

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 05:32:16 ; Search time 2909 Seconds

(without alignments)
5791.302 Million cell updates/sec

Title: US-09-482-788-2

Perfect score: 16128
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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 3611042 segs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2364 | 14.7 | 61944 | 15 US-10-329-079-34 | Sequence 34, Appl |
| 2 | 2325.5 | 14.4 | 37360 | 15 US-10-329-079-6 | Sequence 6, Appl |
| 3 | 2191.5 | 13.6 | 18876 | 15 US-10-329-079-42 | Sequence 42, Appl |
| 4 | 2160.5 | 13.4 | 7788 | 15 US-10-329-079-8 | Sequence 8, Appl |
| 5 | 2011 | 12.5 | 47988 | 15 US-10-402-842-1 | Sequence 1, Appl |
| 6 | 1897.5 | 11.8 | 9748 | 16 US-10-282-122A-11388 | Sequence 31388, A |
| 7 | 1867.5 | 11.6 | 15450 | 16 US-10-282-122A-1449 | Sequence 7449, Ap |
| 8 | 1838.5 | 11.4 | 31263 | 16 US-10-282-122A-25447 | Sequence 25447, A |
| 9 | 1831 | 11.3 | 9590 | 16 US-10-282-122A-33351 | Sequence 33351, A |
| 10 | 1824.5 | 11.3 | 88421 | 9 US-09-976-059-1 | Sequence 1, Appl |
| 11 | 1804.5 | 11.2 | 9025608 | 15 US-10-156-761-1 | Sequence 1, Appl |
| 12 | 1770.5 | 11.0 | 10296 | 15 US-10-282-122A-33665 | Sequence 33665, A |
| 13 | 1752 | 10.9 | 6288 | 16 US-10-282-122A-33846 | Sequence 33846, A |
| 14 | 1749.5 | 10.8 | 939 | 15 US-10-369-493-42604 | Sequence 42604, A |
| 15 | 1749 | 10.8 | 15738 | 15 US-10-329-079-46 | Sequence 46, Appl |
| 16 | 1743.5 | 10.8 | 10002 | 16 US-10-282-122A-14471 | Sequence 14471, A |
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| 18 | 1713.5 | 10.6 | 7347 | 9 US-09-815-242-7773 | Sequence 7773, Ap |
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| 20 | 1713.5 | 10.6 | 7347 | 17 US-10-324-967-17 | Sequence 17, Appl |
| 21 | 1702.5 | 10.6 | 7155 | 16 US-10-282-122A-10403 | Sequence 10403, A |
| 22 | 1696.5 | 10.5 | 7158 | 9 US-09-974-300-2171 | Sequence 2171, Ap |
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| 26 | 1685 | 10.4 | 12951 | 16 US-10-282-122A-31678 | Sequence 31678, A |
| 27 | 1670.5 | 10.4 | 7617 | 16 US-10-282-122A-25471 | Sequence 25471, A |
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| 29 | 1641.5 | 10.2 | 11100 | 15 US-10-329-079-5 | Sequence 5, Appl |
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| 34 | 1605.5 | 10.0 | 7925 | 16 US-10-282-122A-33350 | Sequence 33350, A |
| 35 | 1588 | 9.8 | 7185 | 15 US-10-329-079-48 | Sequence 48, Appl |
| 36 | 1548 | 9.6 | 6408 | 15 US-10-329-079-44 | Sequence 44, Appl |
| 37 | 1524 | 9.4 | 6522 | 16 US-10-282-122A-31533 | Sequence 31533, A |
| 38 | 1522 | 9.4 | 6432 | 15 US-10-329-079-10 | Sequence 10, Appl |
| 39 | 1493.5 | 9.3 | 7155 | 15 US-10-329-079-14 | Sequence 14, Appl |
| 40 | 1486 | 9.2 | 6465 | 9 US-09-974-300-2166 | Sequence 2166, Ap |
| 41 | 1464 | 9.1 | 5127 | 15 US-10-156-761-3630 | Sequence 3630, Ap |
| 42 | 1451.5 | 9.0 | 9723 | 16 US-10-282-122A-13740 | Sequence 13740, A |
| 43 | 1438.5 | 8.9 | 7161 | 16 US-10-282-122A-35022 | Sequence 35022, A |
| 44 | 1428 | 8.9 | 29555 | 8 US-08-781-986A-206 | Sequence 206, App |
| 45 | 1428 | 8.9 | 29555 | 16 US-10-329-624-206 | Sequence 206, App |

ALIGNMENTS

RESULT 1
US-10-329-079-34 Application US/10329079
; Sequence 34, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STAPFA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-11US
; CURRENT FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 61944
; TYPE: DNA
; ORGANISM: Streptomyces refuineus
; US-10-329-079-34
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 Query Match: 14.66% Indels: 722
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Qy      764 roLyS---LeuGlnLeuLeuAsnGlyTyrglyGlnSerGlySer---SerIleCysP 782
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Db      18547 ACTTGAGCTGACGACGACGCGCGCGGTGAGCGCGCGCGCATCATGCGTCCCGCTGG 18606
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Qy      817 lAValGlyGlnLeuValIleGluSerProGlyIleAlaArgAspTyrglyIleValProP 837
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Db      18762 -----GCGCGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18816
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Qy      897 lYAlaIleGlnThriAlaLeuArgGlnIleMetProAspAspLeuThriIleAlaValGluA 917
Db      18877 GAGAGGTGAGCGCGCGCGCGCGCGAC-----CCGAC----- 18911
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Db      18912 -----ATCGCGCAGG 18921
Qy      937 eR-----TyRpheGlyAsnArgProSerAspAlaHisIleLeu----- 949
Db      18922 CGGCGCGCGCTGTCGACGCGGAGACGACCGGATCTGTGTGCTACGCGGCTGC 18981
Qy      950 --AspHisAspAla-----ThriValAlaIleAsnIleLyLeuGlnGlnValLeuP 966

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Qy      1006 lmglyAlaIleValGlnAlaProAlaProIleProValPheAlaAspThraAlaAl 1026
Db      19156 GCGGCG-----GTCGCGCGCGACCGCGCGGAGGAGCGCTGCGCGCGCT 19200
Qy      1026 yLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAsnValGlyA 1046
Db      19201 TCGCCGACGCTCTCGCGCTGAGAGGTACGCGGAC-----G 19239
Qy      1046 lAThrPheGlnIleGlyLyAsnSerIleThraAlaIleLyAsnMetAlaA 1066
Db      19240 CGGACTTCTTGGCGCTGCGCGCGCGCACCTCCGTGCGCGCGGCTCATGACGCGATCC 19299
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Db      19701 --CGCGCGCTGCGCGAGCGCTGCGCATACGCTTACGCTGACCGAGACGACTCCCGCTGC 19758
Qy      1218 rGAlaThrLeuLeuAspGlyGlyIleAspAspHisIleLeuThriIleAlaMetHisI 1238
Db      19759 GGGCGGTGCTGCTGCGACCGCGCGCGCGACGACGATGCTCTCCGTGCTGCGACACA 19818
Qy      1238 lAileSerAspGlyTrpSerIleAspValLeuArgArgAspLeuAsnGlnLeuTySerA 1258
Db      19819 TCGCGCGGACGCGCTGCTGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19878
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Db      19879 CACGCGTG---GAGGCGCGCGCGCG-----CGTGGCGCGCGCTGCGGTGAGTACG 19929
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[illegible]

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| QY | 1670 | sPTrrlaaPProPaaerPllleGluValaThrxaAnaGluPheValaArglleaArgAdaLa | 1690 |
| Db | 21103 | ACACCCCGCCCGGTCGCGCTGTCAACAGS-----GGGAACTGCCCGCCGCA | 21150 |
| QY | 1690 | euaAnaerSerAanaIa-----AapGlyPheGluVallleGluHlaaerSerThLya- | 1707 |
| Db | 21151 | TCACCGCTGCGCGCGCGCTGCGGTGCGCCAGCACCTCTGCGCGCGCGACGCGCACAG | 21210 |
| QY | 1708 | -----ProSerlaThrSerLeuAlaThaValLeuT | 1718 |
| Db | 21211 | GCGCCGGAGCCCTGCGCGAGATGCGCGCGCGCTGCGCGAGCACAGCGCGGTACTGTCTGC | 21270 |
| QY | 1718 | yrThrSerGlySerThGlyArgProbaGlyValaMetIle----- | 1731 |
| Db | 21271 | ACACCTTGGGCTCCAGCGGAAGCGCCCAAGGCGGTGTGTGTACACCGGGGCAACTTGGCA | 21330 |
| QY | 1732 | -----GluHlaaArgVallleaArgThaValThrSerGlyCysIleProaAnt | 1748 |
| Db | 21331 | ACGTGTGCGCGAATCGGAGAGCGGTGCGC-----CTACACCGCGCGG- | 21370 |
| QY | 1748 | yrProSerGluThrArgMetAlaHlaMetAlaThrIlelaaPheaaerGlyAlaSerThyG | 1768 |
| Db | 21375 | -----GACCGGCTGTGTGCGCTGTCAACAGCGCACTTGTGCAATCGCGCCCTGG | 21422 |
| QY | 1768 | IuIleTySerAlaLeuLeuPheGlyArgThLeuValCysValaAapTyMetThThL | 1788 |
| Db | 21424 | AGCTGTCTCTGCGCTGTGTGTGCGCGCGCGCAACTGTGTCTGCGCGACCGCGGACCGCAC | 21483 |
| QY | 1788 | euaAerAlaArgAlaLeuLysaArylaPhePheArgGluHlaaIaalaSerHlaY | 1808 |
| Db | 21484 | GGAGACCGGAGAGCACTG-----GCGCACTGCG | 21510 |
| QY | 1808 | alThrSerSerSerGlnaArylaProleuArgValProaArgaGlyLeuSerArgThLeuH | 1828 |
| Db | 21511 | TCACCGGAGACGCGCGCACCATCTCTCCAGGCGCACCCCGCACCACTGTGACAG- | 21566 |
| QY | 1828 | etPhePhePheLeuValaThrAaerSerThaLaProaAerAlaLeuAerAlaGlnGlyL | 1848 |
| Db | 21561 | -----CTGCTGAGCGAGACCGCGCCGACGCGCTG-----CGCGGCG | 21597 |
| QY | 1848 | eutyArgIn----- | 1850 |
| Db | 21598 | TGGCGAAACTGTGTGCGCGGAGAGCGCTCCCGCGGTCCGTGCGCTCCGCGCTCACGGCC | 21655 |
| QY | 1851 | --GlyValaGlnCysTyraaGlnGlyTyrglyProThrgluHlaaGlyValaMetSerThIleT | 1870 |
| Db | 21658 | TGGCGCGGCAACTGTGTCAAGCTGTACGCGCGCGCACCGAGCACCACTGTGTCCACCGCG | 21711 |
| QY | 1870 | yrProIleAaerSerThGluSerPheIleaaGlnGlyValProIleGlyArgAlaLeuAna | 1890 |
| Db | 21718 | CCACCTGTGACCGGCGCACCGGG-----AGCGCACCGCCCAATGGCGCGGCGCTGGCA | 21777 |
| QY | 1890 | snaSerGlyAlaTyraValaArylaAerProGluGlnGlnLeuValaGlyIleGlyValaMetGlyG | 1910 |
| Db | 21772 | ACACCGCGGCGCTAGTGTGTGAAGAGTGTGTGACCGCGCGCGCGCGCGGCGGTCCCGCGG | 21833 |
| QY | 1910 | IuLeuValaValaThrGlyAaerGlyLeuAlaAaArglyTyrgSerAaRlyS--AlaLeuAaerG | 1929 |
| Db | 21832 | AGCTCTACTGTGCGCGCGCGCGGTGTGCGCGCGCTACTGTGCGCGCGCGCGCTTACCG | 21891 |
| QY | 1929 | IuaAnaArgPheValaHlaIleThValaAaerGlnThThValaValaTyraGThGlyA | 1949 |
| Db | 21892 | CCGAGCGCTTACCGCGCACCCCTTGGCGCGCGCGCGCGCGCGCGCGCAAGTACCGACGAGCG | 21955 |
| QY | 1949 | sPaArgValaArgTyraGlnIleGlyAaerGlyLeuIleGluPhePheGlyArgMetAaerThrG | 1969 |
| Db | 21952 | ACCTGTGTCCGCGCGCGC---GCGAGCGGAGAGCTGAATTTCTGTGAGACGACCGACACAC | 22000 |
| QY | 1969 | IuPheLysIleArgGlyAaerArgTlleGluSerAlaGluIleGluAlaAlaLeuLeuArga | 1989 |

| | | | | | | | | | |
|----|-------|---|--|--|--|--|--|--|-------|
| Dh | 22009 | AGGTCAGAGCTCCGGGCTTCCGATCGAGCTGGGCGAGATCGAGACGGCCCTCGGTGGCC | | | | | | | 22068 |
| Qy | 1989 | spSerSerValArgAspAlaAlaValValLeuGlnGlnAsnGlnAspGlnAlaPro---- | | | | | | | 2007 |
| Dh | 22069 | ACCGGACGTCCTCGGGGCGGTGTGGTGCSCCGGCGCGGTCCGGCCCGGCCCGCCGCGC | | | | | | | 22128 |
| Qy | 2008 | -----GluIleLeuGlyPheValValAlaSerH | | | | | | | 2017 |
| Dh | 22129 | CGGACGACGGCGGACCGCGGCCCGCCCGGACGTGGTGGCTGGTGGTGGCGGAC | | | | | | | 22188 |
| Qy | 2017 | IsaPrlHisSerGluAsnAspLysGlyGlnSerAlaAsnGlnValGlnGlyTPGlnAspH | | | | | | | 2037 |
| Dh | 22189 | CCGACCGGGCGGCGACGAGCGGAGCCGGGAGCGGGCCGGCTCGACGAGTGGCGGAGA | | | | | | | 22248 |
| Qy | 2037 | IsPheGlnSerGlyMetTyrSerAspIleGlyGluIleAspProSerThrIleGlySerA | | | | | | | 2057 |
| Dh | 22249 | CTTACGACACC-----TCCGACCCGACCCCTGGGCGCGG | | | | | | | 22296 |
| Qy | 2057 | spPheLysGlyTPRThrSerMetTyrAspGlySerGlnIleAspPheAspGlyMetHisG | | | | | | | 2077 |
| Dh | 22297 | ACTTCGGAGATCTGGCGGAGAGTACGACGAGCGGCCCATCCCGTCGAGAGATGCTTC | | | | | | | 22366 |
| Qy | 2077 | IuTPRLeuGlyGluThrThrArgThrIleuHisAspAsnArgSerLeuGlyAsnValLeuG | | | | | | | 2097 |
| Dh | 22357 | AGTGGCGGGCGGCCCGGTGACCGGATCCGGGCGGTGGCC-----GGCGGCTGTGG | | | | | | | 22413 |
| Qy | 2097 | IuIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAspSerAArgLeuGlySerTyrV | | | | | | | 2117 |
| Dh | 22414 | AGATCGGGGGTGGGACCGGACTGTCTGTTCGGAACTGGACCGGACTGACACCGCTTAC | | | | | | | 22473 |
| Qy | 2117 | alGlyLeuGluProSerArgSerAlaAlaAlaPheValAsnLysValaThrGlySerIleP | | | | | | | 2137 |
| Dh | 22474 | ACGGAACCGACTGTCCGACCGGTGATCGAGACCTCGACGAGCAGTGGCGGCGGACG | | | | | | | 22533 |
| Qy | 2137 | roSerLeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIleGlyGlnValA | | | | | | | 2157 |
| Dh | 22534 | CCGGCTGGAAGAGAAAGTGGAGCTGCACCTCCGCCCGGACAGACTTACCGGTCTGC | | | | | | | 22593 |
| Qy | 2157 | spAspLeuHisProAspLeuValValLeuAsnSerValIleGlnTyrPheProSerSer | | | | | | | 2177 |
| Dh | 22594 | GCAAGGGTTCTACGACACCATGTGTCTCACTCCGTCTCGAGTACTTCCCGGGCGG | | | | | | | 22653 |
| Qy | 2177 | IuTyrLeuAlaGluIleAlaAspThrLeuIleHisLeu-----ProAsnValGlnArgI | | | | | | | 2195 |
| Dh | 22654 | ACTACCTCTCCCGGGTCTGCGCGGCGCATTCGACGCTGTGAGCGCCG-----GGACGCG | | | | | | | 22710 |
| Qy | 2195 | LePhePheGlyAspValArgSerGlnAlaThrAsnGlnHisPheLeuAlaAlaArgAlaI | | | | | | | 2215 |
| Dh | 22711 | TCTTCGTGGCGAGCTGCGGACGCTGGCTGGCTGGCGGGCTTC-----CGGCGCT | | | | | | | 22761 |
| Qy | 2215 | LeHisThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLysMetGluGlyLeuG | | | | | | | 2235 |
| Dh | 22762 | CGGTGGAGATGGGAGACCGCGCGCGGCGGACCGCCCGGCGCGGTGTGGCGGCGCGG | | | | | | | 22821 |
| Qy | 2235 | Iu-----AspMetGluGluGluLeuLeuValGluProAlaPhePheThrSerLeuI | | | | | | | 2252 |
| Dh | 22822 | ACCGCAGAGCGGCCACGAGAAAGAACTGCTCGTGACCCGGGCTACTTCCGCGGCTGC | | | | | | | 22881 |
| Qy | 2252 | YAspArgPheProGlyLeuValGluHisValGluIleLeuProLysAsnMetGluAlaV | | | | | | | 2272 |
| Dh | 22882 | GC---CGGAGACCGGGAACCCCTGCTCTGGACGTGGCGGGTCCGCGCGGAGGCGCC | | | | | | | 22938 |
| Qy | 2272 | alaAsnGluLeuSerAlaTyrArgTyrAlaAlaValAlaHisValArgGlySerLeuGlyA | | | | | | | 2292 |
| Dh | 22939 | TCAACGAGCTGACCGCTTACCGCTAC--GACGTCTGTGGCGCAAGCCGAGGCGGGGA | | | | | | | 22995 |
| Qy | 2292 | spGluLeuValLeuProValGlnLysAspAspTrpIleAspPheGlnAlaAsnGlnLeuA | | | | | | | 2312 |
| Dh | 22996 | CCGCGGTCCGGGCCCGCGCGCGGAGATGGCGTGGGGGAG----- | | | | | | | 23036 |
| Qy | 2312 | snGlnLysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValaSerL | | | | | | | 2332 |

| | | | |
|----|-------|---|-------|
| Db | 23037 | -----GAGGTGGAGAC-----CGCGCGGCGTGGCGGAGTCTGGCGGCACACC | 23082 |
| QY | 2332 | ysIIePProPhegluIleThrAlaPheglu-----ArgInuValAlaSerL | 2348 |
| | | ::: | |
| Db | 23083 | CGCGCGCGCTGGCGGCTACCGCATCCCAACCGCGCGGTGGCGGCAGACGGCGGCC | 23142 |
| QY | 2348 | euaAnsSerAmIleAspGluTrpGlnLeuSerThrIleArgSerSerAlaGluGlyAspS | 2368 |
| Db | 23143 | TCGCGCGGCTGGAGAGACGGCGCGCTGCCCGCGCGCGCGGCGGTCTGGAGAGGCCCCG | 23202 |
| QY | 2368 | er---SerLeuSerValProAspIlePheArgIleAlaGluGlyAlaGlyPheArgValG | 2387 |
| Db | 23203 | CGCGCGGAGTGGACCCCGGAGACCTGTACACACTGGCGCGCGCGCGCGCCGACCGCGCT | 23262 |
| QY | 2387 | IuValSerSerAlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAlaValPheHisG | 2407 |
| Db | 23263 | GGGTGTGC-----TGGTCGGCGGAGGAGACCGCGCGACACCGTG----- | 23300 |
| QY | 2407 | ysCySerGlnGlyArgThrLeuValAsnPheProThrAsp | 2420 |
| Db | 23301 | -----GACTGTGTGTGGCCCCCGGCGGACGGGGCGGCGCGCGGAGC | 23343 |
| QY | 2421 | -----HisIleuArgGlySerAspLeuLeuThrAspA | 2432 |
| Db | 23344 | TGGACACCGCGCGCGGACSTGGCCGTACGACCGCGGACCGGACCGCGCGGACGACG | 23400 |
| QY | 2432 | rgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValaArgIuArgLeuArgS | 2452 |
| Db | 23404 | ACCGGTCCGCGCGCGCTGGCACAACGGGAGATGGCCCGCGGCGGTGCGCGGTACTGGCGCG | 23463 |
| QY | 2452 | erLeuLeuProSerTyrMetIleProSerAsnIleValValLeuAspArgMetProLeuA | 2472 |
| Db | 23464 | GACGCGTCCGCGACCTACATGATGTGCTCCCTCGCGCGCTGTCTCTCGCGCGCTCCGCTCA | 23523 |
| QY | 2472 | snAlaAsnGlyIysValaAspArgIleGluLeuSerAsnArgAlaIysValaValProLysG | 2492 |
| Db | 23524 | CGCGCAACGGGAGAGTGGACCGGCGCGCTGCCAC-----CCCGACC | 23566 |
| QY | 2492 | IngInThrAlaAla-----ProLeuProThrPheProIleSerGluValGluValI | 2509 |
| Db | 23569 | CGCGGGCGCGCGCGCGCGCGGCA-----CCGCGACACGCGCGGAGAGAC | 23618 |
| QY | 2509 | IeLeuCyGluGluAlaIleThrGluValaPheGlyMet---LysValaPrlIeThrAspHisP | 2528 |
| Db | 23617 | TGCTGTGCTGGCTCTTGGCGGACCTGTGGCTGTGGCTGTAGCGGGGTGGACCGGAGACST | 23676 |
| QY | 2528 | hePheAsnLeuGlyGlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspArgA | 2548 |
| Db | 23677 | TCCTTCAGCTTGGCGGACAGCATCTGTCTCCCTCGGCTCGGACCGCGGACCGGAGAAC | 23786 |
| QY | 2548 | rgLeuLysValArgIleThrValaLysAspValaPheAsnHisProValaPheAlaAspLeuA | 2568 |
| Db | 23737 | AG---GGGCTCCGCTTACACACCGGACCTCTTCAGACACACACCGGCGCGCGCTGG | 23799 |
| QY | 2568 | IaSerValIle--ArgGlnGlyLeuGlyLeuGlnGlnProValaSerAspGlyGlnGlyI | 2587 |
| Db | 23794 | CGGCGGCGCTGGACGGCGAG-----GGAGCCGGAGC | 23822 |
| QY | 2587 | nAspArgSerAlaHisMetAla---ProArgThrGluTrpGlnAlaIleLeuCyAspArgI | 2606 |
| Db | 23824 | AGACCGCGCGGACGCGCGCGGACCCCGCGCGCGGACCGCGCGCC----- | 23866 |
| QY | 2606 | uPheAlaLysValLeuGlyPheGlnValGlyIleThrAspAsnPheAspLeuGlyI | 2626 |
| Db | 23869 | ----- | 23866 |
| QY | 2626 | yHisSerLeuMetAlaThrLysLeuAlaValaArgIleGlyHisArgLeuAspThrThrVa | 2646 |
| Db | 23870 | -CATTCACGCGCGGAGAACTCGC-----CGAGCTGGAGAGAGCTCGCGCGCGACT | 23919 |
| QY | 2646 | ISeValLysAspValaPheAspHisProValaLeuPheGlnIleuAlaIleAlaLeuAspAs | 2666 |
| Db | 23920 | GGGA----- | 23923 |

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QY 2666 nleuValGlnSerIythrAngluValGlyArgGluMetAlaGluTyrSerPr 2686
Db 23924 -----GGAGATGCATGAGGAGGCTCG----- 23944
QY 2686 orpheGlnLeuLeuPheThrGluAerProGluGluPheMetAlaSerGluLeuYsProG 2706
Db 23944 ----- 23944
QY 2706 nleuGluLeuGlnGluLeuIleGlnAerIleTyrProSerThrGluMetGlnYsAlaPh 2726
Db 23945 -----CAGCGCATGCTCGAAGAGTCTTCGCGTACACCCGCTCGAGAGGGGCT 23994
QY 2726 eleuPheAerPheThrAlaArgProArgProPheValProPheTyrIleAerPhePr 2746
Db 23995 GCTCTTC--CAGCGGCTC-----TTGACAGAGAGCGTCCC 24027
QY 2746 oSerThr-----SerGluProAerAlaAlaGlyLe 2756
Db 24028 CGACGCGCTACGTACGCGGCTGCTCGCCCTCGCGGCGACCTGACCGCGCGGCT 24087
QY 2756 uilelyValACyAGluSerIeValAerH1sleuAerIlePheArgThrValPheAlaG 2776
Db 24088 GAGACGGGCGCCGAGCGCTGAGTGGAGCGGACCGCGCTGCGCTCGCGCTTCGCGCA 24147
QY 2776 u--AlaSerGlyLeuTyrGlnValValLeuSerCyLeuAerProIleGlnVa 2795
Db 24148 GCGGCGCTGGGGGAGTGTTCACAGTGTGCGGTCCGCGCGGCTGCGTGGAGAGA 24207
QY 2795 lileGluThrGluAerAerH1leAerH1AlaThrAnglu-----PheLe 2810
Db 24208 GCTGGACCTGCGGTCCGCGGGGCGCGCGGCGGACGAGCGGACCTGAGCGGCTCT 24267
QY 2810 uAerGluPheAlaLeuGluProValArgLeuGlyH1s--ProleuIleArgPheThrI 2829
Db 24268 GAGCGAGACACCGGACCGGCTTCGACCTCGCGCGCGCGCTGCTGGGCTTCGCT 24327
QY 2829 eilelyGlnThrIySerMet--ArgValIleMetArgIleSerH1AlaLeuTyrAs 2848
Db 24328 CGCGAGAGCGGGGAGAGACCGGACCGCGGTGGCGGTACCTACACACATCATCTCGA 24387
QY 2848 rGlyLeuSerLeuGlnH1sValValArglyVleuH1MetLeuTyrAnGly----- 2865
Db 24388 CGGCTGCTCGTCCGATCTGATGAGGAACTGCTGCGCTGACCGGACGCGGGGCGA 24447
QY 2866 --ArgSerLeuLeuProProH1sGlnPheSerArgTyrMetGlnTyrThrAla----- 2882
Db 24448 CCCCTCGCGCTCGCGCGGCTCGCGCGGACCGGACCGGACCTGACTGGCGCGGACG 24507
QY 2883 -AerGlyArgGluSerGlyH1sGlyPheTyrArgAerValIleGlnAerThrProMetH 2902
Db 24508 CCGGTCCGAGAGGAGCGGACCGGCT--TGGCGGACAGCGCTGGCGGGA----- 24553
QY 2902 rIleLeuSerAerAerThrValVal-----AerGlyAerAerAlaThrCySly 2918
Db 24554 ----CTGTCCGAGCCGACGTGTGTGGCGCGGCGGCGGACCGGACCGGCGG----- 24601
QY 2918 sAlaLeuH1sLeuSerIythrValAerH1leProSerGlnVal----- 2932
Db 24602 -----CTGCGCGACAGGTGTGGACCGGCGGCTGACCGGCTGACCGA 24633
QY 2933 -----LeuArgIySerSerAerH1leIleTh 2941
Db 24634 ACGGAGACCGCGGCGCTCACCGGCTGGGGCGCGCGCGCGGCG-----GTGAC 24681
QY 2941 rGlnAlaThrValPheAerH1AlaCyValAlaLeuValLeuSerArgGluSerAerIy 2961
Db 24682 GGTGAATCTGGCGGTGAGCGCGCTGGGCGACGCTGCTCGCGCTCCACCGGCGCGA 24741
QY 2961 sAerValAlaPheGlyArgIleValAerGlyArgGlnGlyLeuProAlaGluTyr----- 2979
Db 24742 CGAGTGTGTCTTGGGAGACCGGTGTGGGGCGG-----CGGCGGAGCTGCCCGG 24792

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QY 2980 ----GlnAerIleValGlyProCyThrAerAlaValProValArgAlaH1leGluSe 2998
Db 24793 TGGCGAGGACATGTGTGGGTCTTCATCAACGAGCGCGCTGCGGATGCGGCGC 24852
QY 2998 rSerAer---TyrAerGlnLeuLeuH1sAerIleGlnAerGlnTyrLeuLeuSerIePr 3017
Db 24853 GAGCGAGCGGATGGGAGACTGTGCTCCCGGATCCAGCGGACAGACCGGCTCATGA 24912
QY 3017 oH1sGluThrIleGlyPheSerAerLeuYsArgAerCyThrAerTPProGluAlaI 3037
Db 24913 GACACGACAGCTGAGACTGTCCGACATCCAGCGC-----TGGCGGAGACAGC 24960
QY 3037 eThrAerPheSerCyCyelleThrTyrH1sAerPheGluTyrH1sProGluSerGlnPr 3057
Db 24961 CGAATCTTCGACACCTCCACGCGCGCTTCGAGAACTAC----- 24997
QY 3057 eGluGlnArgValGluMetGlyValLeuThrIyPheValAerH1leGluMetAerP 3077
Db 24997 ----- 24997
QY 3077 uProLeuTyrAerPheAlaIleAlaGlyGluValGluProAerGlyAlaGlyLeuYsVa 3097
Db 24998 -CCGCGGACAGACTCTGCGCGCGCTCGG-----TCTCGGACGACGCGCGCTGCGGT 25050
QY 3097 1 3097
Db 25051 G 25051

RESULT 2
US-10-329-079-6
; Sequence 6, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STRAPA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-11US
; CURRENT APPLICATION NUMBER: US/10/329, 079
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 37360
; TYPE: DNA
; ORGANISM: Streptomyces fradiae
US-10-329-079-6

Alignment Scores:
Pred. No.: 5,77e-187 Length: 37360
Score: 2325.50 Matches: 887
Percent Similarity: 41.70% Conservative: 502
Best Local Similarity: 26.63% Mismatches: 1212
Query Match: 14,42% Indels: 734
DB: 15 Gaps: 131

US-09-482-788-2 (1-3129) x US-10-329-079-6 (1-37360)
QY 51 ProCyThrProPheGlnLeuAerMetIleAerCyAerAlaLeuAerIyGlnSerAla 70
Db 62 CCCCTGCGCGCGCGGACCGGACGCTGTGCTCTCAACGCTACAGAGAGGCGCGC 121
QY 71 lileGlyH1s-----AlaValTyrAerValProThrAerPheAerIleAerArgPheAla 88
Db 122 GGTACACATACAGCTGCGGCTGCGGCTCACCGGAGTCTGACGCTCGACCGCTCCAC 181
QY 89 LeuAlaTrpIyGluIleValAerGlnThrProAlaLeuArgAlaPheAlaPheThrSer 108
Db 182 GCGGACACTGGGACCTGACCGCGCGGACGAGAGGCTGCGGACCG--GTCTTCGCGGAG 238
QY 109 AarSerGlyIyThrSerGlnValIleLeuIyAerSerPheAlaH1sSerTPMetCyS 128
Db 239 GACGAACAGGGCGGACGACGAGTGTGAGACCG----- 274

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| | | | | |
|----|------|---|--------|------|
| Oy | 129 | TrpSerSerSerSerPro----- | AspVal | 138 |
| | | | | |
| Db | 275 | ---GGGGCCCCCGCCACCCGGCGTCCGGCTGCCGGCCACCGCATGACGCCCTG | | 331 |
| Oy | 139 | ValArgArg-GluAlaAlaAlaAlaAlaSerGlyProArgGlySerAsnArgPheValLeuLeu | | 158 |
| | | | | |
| Db | 332 | GTCGGCGAAGCGGTGGCCGCCCTTCCAGCTGGCCGACAGATCCGCTGGCGACACC | | 391 |
| Oy | 158 | uGluAsp---MetGlnThrIlyIyIyGlyCysGlnLeuValThrTrpPheSerHisAlaLeuVal | | 177 |
| | | | | |
| Db | 392 | CTTTACAGCTCCCGGAGCGCGACAGACGTCTGCTCTGTATG-CACCAATGCGGC | | 450 |
| Oy | 177 | AspValThrPheGlnGlnArgValLeuSerArgPheAlaAlaTyrLeuIleGlyIu | | 197 |
| | | | | |
| Db | 451 | CGAGCGGTGTGCATGGGGCGCGCTGGACCGGACCTGGCCGCGCTACCGGCGCGGCG | | 510 |
| Oy | 197 | AspThrHisArgProGluThrPro----- | | 205 |
| | | | | |
| Db | 511 | CG | | 570 |
| Oy | 206 | ---GluSerSerAspAlaThrAspThrAspSerGlnSerValSerValSerMetSer | | 224 |
| | | | | |
| Db | 571 | ACAGACGCGCGACGACGTGGACGACACAGCTGGACCGCGCGCTCGCC----- | | 616 |
| Oy | 224 | rCysGluAspAsnAlaValSerAlaThrHisPheTrpGlnThrHisIleuAsnAspLeuAs | | 244 |
| | | | | |
| Db | 617 | ---CACTGGCGCGAGAACTGGCGGCA----- | | 640 |
| Oy | 244 | nAlaSerValPheProHisIleuSerAspHisIleuMetVal-----ProAsnPr | | 260 |
| | | | | |
| Db | 641 | ---CTGCCGACGAATCGCGCTGCGCTTACGACCGGCTCGCGCC | | 681 |
| Oy | 260 | oThrThr----- | | 262 |
| | | | | |
| Db | 682 | CACAGACACCCCGCGCTACGCCGAGCGGGTCCCTTCGCGGTGCAGCGCGCGCTACGG | | 741 |
| Oy | 263 | -----ThrAlaGlnHisArgIleThr--PheProIleuSerGlnIlyAl | | 276 |
| | | | | |
| Db | 742 | GGACGTGCGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | | 801 |
| Oy | 276 | AlaIleuSer----- | | 278 |
| | | | | |
| Db | 802 | CTTGGCGCGCTGTGGACCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | | 861 |
| Oy | 279 | -----AsnSerAlaI | | 282 |
| | | | | |
| Db | 862 | CGCGCGCGCGACCG | | 921 |
| Oy | 282 | eCysArgThr-----AlaIleuSerIleIleuIleuSerArgIlyThrHis | | 296 |
| | | | | |
| Db | 922 | CTGTGGACCGACACCTGGCGGACCGCGCGCTTCCGCGAAGTGTGTGACCGGGTGGCG | | 981 |
| Oy | 296 | sSerArgGlnAlaIleuPheGlyAlaValThrGlnIleuSerLeuProPheArgHisIleTy | | 316 |
| | | | | |
| Db | 982 | GACGAC-----CTGGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCG | | 1022 |
| Oy | 316 | rIleuAlaSerGlyThrTyrGlnThrValAlaProIleuArgValHisCysGlnSerAsnIle | | 336 |
| | | | | |
| Db | 1028 | CTGTGTGAGCGGTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | | 1066 |
| Oy | 336 | uArgAlaSerAspValMetAspAlaIleSerSerTyrIAsnAsp-----ArgIle | | 352 |
| | | | | |
| Db | 1067 | ---CACCGCGTGTCCAGCGATGTCTACCTTGCACACAGCGCGCGCGCGCGCGCG | | 1119 |
| Oy | 352 | uGlyHisIleuAlaProPhe---GlyIleuArg---AspIleArgAsnThrGlyAspAsnG | | 370 |
| | | | | |
| Db | 1120 | CGATCACCCTCTCGACCTGCGCGCGGTGGCGCGGAGACGTGTGCGACCGCGCGAG--GG | | 1176 |
| Oy | 370 | ySerAlaIlaCysAspPheGlnThrValIleuIleuValThrArgIlySerHisValAsnAs | | 390 |
| | | | | |
| Db | 1177 | CACGCGCGACACCGCATGTACGTACCTTACCGAGACACAGCGCGGACACCGACGCGG | | 1236 |

| | | |
|----|---|------|
| QY | nglylLaasnlylhelengInglInIethGluSerSerHisphMetProCysAsnAs | 410 |
| Db | 1237 CGAACTCGAAGCGGCTCCGCGC----- | 1258 |
| QY | 410 nArGAlaleuDeuLeuHisCySGImetGluSerSerGlyAlaleuEuValAlaTYrTY | 430 |
| Db | 1259 -----TA | 1266 |
| QY | 430 rAspHisAnValIleAspSerLeuGlnThrTrArgLeuLeuGlnIlePheGlyHisLe | 450 |
| Db | 1261 CCGGCCCCGACCTGTTCGACCGCACGACCGCGGGCTCTGGCGGAGGGTTCAAGCGCGCT | 1320 |
| QY | 450 uIlLeuSeCySLeuGln-----SerProLeuArlleuSerSerMe | 463 |
| Db | 1321 GCTCGGACCGTTCGACCGCGGACCGCGGCGGCTCTGGCGGAGGGTTCAAGCGCGCT | 1380 |
| QY | 463 tAlAGluValAsnIleuMetThrGluTYrAspArgAlaGluIleGluSerTrpAsnSerG1 | 483 |
| Db | 1381 CCGGGAAACCGCGGGCGCTGGCGGACCGGAGCGCGCGGCAAGGGAGAGACCGCGCCAC | 1440 |
| QY | 483 nProLeuGluValGlnAspThrIleuIleHisGluMetLeuValAlaValSerHisSe | 503 |
| Db | 1441 CGCGGTGCGCGCTCCGCGCGCGCTCTTC-----GCGCGCTCGGCCA | 1482 |
| QY | 503 rProThrIleThrAlaIleGlnAlaTrpAsnGlyAspTrpThr-----TyrSerGlyLe | 521 |
| Db | 1483 TCGCACGCGCGCGCGCGCGCGCGCTCACCGAGCGCGCGGACCTTGACCTAGCGGAACT | 1542 |
| QY | 521 uAspAsnValSerSerArgLeuAlaValHisIleIleYSerLeuGluLeuArgAlaGlnG1 | 541 |
| Db | 1543 CGAGCGCGCGCTCCAAAGCTCTCGCGCGGGCGCTCTCGAGTCCGCGGTG---GGGCGGGA | 1599 |
| QY | 541 nAlaIleIleProValTYrPheGluTYrSerTYrTrpValIleAlaSerMetLeuAlaVa | 561 |
| Db | 1600 GGACTGTGTCGCGCTGGGCGGCGCGCGCGCTGCGGAGACTGGTGGTGCGGCTCGCGGT | 1659 |
| QY | 561 lLeuIleYSerG1YAsnAlaPheThrLeuIleAspProAsnAspProAlaArgThrAl | 581 |
| Db | 1660 GCTAAAGTCGGGCGCGCGCTTACCTCGCGCTGACCGGACCGGACCGCGCGGACCACTTC | 1719 |
| QY | 581 aGlnValValThrGlnThrArgAlaThrValAlaLeuThrSerTYrLeuHisArgGluTh | 601 |
| Db | 1720 GTAACTCTTCACGACTCCGCGCGCGCGCTCTCTTCCACGACCGCGCTCCGCGGAGAC | 1779 |
| QY | 601 rValGlnIleuLeuValGlyArgCysVal-----ValAlaAspAspG1 | 615 |
| Db | 1780 CTTGACGACGACCGGTGGGCGAGGGGTGCGGAGTCCCGGAGGCTGCTGACGACGAGCC | 1839 |
| QY | 615 uLeuLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrIleYSer----- | 632 |
| Db | 1840 CGCCACCGCGCGCGCGCGCGCGGCTCGGCGGACCGGCTCCACCGACCGCGCGCGCG | 1899 |
| QY | 632 -----GlnAspLeuAlaTYrValIlePheThrSerGlySerThrGlyAs | 647 |
| Db | 1900 GTGCGCCCTGCTCCCGACACACCGGCGCTACCATCTACCTCGGCTTGACCGAGAGC | 1959 |
| QY | 647 pProIleG1YleMetIleGluHisArgAlaPheSerSerCysAlaLeuTYrPheGlyAl | 667 |
| Db | 1960 GCCCAAGGCGCTGCTGTCAGCTACCGGCAACGTTCAAGCTGTCAGCCGCGCGCGC | 2019 |
| QY | 667 aSerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAl | 687 |
| Db | 2020 GGGCGGTGACTTCGGGCGCGCGACGCTGTGACCGCTTCCACTCCAGCGGCTTCGACTT | 2079 |
| QY | 687 aCyLeuLeuGlnIleMetThrThrIleuIleAsnGlyGly---CysValCysIleProSe | 706 |
| Db | 2080 CTGCGTGTGGAGATGTGGGGCGCTGGCGGACCGCGCGCGCTGTGCTGTCCGCA | 2139 |
| QY | 706 rAspAspAspArgMet---AsnSerIleProSerPheIleAsnArgTYrAsnValAsnTYr | 725 |
| Db | 2140 CGAGGTGGCCAGATCACCGCGCGACCTCTGAGACTGTGGCGCGCGGACGCGGTCAAGCT | 2199 |
| QY | 725 pMetMetAlaThrProSerTYr-----MetGlyTh | 735 |

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Db      2200 GCTCAGCAGACGCGCCCTTCCTTCTCAAGCTCTCGGCGGAGTCCGACCTCGCGCT 2259
Qy      735 rPheSerProGluAapValProGluLeuAlaThrLeuValValGlyGluGlnMetSe 755
Db      2260 C---CCCCAGAGACACCGCGCGCTCGGAGTACGTCTCTCGGCGGAGAGAGCGCTGGA 2316
Qy      755 rSerSerValAaAlaLeuTrpAlaProLys---LeuGlnLeuLeuAaGlyTrpGly 774
Db      2317 CACCGCCCAACTCGCCCTCGGCGGAGCGCGCGCTCGCTGATCAATGTACGGGAT 2376
Qy      774 nSerGluSerSer---SerLeuCySPheAlaSerAaMetSerThrGluProAaAaMet 793
Db      2377 CACCGAGACGCGCTCCACGCTCACCCACCTGAGCTGAGACGACCGCCCGTGAACCGCG 2436
Qy      793 rGlyAaGlyAlaValGly-----AlaHisSerTrpValIleAapPr 806
Db      2437 CCGGACCGCCATCGGACACACCCCTGAAAGACCTCGCGGCCAC-----GTGCTCGACCA 2490
Qy      806 oAaAaPrlAaAaAaArgLeuValProIleGlyAlaValGlyLeuLeuValIleGluSerPr 826
Db      2491 GGGGCTGCTCC-----GTGCGGTGGGGGTGTGGGCGAGCTGTACGTCGCGCGCC 2544
Qy      826 oGlyIleAlaAaAaPrlTrpIleValProProProProGluLysSerPro-PhePheThrA 846
Db      2545 CCGCGCTGCGCGCGCTACCG--CCGCGCGCGCGCTGAGCGCACCGCTTCGTCGCG 2603
Qy      846 rPrlProSerTrpTrpProAlaAaAaThrPheProAaPrlGlyAlaValGlyTrpArgThg 866
Db      2604 AC-----CCGTTCCAGACCGCGCGCGCGCGATGTACCGGACCG 2639
Qy      866 lAaSPheLeuAaAaArgTrpAlaSerAaPrlGlySerIleValCyLeuGlyAaTrpIleAaSPe 886
Db      2640 GCGACCTCGCTCGCGCGCGACCGACCGCGCGCTCCACTAGCGCGGTCCCACTCCC 2699
Qy      886 lAaValysIleAaArgGlyGlnAaValGlnLeuGlyAlaIleGluThrHisLeuAaArgLing 906
Db      2700 AGGTGAACATCGCGCTACCGCATCGACGCGCGCGAGTCGAGACCGCGCGCGCGCC 2759
Qy      906 lAaMetProAaAaPrlLeuThrIleValAlaGlnAaThrLysAaSerGlnSerAlaAaNs 926
Db      2760 AC---CCGAC-----GTGCGCGACGCG----- 2779
Qy      926 eXrThrSerLeuIleAlaPheLeuIleGlySerSerTrpPheGlyAaAaArgProSerAaP 946
Db      2780 -----GCCACCGCGCGTGCACGCGGAGACCGGACGACCG 2813
Qy      946 lAaHisIleLeuAaPrlAaAaPrlAaThrLysAa-----IleA 958
Db      2814 GTTACCTGTGTCTGTACGTGTGTGCGCGCGCGGACGACCGACCGCGACCGGACCGAGTGC 2873
Qy      958 aNlleLysLeuGlnGlnValLeuProAaArgHisSerIleProSerPheTrpIleCyAaMetL 978
Db      2874 GCGCCCACTCGCGCGACCGCTGCGCGCTATATAGTGTCCCGCGCGGTGTGCGGTGA 2933
Qy      978 eGluLeuLeuProAaArgThrAlaThrGlyLysIleAaPrlAaArgAaArgLeuAaTrpIleMetGly 998
Db      2934 CCGCGCGCTGACCGCGCGACCGGCAAGGTGTGACCGGACGCGCGCTG----- 2980
Qy      998 yAaAaPrlLeuAaPrlGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleP 1018
Db      2981 -----CCGCGCGCG----- 2989
Qy      1018 rOValPheAlaAaPrlAlaAla----- 1025
Db      2990 -----GACCGCGCGCGCGTGGGCGCACCGCGCGCGCGCGCGACCGGACCGCGCGAG 3038
Qy      1026 --LysLeuHisAaSerIleTrpValGlnSerLeuGlyIleAaPrlAlaThrValAaAaValG 1045
Db      3039 AAGCGCTGCGCGCGCTGCGCGACGTCCTCGCGCGTCCAG-----GAGGTGACGCGCG 3092
Qy      1045 lAaLThrPhePheGlnLeuGlyGlyAaAaSerIleThrAlaIleLysMetValAaAaMetA 1065

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Db      3093 AGCGCGACTTCTTCCCTGAGAGGCCATTCTCTCGCGCGCTCGGCTCATACCGCGGA 3152
Qy      1065 lAaArgSer---ValGlyMetAaPrlLeuLysAaSerAaMetIleTrpGlnHisProThrLeuA 1084
Db      3153 TCAAGTTCGCGCGCTCGGAGTGTAGATCGGCATCGGACGCTCTTCGAGAGCGCCACGCGCG 3212
Qy      1084 lAaGlyIleSer-----AlaValAlaValGlyAaPrlProLeuSerTrpThrLeuI 1100
Db      3213 CCGCGCTGTCTCCGCGCTTCGACACCGCGCGGACCGGACCGCG-----CGCTCC 3263
Qy      1100 lAaPrlAaSerTrpHisGlnGlyProValGlnGlnSerTrpSerGlnGlyAaArgLeuTrp 1120
Db      3264 TCGCGCGCGCGCGACCGGAC---CGGCTCCGCTCTCTCTCCGCGCGAGCGGTGTGT 3320
Qy      1120 hAaLeuAaPrlLeuAaAaPrlValGlySerLeuTrpTrpIlePrlProTrpAlaValAaArgMetA 1140
Db      3321 TCTTCGAGAAATCGAAGAGACGAGCGGACCTTAAACATCCGCTCGCGCTCGCTGCG 3380
Qy      1140 rGlyLysProValAaAaAaPrlAaPrlAaLeuAaAaAlaLeuGlnGlnAaArgHisG 1160
Db      3381 GCGCGCGCTTCGACGTCGACGCTCGACCGCTCGGCGCGCGCGGAGCGGTGGCGCGACG 3440
Qy      1160 lAaThrLeuAaArgTrpThrPheGlnAaPrlAaAaPrlValGlyValGln-----IleValH 1178
Db      3441 AGCGCTTCGCGCACCTCTCTCCGTCGAGAGACGCGCGCGCTTACGACAGTGTGCGCG 3500
Qy      1178 lAaGlyLysLeuSerGlnGlnMetLysValIleAaPrlLeuCyGlySerAaPrlAaAaPrl 1198
Db      3501 CCGAAGCGCGCGCGCGCGCTGACGTCGTCGAGTGCACCGAAGAAAGACTGCC----- 3556
Qy      1198 hAaGlnValLeuAaGlnGlnGlnThrThrProPheAaAaLeuSerSerGlnAlaGlyTrpA 1218
Db      3557 --CGCGCGCTCGCGAGCGCGCGCGCACACGCTTACCTTCACCGAGAGACTTCCGCTGC 3614
Qy      1218 rGlyAaThrLeuLeuAaArgLeuGlyGlyAaAaPrlHisIleLeuThrIleValMetHisI 1238
Db      3615 GGGCGCTGCTGCTCGGAGCGCGCGCGCGCGCACACGCTCTCTCTCTCTCTCACACCA 3674
Qy      1238 lAaIleSerAaPrlGlyTrpSerIleAaPrlAaAaArgAaPrlAaAaGlnLeuTrpSerA 1258
Db      3675 TCGCGCGCGCGCGCTGCTGCTGCGCGCGCTCGCGCGCGCGCGCTGACGACCGCTAC--G 3731
Qy      1258 lAaAlaLeuLysAaAaPrlLysAaPrlProLeuSerAlaLeuThrProLeuProIleGlnTrpS 1278
Db      3732 CCGCACGCTCGGAGGCGCGCGCGCG-----CAGTGCGCGCGCTCGCGCTGACAGTACG 3785
Qy      1278 eAaSPheAlaLysTrpGlnLysAaPrlAaPrlLeuGlnGln----- 1292
Db      3786 CCGACACACCTCTGGAAGAGAGAGTGTGCGCGCGCGCGGACGACCGCGAGAGCTTC 3845
Qy      1293 ----LysGlnLeuAaAaTrpTrpLysLysGlnLeuLysAaPrlAaAaValIle- 1310
Db      3846 TCGCGCGCGCAATCGCTTGTGCGCGAGGCGCTG---GAGGCGCGCGCGGACAGATCG 3902
Qy      1311 ----ProThrAaPrlAaAaArgProAlaLeuLeuSerGlyAaPrlAaGlyCyValHis- 1328
Db      3903 AGCTTACCGACGACGCGCGCGCGCGCGCGCATGAGAGC---CACCGCGCGCGATTCAC 3959
Qy      1329 --ValThrIleAaPrlGlyLeuLeuTrpGlnSerLeuAaPrlAaPheCyAaAaGlnHisAa 1348
Db      3960 GCTTACACCTCCCGCGCTGCTGCGGACCGGCTGCTGACCTCGGACCGCGCGCGCG 4019
Qy      1348 hAaThrSerPheValValLeuLeuAlaAlaPheAaAaAlaAlaValAaArgLeuThrAlaV 1368
Db      4020 CCAACCTCTTCAAGCGCTCGAGGCGGACCTGCGCGCGGACCTGCGCACCTGAGGCGCG 4079
Qy      1368 aLGIaAaPrlAaValIleGlyThrProIleAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 1388
Db      4080 GCGGAGACATGCTCTCGGACGCTGCTGCGCGCGCGCGCGCGCGGACGCGCGGACGAC 4139
Qy      1388 lAaIleGlyCySPheValAaAaThrGlnCyAaMetAaArgIleAaAaPrlAaHisAaPrlAa 1408
Db      4140 TCGTGGCTTCTTGTACACACCTGCGCTCGGACGACCTGCGCGGAGCGGACCGGACCT 4199

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QY 2754 AlaGlyLeuLeuLeuValaCysGluSerLeuValaAsnHisLeuAspIlePheArgThrVal 2773
 DB 7933 GACCGGCTGGACAGAGCCGCCCAAGCCCTGGTGGACAGCCACCGCGGCTGGCTGGCC 7992
 QY 2774 PheAlaGlu---AlaSerGlyLeuLeuValaValaLeuSerCysLeuAspLeuPro 2792
 DB 7993 TTCGCGACGGCGGCTGGGGAGTGGTTCACACTGGTTCGACCCGCCCGCGGTCGCC 8052
 QY 2793 IleGlnValIleGluThrGluAspAsnIleAsnThrAlaThrGlnGlu----- 2808
 DB 8053 TGGCAGAGCTTCACCTGGCGCGCTGGGAGCCCGGAGCCGAGCAAGACCTGGAG 8112
 QY 2809 ---PheLeuAspGluPheAlaValaGluProValArgLeuGlnHis---ProLeuIleArg 2826
 DB 8113 GCGCTGTGGACAGACACACCGACCGGCTGGACTTCGCGCGCGCGCTGGCTGGCC 8172
 QY 2827 PheThrIleIleLeuGln---ThrLysSerMetArgValIleMetArgIleSerHisAla 2845
 DB 8173 TTCCTGTGGCAGACCGCGGACAGACACCGGCTGGCGGCTGGCTGGCTGGCTGGCC 8232
 QY 2846 LeuTyrAspGlyLeuSerLeuGlnHisValaValaArgLeuHisMetLeuTyrAsnGly 2865
 DB 8233 GTCCTGACGCGCTGGCTTCATGCTCATGCGGAGACTGGCGCTGGCTGGCTGGCC 8292
 QY 2866 ---ArgSerLeuLeuProProHisGlnPheSerArg---TyrMetGlnTyrThr 2881
 DB 8293 GCGCGGACCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCC 8352
 QY 2882 Ala---AspValArgGluSerGlyHisGlyPheThrArgAspValIleGlnAsnThrPro 2900
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 QY 2901 ---MetThrIleLeuSerAspThrValaValaAspGlyAsnAspAlaThrCysVala 2919
 DB 8413 GCGCGGACGCTGATCG 8451
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 DB 8452 ---CGCTCCGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCC 8490
 QY 2933 ---LeuArgGlySerSerAspAsnIleIleThrGln 2942
 DB 8491 GACACCCATGCTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8538
 QY 2943 AlaThrValPheAsnAlaAlaCysAlaLeuValLeuSerArgGluSerAspSerLysAsp 2962
 DB 8539 AACTCGCGGCTGGAGCGCGCTGGCGCGCGCGCTGATCGCGCGCTGCACCGCGCGCGCG 8598
 QY 2963 ValValaPheGlyArgIleValaSerGlyArg---GlnGlyLeuProValaGluTyrGlnAsp 2981
 DB 8599 GTCGTCTTCGCGACGACGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8655
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 DB 8656 ATGGTGGGCTTCATCAACACCGCTGCACCGCGCTGGAGTGAAGCGCGCGCGCGCGCG 8715
 QY 3001 TyrAsnGlnLeuLeuHisAspIleGlnAspGlnTyrLeuLeuSerLeuProHisGlnThr 3020
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 QY 3041 SerCysCysIleThrTyrHisAspHis 3049
 DB 8824 GACACCTCCACCGCGCTTCGAAATACTAC 8850

; GENERAL INFORMATION:
 ; APPLICANT: FARNET, Chris
 ; APPLICANT: ZAZOPOULOS, Emmanuel
 ; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 ; FILE REFERENCE: 3002-1105
 ; CURRENT APPLICATION NUMBER: US/10/329,079
 ; CURRENT FILING DATE: 2002-12-24
 ; NUMBER OF SEQ. ID NOS: 66
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ. ID NO 42
 ; LENGTH: 18876
 ; ORGANISM: Streptomyces refuineus
 ; US-10-329-079-42
 Alignment Scores:
 Pred. No.: 6,26e-176 Length: 18876
 Score: 2191.50 Matches: 795
 Percent Similarity: 43.91% Conservative: 445
 Best Local Similarity: 28.15% Mismatches: 1069
 Query Match: 13.59% Indels: 517
 DB: 15 Gaps: 110
 US-09-482-788-2 (1-3129) x US-10-329-079-42 (1-18876)
 QY 51 ProCysThrProPheGlnLeuAspMetIleAspCysAspAlaLeuAspLysGlnSerAla 70
 DB 11125 CCCCTGCTCCGCCCGACGCGACAGCTGTGTTCTTCAACCGCTACAGACAGAGAGCCGCC 11184
 QY 71 IleGlyHis-----AlaValTyrAspValProThrAspIleAspIleSerArgPheAla 88
 DB 11185 GCGTACACATACAGCGCGCGCGCTGGCGCTGACCGCGACCTGCACGTCGCGCGCGCTGCAC 11244
 QY 89 LeuAlaTribLysGluIleValaGlnThrProAlaLeuArgAlaPheAlaPheThrSer 108
 DB 11245 GCGGCGTGGGACAGCG 11301
 QY 109 AspSerGlyLysThrSerGlnValIleLeuLysAspSerPheValPheSerTrpMetCys 128
 DB 11302 GACGAGAGAGGCGCTTACACAGTGTCTCTG----- 11331
 QY 129 TrpSerSerSerSerPro-----Asp 136
 DB 11332 ---CGCGCGCGCGCTCCCG 11388
 QY 137 GluValaValaArgAsp-GluAlaAlaAlaAlaAspGlyProArg----- 151
 DB 11389 GCGCTGGTGGCGAAGCG 11448
 QY 152 ---CysAsnArgPheValLeuLeuGluAspMetGlnThrLysLysCysGlnLeuVala 169
 DB 11449 CACACCTGTTCGCGC-----TCCCGGACCGCGAGCAGCTCTGCTC 11490
 QY 169 ITrpThrPheSerHisAlaLeuValaAspValaThrPheGlnGlnArgValaLeuSerArgVala 189
 DB 11491 CTGGTG-ATCCACACATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 11549
 QY 189 ILeuAlaAlaTyrLys----- 194
 DB 11550 GCGCGCGCTTACCG 11609
 QY 195 ---HisGlyLysAspThrHisArg---ProGlnThrProLysSerArg 209
 DB 11610 GAGCCACCGCGATCAGCTGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11663
 QY 209 AlaThrAspThrAspSerGlnSerValaSerValaSerMetSerCysGluAspAsnAla 229
 DB 11664 GCGCGGAGACCG 11694
 QY 229 aValaSerAlaThrHisPheThrGlnThrHisLeuAsnAspLeuAsnAlaSerValaPhePr 249
 DB 11695 ---CACTGGCGCGAGAGCTGCGCGA----- 11718

RESULT 3
 US-10-329-079-42
 ; Sequence 42, Application US/10329079
 ; Publication No. US20030198981A1

249 OHISLeuSerAspHisLeuMetVal-----ProAsnProThrThr----- 263
11719 -----CTGCCGAGAGATTCCCGCTCCCTACGACCGGCGCCGCCACGACCCCGG 11774
264 ----AlaGluHis-----Arg11eThrPheProLeuSerGlnLysLeuSerAs 279
11775 GTACCGCGAGCGGATCGCTTCCGGATGACCGCGGACTGTACCGGCTGGGCTT 11834
279 nserAla-----IleCysArgThrAlaLeuSerIleLeuLe 291
11835 GGGGCG 11894
291 userArgTyrThrHisSerAspGlnAlaLeuPheGlnAlaValThrGlu----- 307
11895 GACCCGG-----CTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 11930
308 ----GlnSerLeuProPheAspLysIleTyrLeuAlaAsp-----GlyThrTyrGlnm 324
11931 CACCCCTCG 11990
324 ValAlaProLeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAl 344
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364 gaenThrGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAs 384
12101 AACGGCTGTGTGAGCGCGTCAACCCCGCTCGCGCGCGCGCGCGCGCGCGCGCG 12160
384 gLySerHis-ValAsnAsnGlyIleAsnGlyPheLeuGlnIleThrGlyuserSerH 404
12161 CATTGCTCACTCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12213
404 iAspMetProCysAsnAsnArgAlaLeuLeuLeu-----HisC 417
12214 -----CTGCCG---GGGTGCGAGCGGAGCTGTGCGCGCGCGCGCGCGCGCG 12265
417 yAsnMetGlu-----SerSerIle 424
12266 CCGACCTCGACCTGACCTTCGCGCGAGACCGGCTCGCGCGCGCGCGCGCGCGCG 12325
424 laLeuLeuValAlaTyrTyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeu 444
12326 TCAGCGGAGACCTCGCACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12385
444 euGlnGlnPheGlyHisLeuIleLysCysLeu---GlnSerPro----- 457
12386 TGGAGCGGCTCGTGGCGCTGCGCGAGCGGTGACCGCGCGCGCGCGCGCGCGCG 12445
458 --LeuAspLeuSerSerMetAlaGlnValAsnLeuMetThrGlyTyrAspArgAlaIu 477
12446 GGTTCGACGTCACCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12501
477 leGluSerTrpAsnSerGlnProLeuGlnValGlnAspThrLeuIleHisIleGluMet 497
12502 -----GCCCG 12547
497 euLysAlaValSerHisSerProThrIleArgThrAlaIleGlnAlaTrpAspGlyAspTrp 517
12548 TGTTCGCGCGCTGGCGGAGCGAGCGCGCTTCGCGCGCGCGCGCGCGCGCGCG 12607
517 hr-----TyrSerGlnLeuAspAsnValSerSerArgLeuAlaValHisIleLysSer 535
12608 CCGTGAAGTACGCGGAACTGACCGCGCTCAACCGCGCGCGCGCGCGCGCGCG 12667
535 euGlyLeuAspAlaGlnGlnAlaIleIleProValTyrPheGluLysSerIleTrpVal 555
12668 TCGGCGGTG---GGCGCGGAGACTTTCGCTCGCGCGCGCGCGCGCGCGCGCG 12724

555 leAlaSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIleAspProAsn 575
12725 TGTGAGCGGTGCTCGCGCTGCTGAAGCGGCGCGCGCGCGCGCGCGCGCGCG 12784
575 sPrProAlaAlaGlyThrAlaGlnValValThrGlnThrArgAlaThrValAlaLeuThr 595
12785 ACCGCGCGGAGCGACCTCTTACATCTCGGAGCATGCGCGCGCGCGCGCGCG 12844
595 eLysLeuHisArgGluThrValAlaGlnLysLeuValGlyArgCys----- 609
12845 CGACCGCGGTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12904
610 --ValValAlaAspAspGlnLeuLeuGlnSerValSerAlaSerAspAspPheSer 629
12905 GCGTGTGCTGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12964
629 euThrLysSer-----GlnAspLeuAlaTyrValIlePheTr 641
12965 TCACCGAGCGCGACCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13024
641 hrSerGlySerThrGlyAspProLysGlyIleMetIleGluHis-----Arg 657
13025 CTTGCGGATGACCG 13084
657 laPheSerSerCys-----AlaLeuLysPheGlyAlaSerLeuGlyIleAsnSerAsp 675
13085 TGTGTGACGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13129
675 hrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGluIleMetThr 695
13130 TGTGAGCGCTC---TTCACTCAAGCGCGCTTCACTTCTCGGTGTGGAGATGCGGAG 13186
695 hrLeuIleAsnGlyGly---CysValCysIleProSerAspAspArgMet---Asn 713
13187 CCTGCGCGGACCG 13246
713 eLrLeProSerPheIleAsnArgTyrAsnValAsnTrpMetValThrProSer--- 721
13247 ACCTCTGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13306
732 -----TyrMetGlyThrPheSerProGluAspValProGlyLeuAlaThr----- 746
13307 TCCTCCAGCTCTCGCGCGCGAGACCGAGCGGAGCGTCCCGCGGAGCGCGCGCG 13366
747 -----LeuValLeuValGlyGlnImetSerSerValAsnAlaIleTrpAlaP 764
13367 TGAAGTACGTGCTTTCGCGGAGCGGTGACACCGCGCGCGCGCGCGCGCGCG 13426
764 rLys---LeuGlnLeuLeuAsnGlyTyrGlyGlnSerGlyuserSer---SerIleCysP 782
13427 GCGCGCGGTCCCGCTGTGACATGTACCGGATCACCGAGACCGCGCGCGCGCG 13486
782 heAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAlaValAlaIle----- 799
13487 ACCTGAGCTGACGACGCGCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCG 13546
800 -----HisSerTrpValIleAspProAsnAspIleAsnArgLeuValProIleGly 817
13547 ACGACGTGCG 13600
817 laValGlyLeuLeuValIleGluSerProGlyIleAlaArgAspTyrIleValProProp 837
13601 TCGTTCGCGAGCTGTACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13660
837 rPrProGluLysSerProPhePheThrAspIleProSerTrpTyrProAlaAsnThrPhe 857
13661 GCGTGAAGCGCGCGCGCTTGTGCGGAC-----CGTCCGAGCGC--- 13701
857 rAspArgAlaLysLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySer 877
13702 -----GGCGCGCGAGTACCGGACCGGCGATCTGTGACGCGCGCGCGCGCG 13756
877 leValCysLeuGlyArgIleAspSerGlnValLysIleArgGlyGlnArgValGluLeu 897

| | | | |
|----|-------|--|-------|
| Qy | 1570 | lnthrglnvalseralaatyProabsertglaalaValaAaPserSerCybAtgLeuT | 1590 |
| Db | 15779 | GCGCCCGGCCACCGCCAGCCCGGAGCGGTGGCGCTCCGCTGCCCGGGAGAGCTCA | 15838 |
| Qy | 1590 | hrrYrthrglueuAaPArgrGlnserAhrllleuAaaglyrTrieuAaGrArgrSem | 1610 |
| Db | 15839 | CGTACCGCGAGCTCGCGAGCGAGCGGCGAAGCGGTGGCGCGCGCTGACCGGCGGGCGCG | 15898 |
| Qy | 1610 | etProAlaGluThrLeuValAlaValAheAlaProAaGrSerCybGluThrllleValAlaP | 1630 |
| Db | 15899 | CCGGCCCCGAAACGGCGGCTGGCGGTGGCTGGCGCGAGCCGCGACCTGGTAGCTGCC | 15958 |
| Qy | 1630 | hePheglYValleuYAlaAaInleuAaIaTyrlleuProleuAaPAlaGrSerProSeA | 1650 |
| Db | 15959 | TGCTCGGAGTCTCTCGCGCGCGCGCGCTCAAGTGGCGCTGAGCCGGAGTACCGGAGC | 16018 |
| Qy | 1650 | laArGValAlaAhrllleuAaSerClyleuSerGlyProThrlleValleuIleGlyHbA | 1670 |
| Db | 16019 | AGCCCATCTCGCGCGCATCTGTCTCC-----G | 16042 |
| Qy | 1670 | spTrrAlaProProAaPrlleGluValThraAaValGluPheValaGrIleArGrAaPAla | 1690 |
| Db | 16043 | ACACCCCGCGGTGGCGCTGCTACACAG-----GGGACTGCCCGCCGCA | 16090 |
| Qy | 1690 | euaAaAPserAaAaIa-----AaPrlYpheGluValIleGluAaAPserThrlYs- | 1707 |
| Db | 16091 | TCACCGCTGCGCGCGCGCTGGCGGTGCCCAACCTCTGGCGCGGACGCGGACAG | 16150 |
| Qy | 1708 | -----ProSerAlaThrSerleuAaIaTyrrValleuT | 1718 |
| Db | 16151 | GCGCCGAGCCCTGCCAGAGTCCGCGCGCTGCCGCGACAGCGCGGTACGTCTCC | 16210 |
| Qy | 1718 | yrThrSerGlySerThrGlyArGrProlyGlyValMeIle----- | 1731 |
| Db | 16211 | ACACCTCGGGCTCCAGCGAGCGGCCAAGGCGGTGGCGTCAACCGGGGAACTTGCCA | 16270 |
| Qy | 1732 | -----GluHleArGValIleIleArGThrValThrSerGlyCybIleProAaT | 1748 |
| Db | 16271 | ACCTGTCGGCGGACATGCGGAGCGGCTGGCC-----CTCACCGCGCGG | 16314 |
| Qy | 1748 | yrProSerGluThrArGMeAlaHleAaMerAlaThrlIleAlaPheArGrIlaSerTyrg | 1768 |
| Db | 16315 | -----GACCGGCTGGTGGCGCTACACAGCTGCACTTCGACATCGCGCGCTGG | 16363 |
| Qy | 1768 | IuIleYrSerAlaLeuAaPheGlyArGThrThrLeuValCybAlaAPTyrMeThrThrl | 1788 |
| Db | 16364 | AGCTGTCCTGCGCCCTGATCGGCGCGCCGCAACTGCTGGCGGACCCGCGGACCGGCAC | 16423 |
| Qy | 1788 | euaAaPAlaArGAlaLeuYlaAaPValAhePheArGrGluHleAaAlaAaSerHbA | 1808 |
| Db | 16424 | GGGACCCGGAAGCACTG-----GGCGCACTCG | 16450 |
| Qy | 1808 | alThrSerSerSerGlnAaPValProleuArGValProArGrAaGrleuSerArGrThrlleuM | 1828 |
| Db | 16451 | TCACCGGAGGCGGCGCACCATCTCCAGGCGACCCCGACACCTGGAG----- | 16500 |
| Qy | 1828 | etPhePhePheLeuValValThraPserThrAlaProAaPAlaLeuAaPAlaGlnGlyL | 1848 |
| Db | 16501 | -----CTGCTGGCCGAGACCGCGCCGACGCGCTG-----CGCGGGCG | 16537 |
| Qy | 1848 | euryTyrgln----- | 1850 |
| Db | 16538 | TGGCGAAATGTTGGGCGCGGAAGCTCCCGCGTCCCTGGCTCCCGCTGACAGGCC | 16597 |
| Qy | 1851 | --GlyValGlnCybTyraAaGlyTyrlYrProThrgluAaGlyValMetSerThrlleT | 1870 |
| Db | 16598 | TGGCGGCGGAATGATGATCAAGTCAAGGCGCCACCGAGACCAACATCTGGTCCACCGCGC | 16657 |
| Qy | 1870 | yrProIleAaPserThrGluSerPheIleAaGlyValProIleGlyArGrAlaLeuAaAa | 1890 |
| Db | 16658 | CCCACTCGACCGGCGCACCGGG-----AGCGACCGCCCATCTGGCGCGGCGCTGCGCA | 16711 |

QY 1690 snsergYAlATYrVAlValAAspProgluInlInleuValAGlyllegYValMetGlyG 1910
 Db 16712 ACACCCCGGGCTTAAGTCTTGAAGAGTGGCTGACCCGGTCCCGCGGGGTCTCCGGAGG 167712
 QY 1910 luleuValValAThnglYAspGlyLeuAlaArglyTYrSerAspYs---AlaleuAspG 1929
 Db 16772 AGCTTACCTTGGCGGGCGGGGGGTGGCCGGGGCTTACCTGGAGCGCGGGCGCTTACCG 168312
 QY 1929 lueAnaArgPheValHisIleThrValAsnAspGlnThrVallyValATYrAghThnglYA 1949
 Db 16832 CCGAGCGCTTCACCGCGGACCCCTTCGGCGCGCGCGGACGCGCAAGTCACTGACCGAGGG 168912
 QY 1949 sPArgValATgTYrATgTllegYAspGlyLeuulleglPhePhegYATgMetAspThrs 1969
 Db 16892 ACCTGGTCCGCGGGCGC--GCGAGCGGAGAGCTTGAAGTCTTCGGAGCGACCGACCCACC 169484
 QY 1969 lnpheYsIleArgGlyAsnArgllegluserAlagluileglualAlaleuLeuAdga 1989
 Db 16949 AGCTCAAGGTCCGGGGCTTCCCATGAGCTGGGCGAGATCGAGAGCGCTCTCGTGGCC 170080
 QY 1989 sPserSerValArgAspAlaIleValValleuGlnlInngluAspGlnAlaPro--- 2007
 Db 17009 ACCGGAGAGTCTCGGGGGCGGTGTGGTCCGCGGAGCGGTCTGGCGCGCGCGCGCGCG 17068
 QY 2008 -----gluleuGlyPheValAlAlAspH 2017
 Db 17069 CGAGACGAGCGGACCGCGCGCGCGCGCGCGAGAGCTGGAGCTGAGTGTGGCGGAGC 171280
 QY 2017 lAspHlAserGluAsnAspLyAGlylnserAlaIngInValAGluTYrTrpGlnAspH 2037
 Db 17129 CCGAGCGGGCGCGGACGAGCGGAGCGGAGCGGGCGCGGCTCGACGAGTGGCGGAGA 171880
 QY 2037 lAspHgluserGlyMetTYrSerAspIleGlyGluIleAspProserThrIlegYserA 2057
 Db 17189 CCTACGACACC---CTCTACGACAAC-----TCCGAACCGAGCCCCCTGGCGCGGG 172380
 QY 2057 sPheYsGlyTYrTrpThrsMetTYrAspGlyserGlnIleAspPheAspGluMetHisG 2077
 Db 17237 ACTTCGGAGATCTGGCGGAGAGCTACGACGAGCGCCATCCCGCTGGAGAGAAATCTCC 172980
 QY 2077 lUTrPleAGlyGluThrThrArgThrLeuHisAspAsnAspSerLeuGlyAsnValleug 2097
 Db 17297 AGTGGCGGGCGGCGACGAGTGGAGCCGATCGGGCGCGTGGCGCC---GGCGGGCTGTGG 173580
 QY 2097 lUIleglYThnglYserGlyMetIleleuPheAsnleuAspSerArgleuGlyserTYrV 2117
 Db 17354 AGATCGGGGTGGGACCGGACTGTCTGTGGAACTGGGACCGGACTGACCGCGCTTACC 174130
 QY 2117 alGlyleuGluProserArgserAlaAlaIlePheValAsnlyValAThngluserIleP 2137
 Db 17414 ACGGAAACCGACTGTCCGACCGGGGTATCGAGACCTTGCAACGAGAGGTGCGCGCGAGAC 174730
 QY 2137 roserleuAlaGlyLyAlaIleValAGlnValAGlyThrAlaThsAspIleGlylnValA 2157
 Db 17474 CCGGGCTTGAAGAGAGAGTGAAGTGAAGTCCGCGCGCGGACGACCTTACCGAGTCC 175330
 QY 2157 sPAspLeuHisProAspLeuValValleuAsnserValIleglTYrPheProserSerG 2177
 Db 17534 GCAAGGGGTCTTACGACACCATGTGTCTAACTCCGTCGCGCATCTTCCCGGCGCGG 175930
 QY 2177 lUTYrLeuAlaGluIleAlaAspThrLeuIleHisleu-----ProAsnValGlnArgT 2195
 Db 17594 ACTACCTCTCCCGGGCTCTCGCGGCGGACCTTCACTGACCTGTGAGACCGCGC--GAGCGCG 176530
 QY 2195 lePhePheGlyAspValArgserGlnAlaThsIngInHisPheleuAlaAlaArgAlA 2215
 Db 17651 TCTTCGTGGGAGAGTGGAGCTGGCGCTGGCGCTGTCTCGCGGCTC-----CGGGCT 177080
 QY 2215 leHisThrleGlyLyAsnAlAThrLyAspAspValArgGlnlybMetAlaGluLeuG 2235
 Db 17702 CCGTGGAGATCGGAGACCGCGCGCGGAGACCGCCCGGCGCGGTGGTGGCGCGCGG 177680
 QY 2235 lu-----AspMetGluGlnGluLeuValAGluProAlaPhePheThrserleu 2252

| | | | | | | |
|---|-------|--|-------|-------|--|-------|
| D | 17762 | ACCGCAGGAGCGCCACGGAGAGAAAGAACTCGCTGACACCCGGGCTACTTCGCGCGCTCG | 17822 | 17762 | ACCGCAGGAGCGCCACGGAGAGAAAGAACTCGCTGACACCCGGGCTACTTCGCGCGCTCG | 17822 |
| Q | 2252 | ysAspArgpHeProGluLeuValGluHisValGluIleLeuProLysAsnMetGluAlaVal | 2272 | 2252 | ysAspArgpHeProGluLeuValGluHisValGluIleLeuProLysAsnMetGluAlaVal | 2272 |
| D | 17822 | GC---CGGAGAACCGGGGAACCCCTCGTCTGTGACGCGGGGCGCGCGGGAGAGCGCG | 17878 | 17822 | GC---CGGAGAACCGGGGAACCCCTCGTCTGTGACGCGGGGCGCGCGGGAGAGCGCG | 17878 |
| Q | 2272 | aLaMetGluLeuSerAlaTyrArgTyrAlaAlaValHisValAlaArgGlySerLeuGlyA | 2292 | 2272 | aLaMetGluLeuSerAlaTyrArgTyrAlaAlaValHisValAlaArgGlySerLeuGlyA | 2292 |
| D | 17879 | TCAACGAGCTGACCGCGTACCGCTAC---GACGTCTGTGCGCAACCGGAGCGCGGGA | 17939 | 17879 | TCAACGAGCTGACCGCGTACCGCTAC---GACGTCTGTGCGCAACCGGAGCGCGGGA | 17939 |
| Q | 2292 | spGluLeuValLeuProValIGluLysAspArgTrpIleAspPheGlnAlaAsnGlnLeuA | 2312 | 2292 | spGluLeuValLeuProValIGluLysAspArgTrpIleAspPheGlnAlaAsnGlnLeuA | 2312 |
| D | 17936 | CCGCGCGTCCGCGCCCGCGCGCGGAGATGCGCGTGGCGGAG----- | 17976 | 17936 | CCGCGCGTCCGCGCCCGCGCGCGGAGATGCGCGTGGCGGAG----- | 17976 |
| Q | 2312 | snGlnLysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValSerL | 2332 | 2312 | snGlnLysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValSerL | 2332 |
| D | 17977 | -----GAGGTCCGAGAC-----CGCGCGCGGTGCGCGAGGTGCGCGGACAC | 18022 | 17977 | -----GAGGTCCGAGAC-----CGCGCGCGGTGCGCGAGGTGCGCGGACAC | 18022 |
| Q | 2332 | ysIlePheProHeGluIleThrAlaPheGlu-----ArgGlnValAlaIleSerL | 2348 | 2332 | ysIlePheProHeGluIleThrAlaPheGlu-----ArgGlnValAlaIleSerL | 2348 |
| D | 18023 | CGCGCGCGCTCGCGCTACCGCGCATCCCAACCGCGCGGTGCGCGCGAGACCGCGCGCC | 18082 | 18023 | CGCGCGCGCTCGCGCTACCGCGCATCCCAACCGCGCGGTGCGCGCGAGACCGCGCGCC | 18082 |
| Q | 2348 | euaAsnSerAsnIleAspGluTrpGlnLeuSerThrIleArgSerSerAlaGlnGlyAsps | 2368 | 2348 | euaAsnSerAsnIleAspGluTrpGlnLeuSerThrIleArgSerSerAlaGlnGlyAsps | 2368 |
| D | 18083 | TGCGCGCGCTGAGAGACCGCGCGCGCTCGCGCGCGCGCGCGCGCTGAGAGCGCGCG | 18142 | 18083 | TGCGCGCGCTGAGAGACCGCGCGCGCTCGCGCGCGCGCGCGCGCTGAGAGCGCGCG | 18142 |
| Q | 2368 | er---SerLeuSerValProAspIlePheArgIleAlaGlnGlyAlaGlyPheArgValG | 2387 | 2368 | er---SerLeuSerValProAspIlePheArgIleAlaGlnGlyAlaGlyPheArgValG | 2387 |
| D | 18143 | CCGCGCGAGTGAACCGCGAGACCTGTACACGCGGGCGCGCGCGCGCGCGACCGCGT | 18202 | 18143 | CCGCGCGAGTGAACCGCGAGACCTGTACACGCGGGCGCGCGCGCGCGCGACCGCGT | 18202 |
| Q | 2387 | luValSerSerAlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAlaValPheHisGlc | 2407 | 2387 | luValSerSerAlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAlaValPheHisGlc | 2407 |
| D | 18203 | GGGTGTCC-----TGTGCGCGCGAGGACCGCGCGGACCGGTG----- | 18240 | 18203 | GGGTGTCC-----TGTGCGCGCGAGGACCGCGCGGACCGGTG----- | 18240 |
| Q | 2407 | ysCysSerGlnGlyArgThrLeuValAsnPheProThrAsp----- | 2420 | 2407 | ysCysSerGlnGlyArgThrLeuValAsnPheProThrAsp----- | 2420 |
| D | 18241 | -----GACGTGCTGTGCGCCCGCGGACCGGGGCGCGCGCGGAG | 18283 | 18241 | -----GACGTGCTGTGCGCCCGCGGACCGGGGCGCGCGCGGAG | 18283 |
| Q | 2421 | -----HisValLeuArgGlySerAspLeuLeuThrAsnA | 2432 | 2421 | -----HisValLeuArgGlySerAspLeuLeuThrAsnA | 2432 |
| D | 18284 | TGGACCGCGCGCGGACCTGTGCGCGGTACGACCGCGACCGCGACCGCGCGGACCGA | 18344 | 18284 | TGGACCGCGCGCGGACCTGTGCGCGGTACGACCGCGACCGCGACCGCGCGGACCGA | 18344 |
| Q | 2432 | rgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeuArgS | 2452 | 2432 | rgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeuArgS | 2452 |
| D | 18344 | ACCGGTCCGCGCGCGCTGCGCAACCGGAGACTGGCGCGCGGTGCGGTACTGCGCGG | 18403 | 18344 | ACCGGTCCGCGCGCGCTGCGCAACCGGAGACTGGCGCGCGGTGCGGTACTGCGCGG | 18403 |
| Q | 2452 | erLeuLeuProSerTyrMetIleProSerAsnIleValValLeuAspLysMetProLeuA | 2472 | 2452 | erLeuLeuProSerTyrMetIleProSerAsnIleValValLeuAspLysMetProLeuA | 2472 |
| D | 18404 | GACGCGTCCGCGACTACATGATGTGCTCGCGCGGTGTCTGTCTGCGCGCTCCGCTGA | 18463 | 18404 | GACGCGTCCGCGACTACATGATGTGCTCGCGCGGTGTCTGTCTGCGCGCTCCGCTGA | 18463 |
| Q | 2472 | snAlaAsnGlyLysValAspArgGlyLeuLeuSerArgArgAlaValValProLysG | 2492 | 2472 | snAlaAsnGlyLysValAspArgGlyLeuLeuSerArgArgAlaValValProLysG | 2492 |
| D | 18464 | CCGCGCAACCGGAGGTGACCGCGCGCGCTGCCAC-----CCGAC | 18508 | 18464 | CCGCGCAACCGGAGGTGACCGCGCGCGCTGCCAC-----CCGAC | 18508 |
| Q | 2492 | IngInThrAlaAla-----ProLeuProThrPheProIleSerGluValGluValI | 2509 | 2492 | IngInThrAlaAla-----ProLeuProThrPheProIleSerGluValGluValI | 2509 |
| D | 18509 | CGCGCGCGCGCGCGCGCGCGCGCA-----CGCGCACGCGCGCGGAGAGAC | 18556 | 18509 | CGCGCGCGCGCGCGCGCGCGCGCA-----CGCGCACGCGCGCGGAGAGAC | 18556 |
| Q | 2509 | leLeuCyArgGluAlaThrGluValPheIleMet---LysValAspIleThrAsnHisP | 2528 | 2509 | leLeuCyArgGluAlaThrGluValPheIleMet---LysValAspIleThrAsnHisP | 2528 |
| D | 18557 | TGCTGTGCGCGCTTTCGCGACCTGTGTGGCGCTGAGCGCGGAGGACACCGAGACGT | 18616 | 18557 | TGCTGTGCGCGCTTTCGCGACCTGTGTGGCGCTGAGCGCGGAGGACACCGAGACGT | 18616 |
| Q | 2528 | hePheAsnLeuGlyGlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnA | 2548 | 2528 | hePheAsnLeuGlyGlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnA | 2548 |
| D | 18617 | TCTTCACGCTGGCGGAGACACATCTGTGCGCTCGCGCTGTCAAGCGCGACCGGAAAC | 18678 | 18617 | TCTTCACGCTGGCGGAGACACATCTGTGCGCTCGCGCTGTCAAGCGCGACCGGAAAC | 18678 |
| Q | 2548 | rgLeuLysValArgIleThrValLysAspValPheAsnHisProValPheAlaAspLeuA | 2568 | 2548 | rgLeuLysValArgIleThrValLysAspValPheAsnHisProValPheAlaAspLeuA | 2568 |
| D | 18677 | AG---GGGCTGCGGTGACACCGCGGACGCTTTCGAGCACACCGGTGGCGCGCTGG | 18733 | 18677 | AG---GGG | |

Db 18734 CGGGGGCCCTG---GACGGCAAGAGCGGAGAGACCGGGCGCGACCGCGCGGAC- 18789

Qy 2588 spargSerAlaHisMetAlaProArgThrGluThrGluAlaIleLeuCyAspGluPheA 2608

Db 18790 -----CCGGCGCGCGGACCGCGCGCCATCAGCGCCGAGGAACCTCG 18829

Qy 2608 IaLyVal 2610

Db 18830 CCGAGCTG 18837

RESULT 4
US-10-329-079-8
: Sequence 8, Application US/10329079
: Publication No. US20030198981A1
: GENERAL INFORMATION:
: APPLICANT: FARNET, Chris
: APPLICANT: ZAZOPOULOS, Emmanuel
: APPLICANT: STAFEA, Alfedo
: TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
: FILE REFERENCE: 3002-11US
: CURRENT APPLICATION NUMBER: US/10/329,079
: CURRENT FILING DATE: 2002-12-24
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 8
: LENGTH: 7788
: TYPE: DNA
: ORGANISM: Streptomyces fradiae
US-10-329-079-8

Alignment Scores:
Pred. No.: 7.4e-174 Length: 7788
Score: 2160.50 Matches: 783
Percent Similarity: 43.05% Conservative: 441
Best local Similarity: 27.54% Mismatches: 1059
Query Match: 13.40% Indels: 563
DB: 15 Gaps: 110

US-09-482-788-2 (1-3129) x US-10-329-079-8 (1-7788)

Qy 51 ProCysThrProPheGlnLeuAspMetIleAspCyAsnAlaLeuAspLysGlnSerAla 70

Db 61 CCCCTGTGCCCCCGCCAGCGAGCGTGTCTTCAACCGCTACAGACAGGAGCGCGC 120

Qy 71 IlegIHis-----AlaValTyraAspValProThrAspIleAspIleSerArgPheAla 88

Db 121 GGCTACCAACATCAGCGTGGCGCGCTGCGGCTCACCGGAGATCTGACGTCGACGCGCTCCAC 180

Qy 89 LeuAlaTrpLysGluIleValaGlnThrProAlaLeuArgAlaPheAlaPheThrSer 108

Db 181 GCGGCAAGCGGCGACCTGACCGCCCGGCAAGAGAGCTCGCACCC---GTCTTCCGCGAG 237

Qy 109 AspSerGlyLysThrSerGlnValIleLeuLysAspSerPheValPheSerTrpMetCys 128

Db 238 GACGAACAGGGGCGCCACCAAGGTCTCTGACCCG----- 273

Qy 129 TrpSerSerSerSerPro-----AspGluVal 138

Db 274 ---GGGGCGCGCGCGCAACCGCGGTCTGTCGCGGTCGCGGCCACCGCACTGACGCGCTG 330

Qy 139 ValArgAsp-GluAlaAlaAlaAlaAlaSerGlyProArgCyAsnArgPheValLeu 158

Db 331 GTGGCGGAAGCGTGTGCGCGCCCTTCGACCTGCGCGAGACATCCCGTGTGCGCCACACC 390

Qy 158 uGluAsp---MetGlnThrLysLysCysGlnLeuValTrpThrPheSerHisAlaLeuVa 177

Db 391 CTCTTACGCTCCCGGAGCGGACGACAGTCTGCTCTGTATC-CACCACTGCGCGC 449

Qy 177 IaSPValThrPheGlnGlnArgValLeuSerArgAlaPheAlaAlaTyrlLysHisGlu 197

Db 450 CGAGCGGTGTGCAATGGGGCGCGCTGGACAGGACCTGCGCGCGCTACCGCGCGCGCGC 509

Qy 197 sAspThrHisArgProGluThrPro----- 205

Qy 806 oAaAsp1LeuAsnArgLeuValProIleGlyAlaValGlyGluLeuValIleGluSerPr 826
Db 2490 GGGGGCTGCTTCC-----GTGCCGCTGGCGCTGTGGCGCAAGCTGACGTGGCGGCC 2543
Qy 826 oGlyIleAlaArgAspTyrIleValProProProGluLysSerPro-PhePheThrA 846
Db 2544 CGCGCTGGCGCGCGCTACCG-CCGCCGCCCGCGCTGAGCGCACCGCTTCCTCCCG 2602
Qy 846 sP1LeProSerTyrTyrProAlaAsnThrPheProAspGlyAlaLysLeuTyrThrG 866
Db 2603 AC-----CCGTTGCACCGCGCGCGCGGATGTAACGAGACCG 2638
Qy 866 lYAspLeuAlaArgTyrAlaSerAspGlySerIleValCysLeuGlyArgIleAspSerg 886
Db 2639 GCACACCTCGTCCGGCGACCCAGACCGCGCTCCCACTACGTGGCGCGGCTCCACTCC 2698
Qy 886 lNValIysIleArgGlyGlnArgValGluLeuGlyAlaIleGluThrHisLeuArgGln 906
Db 2699 AGGTGAACCTGGCGCTACCGCATCGACCGCGCGAGATCGAGCGCGCGCGCGCC 2758
Qy 906 lNMetProAspAspLeuThrIleValValGluAlaThrLysArgSerGlnSerAlaAsn 926
Db 2759 AC---CCGAC-----GTCCGCCAGCG----- 2778
Qy 926 eRThrSerLeuIleAlaPheLeuIleGlySerSerTyrPheGlyAsnArgProSerAsp 946
Db 2779 -----GCCACCGCGCTGCACCGCGCGGAGACCGACGAC 2812
Qy 946 lAhIleIleuAspHisAspAlaThrLysAla-----IleA 958
Db 2813 GGTAACCTGCTGTGTAGTGTGGCGGCGCGACACCGACCGCGACCGACGAGGTG 2872
Qy 958 sN1LeIysLeuGlnValLeuProArgHisSerIleProSerPheTyrIleCysMetL 978
Db 2873 GCGGCCACCTGGCGCGACCGCTGCGCTATATGATCGCGCGCGCTGTGGCGCTGA 2932
Qy 978 eugIleuLeuProArgThrAlaThrGlyLysIleAspArgArgArgLeuArgIleMetGlyL 998
Db 2933 CCGCGCTGGCGCTGACCCCGACCGCAAGCTGACCGACCGACCGCGCTG----- 2979
Qy 998 yAspIleLeuAspLysGlnThrGlnAlaIleValGlnAlaProAlaProIleP 1018
Db 2980 -----CCGCGCCCC----- 2988
Qy 1018 roValPheAlaAspThrAlaAla----- 1025
Db 2989 -----GACCGGCGCGCTGGCGCACCGCGCGCGCGCGACCGCGCGAG 3037
Qy 1026 --LysIleuHisSerIleTyrValGlnSerLeuGlyIleAspProAlaThrValAsnValG 1045
Db 3038 AAGCGCTGTGGCGCGCTTGCACCGACGTCTCGCGCTCGAC-----GAGTTCAGCGCG 3091
Qy 1045 lYAlaThrPhePheGluLeuGlyLysAsnSerIleThrAlaIleLysMetValAsnMetA 1065
Db 3092 ACGCGCACTTCTTGGCGCTGGAGGCACTTCTCGCGCGCTCGGCTCATACCGCGA 3151
Qy 1065 lAArgSer---ValGlyMetAspLeuLysValSerAsnIleTyrGlnHisProThrLeuA 1084
Db 3152 TCAGGTGGCGCTGGAGTGAATCGCATCCGACACGCTTTCAGAGCGCGCGCGCG 3211
Qy 1084 lAgIlyIleSer-----AlaValValLysGlyAspProLeuSerTyrThrLeuI 1100
Db 3212 CCGCGCTGTCCCGCGCTCGACACCGCGCGGACCGCGCGC-----CGCTCC 3262
Qy 1100 lProLysSerThrHisGluGlyProValGluGlnSerTyrSerGlnGlyArgLeuTyrP 1120
Db 3263 TGGCGGCGCGCGCGAC-----CGCGTCCGCTCTCTCCGCGCGAGCGCGTGTGT 3319
Qy 1120 heLeuAspGlnLeuAspValGlySerLeuTyrTyrLeuIleProTyrAlaValArgMetA 1140
Db 3320 TCCTCGAGAACTGGAAGACCGGCGCGCACTACCAATCCGCTCGCGCTGCGCTGC 3379

Qy 1140 rGgIyProValAsnValAspAlaLeuArgAlaLeuAlaLeuGlnIleGlnHisG 1160
Db 3380 GCGCGCTTCGACGTGAGCGCTTGGCAACCGCGCTTGGCGAGCGATGTGGCGCGACG 3439
Qy 1160 lNThrLeuAlaGlnThrPheGluAspGlnAspGlyValGlyValGln-----IleValH 1178
Db 3440 AGCGCTTCGACGCGCTTCCGCTCCGTCGAGACCGCGCGCGCTTACACAGGTGTCTCGG 3499
Qy 1178 lAgIlyLysLeuSerGlnLysLeuValIleAspLeuCysGlySerAspLeuAspProp 1198
Db 3500 CGAAGCGCGCGCGCGCGCTCGACGTCTGAGACGTACCGAGACGAGAGCTGCC----- 3555
Qy 1198 heGluValLeuAsnGlnGluGlnThrThrProPheAsnLeuSerSerGluAlaGlyTyrP 1218
Db 3556 --GCGCGCTCGCGAGCGCGCGCGACACCGCTTACCTTCACCGAGACTTCCGCTGC 3613
Qy 1218 rGAlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisHis 1238
Db 3614 GGGCGTACTGTGCGGACCGCGCGCGCGCGACGAGCTCTCCCTGCTCCACACCA 3673
Qy 1238 lElIleSerAspGlyTyrSerIleAspValIleAspValArgAspLeuAsnGlnLeuTyrSerA 1258
Db 3674 TCGCGCGCGAGCGCTGTGTGCTGGCGCGCGCTCGCGCGCGCGACCGCGAGACCTTC 3730
Qy 1258 lAlaIleuLysAspSerLysAspProLeuSerAlaLeuThrProLeuProIleGlnTyrS 1278
Db 3731 CCGCACGTCCGAGAGCGCGCGCG-----CAGTGGCGCGCGCTCGCGTGCAGTACG 3784
Qy 1278 eRAspPheAlaLysTyrGlnLysAspGlnPheIleGlnGlnLys----- 1292
Db 3785 CCGACACACCTTCGGAAGAGAGTGTCTCGCGCGCGCGCGACCGCGAGACCTTC 3844
Qy 1293 -----LysGlnLeuAsnTyrTyrLysGlnLeuLysAspSerProAlaLysIle- 1310
Db 3845 TCGCGCGCACTGCTCTTGTGCGCGAGCGCTG---GAGGCGCGCGGACAGATCG 3901
Qy 1311 ----ProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGlyCysValHis- 1328
Db 3902 AGCTACCCACCGACCGCGCGCGCGCGCGCATGAGAC---CACCGGCGCGCATTCAC 3958
Qy 1329 --ValThrIleAspGlyGluLeuTyrGlnSerLeuArgAlaPheCysAsnGlnHisAsnT 1348
Db 3959 GCTTACACCTCCCGCGCTGACCGCGCGCGCTGTCGTCGCGCACCGCGCGCGG 4018
Qy 1348 hRThrSerPheValValLeuLeuAlaIlePheArgAlaIleHisTyrArgGluThrAlaV 1368
Db 4019 CCACCTCTTCATGCGCTTCAGGCGGAGCTCGCGGACTCGCGGACTGTTGCCACCTTGAGGCG 4078
Qy 1368 alGluAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLeuGluAspI 1388
Db 4079 GCGGAGACATGCTCTCGGACGCGCTGTCCGCGCGCGCGCGCGAGCGCGCGACGAC 4138
Qy 1388 lElIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHisHisAspThrP 1408
Db 4139 TCGCGGCTTCTGTCAACCTTGGCGCTCCGACCGACGCTCGCGCGCGCGACCGCGACCT 4198
Qy 1408 heGlyThrLeuIleAsnGlnValLysAlaThrThrThrAlaIlePheGluAsnGluAspI 1428
Db 4199 TCGAGAACTGTGCGCGCTCAGGAGACCGGACCGGACCTGTGCGCTTGCACAGGACA 4258
Qy 1428 lProPheGluArgValValSerAlaLeuGlnProGlySerArgAspLeuSerSerThrP 1448
Db 4259 TCCGTTTCGACAACTGTGTGAGCGCTCAACCC---ACCGCTCTCTTCAGGCGAC 4315
Qy 1448 roLeuAlaGlnLeuIlePheAlaValHisSerGlnLysAspLeuGlyArgPheLysPheG 1468
Db 4316 CCGCTTTCAGATGCTGTGCTCGCTCCAGAAC---AACGAGCGCGCGAGCGCGCTCATGC 4372
Qy 1468 lNglYLeuGlu---SerValProValProSerLysAlaTyrThrArgPheAspMetGluP 1487
Db 4373 CCGGCTGTGAGGTACCGTGAACCGCGCGCGCGCGCGCGCGCGCAAGACTCTTTCG 4432
Qy 1487 heHisLeuPheGlnLys-----ThrAspSerLeuLysGlySerValA 1501

QY 2169 ValIleGlnTyrPheProSerSerGluTyrLeuAlaGluIleAlaSerThrLeuIleHis 2188
 DB 6472 GTGTCTCAGTACTTCCCGACGCGGACCTTCAACCGGCTACTCGCGCGCGCTGAC 6531
 QY 2189 Leu-----ProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsn 2206
 DB 6532 CTGTGGCGCCCGGCGC---GGGCGGCTCTGTGTGGGACCGTCCGACCTGGACCTGTCTG 6588
 QY 2207 GlnHisPheLeuAlaAlaGlnAlaIleHisThrLeuGlyAsnAlaThrLysAspAsp 2226
 DB 6589 CGCGGCTTC-----CGCGCTCGGTGAGACCGCGCAACGCGGCTCTCGGAACCT 6639
 QY 2227 ValArgGlnLysMetAlaGluLeuGlu-----AspMetGluGluIleLeuVal 2243
 DB 6640 CCGCGCGCGCTACTTGGCGCGCGCGCGGACGAGCGCGCGCGGAGAACGACTGTATC 6699
 QY 2244 GluProAlaPhePheThrSerLeuLys-----AspArgPheProGlyLeuValGluHis 2261
 DB 6700 GCCCGGACTACTTCCGGCGGCTGTGGCGGAGCGCGGACCGGCTCTG----- 6750
 QY 2262 ValGluIleLeuProLysAsnMetGluAlaValAsnGluLeuSerAlaIleTyrArgTyrAla 2281
 DB 6751 CTGACGCTGCGCATTCGCGCGCGGACGCGCTACAACTGACGCTGACCGCTAC--- 6807
 QY 2282 AlaValAlaHisValArgGlySerLeuGly-----Asp 2292
 DB 6808 GACGCTCTGCTGTGTCACAAACAGAGACCGGACCGCGCTCTCGCGCGCGCGGACAC 6867
 QY 2293 GluLeuValLeuProValGluLysAspAspTrpIleAspPheGlnAlaAsnGlnLeuAsn 2312
 DB 6868 GAACCTGGCTGAGACCGCGGAGACCGGCGAT-----GCGGGGCGGCTGTGCC 6912
 QY 2313 GlnLysSerLeuGlyAspLeuLysSerSerAspAlaAlaIleMetAlaValSerLys 2332
 DB 6913 GAG-----ATCTGCGCGCGGACCGCGCGCGCTGCGCGCTGACCGCG 6954
 QY 2333 IleProPheGluIleThrAlaPheGlnArgGlnValAlaSerLeuAsnSerAsnIle 2352
 DB 6955 ATCCCAACCGCGCGCGCGCGGAGACCAACCGCGCTCGCGCGCTGAG----- 7005
 QY 2353 AspGluTrpGlnLeuSerThrIleArgSerSerAlaGlu-----GlyAspSerSerLeu 2370
 DB 7006 GACGGGAGACCGGTGACCGGAGCGCGCGCTGTGAGCAACCGGCTGAC---GAGATC 7062
 QY 2371 SerValProAspIlePheArgIleAlaGlyGlnAlaGlyPheArgValGluValSerSer 2390
 DB 7063 GATCCGAGGACCTGTACGACGCGCGGACCGCGCGGACGACCGGCTGGTGACC--- 7119
 QY 2391 AlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAlaValPheHisLysCysSerGln 2410
 DB 7120 -----TGTGTGCGCGGACCGCGCGGACCGCTG----- 7149
 QY 2411 GlyArgThrLeuValAsnPheProThrAspHisIleLeuArgGlySerAspLeuLeu--- 2429
 DB 7150 -----GACCTGTGCTGCGCGCGCG-----GGCGGGAGACGGGCTGCCG 7188
 QY 2430 -----Thr 2430
 DB 7189 CCGGTGCGCGCGCGCGGAGCTGTGCGCGCGCGCGCGCTGACCGCGCGGAGACG 7248
 QY 2431 AsnArgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeu 2450
 DB 7249 AACGACCGCGCGCGCGGTGACACCGCGGACCTGCGCGCGCGCGCTCTCCACCTG 7308
 QY 2451 ArgSerLeuLeuProSerTyrMetIleProSerAsnIleValAlaLeuAspLysMetPro 2470
 DB 7309 GCGGACCGCTGCGCGGACTACATGTCTCCCTCGCGCTGTCTGTGACGCGCTCCG 7368
 QY 2471 LeuAsnAlaAsnGlyLysValAspArgLysGluLeuSerArgArgAlaLysValValPro 2490
 DB 7369 CTGACCGCGCAACGCGGAGGTGACCGGACCGCGCTG-----CCGACCGCGGACCG 7419

QY 2491 LysGlnGlnThrAlaAlaProLeuProThrPheProIleSerGluValGluValIleLeu 2510
 DB 7420 GCGGCGACGAGACCGCGCGCGCGCGCGCGCGGACCGCGCGGAGGAA-----CTGCTC 7470
 QY 2511 CysGluGlnAlaThrGluValPheGlyMet---LysValAspIleThrAspHisPhePhe 2529
 DB 7471 TGCACGCTCTCCCGGACCTGCTGGGCTGTGGCGGCTGTGGAGTCCGAGACAGCTTCTTC 7530
 QY 2530 AsnLeuGlyLysIleSerLeuLeuAlaThrLysLeuIleSerArgIleAspArgLeu 2549
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 QY 2550 LysValArgIleThrValLysAspValPheAspHisProValPheAlaAspLeuAlaSer 2569
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 QY 2570 ValIleArgGlnLeuGlyLeuGlnProValSerAspArgGlyGlnArg 2589
 DB 7648 GCCCTGACCGGACGAGAACCGGAGCGAACCGGCGCGCGCGCGCGCGCGCGCGCGCC 7707
 QY 2590 SerAlaHisMetAlaProArgThrGluAlaIleLeuLysAspGluPheAlaLys 2609
 DB 7708 ACCGCG-----GCGCGCGCATTCACCTTCGACGAACTGCGCGAG 7746
 QY 2610 Val 2610
 DB 7747 CTC 7749
 RESULT 5
 US-10-402-842-1
 ; Sequence 1, Application US/10402842
 ; Publication No. US20030219872A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Magarey, Nathan A.
 ; TITLE OF INVENTION: NON-RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GENES
 ; FILE REFERENCE: 0630/1J854-US1
 ; CURRENT APPLICATION NUMBER: US/10/402,842
 ; PRIOR FILING DATE: 2003-03-28
 ; PRIOR APPLICATION NUMBER: US 60/368,713
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 47988
 ; TYPE: DNA
 ; ORGANISM: Streptomyces hygroscopicus
 ; US-10-402-842-1
 Alignment Scores:
 Pred. No.: 7,69e-160 Length: 47988
 Score: 2011.00 Matches: 870
 Percent Similarity: 38.15% Conservative: 473
 Best Local Similarity: 24.72% Mismatches: 1301
 Query Match: 12.47% Indels: 878
 DB: 15 Gaps: 138
 US-09-482-788-2 (1-3129) x US-10-402-842-1 (1-47988)
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 DB 15061 GACGCGGACCGCGGACCGCGCTC-----GACGCGCGGACCGCGCGCG--- 15099
 QY 32 TyrGlnGlnLeuPheHisLeuTyrGlyLeuAspSerSerArgIleGluAlaIleLys--- 50
 DB 15100 -----TTCCGCTTCAGCGCTGTGACCGGCTGTGAGCGGCTGACCGCG 15147
 QY 51-----ProCysThrProPheGlnLeuAspMetIleAsp 61
 DB 15148 GACGCGCGCGCGCGGACGAGCGCTTACCGCTGACCGCGATGCG----- 15192
 QY 62 CysAsnAlaLeuAspLysGlnSerAlaIleGlyHisIleValTyrAspValProThrAsp 81

Db 15193 -----AGCGGCTGCTCTTCACACCTGATGACGCCGGAACGCCGC 15234
Qy 82 IleapIleSerArgPhe-----Ala 88
Db 15235 ATGACATTCAGAGCTTCCACTTGCCCTGCACAGCATCCGCGAGCCGAGCTGCTGCC 15294
Qy 89 LeuAlaTrpIyegIuIleValIleAngIlnThrProAlaLeuArgAlaPheAlaPheThrSer 108
Db 15295 ACCGCTGGCAGCGGTGCTGCACCGCACCTGCTGCTCCGT----- 15336
Qy 109 AspSerGlyThrSerGlnValIleLeuIySerPheValPheSerTrpMetCys 128
Db 15337 -----ACGTCA-----CTGACC 15348
Qy 129 TrpSerSerSerSerProAspGluValArg----- 140
Db 15349 TGGGACGCGCTCGCGGAAACCGCTCCAGTCCGTGGCACCGCGCTCGGATACCGGTGCA 15408
Qy 141 -----AspGluAlaAlaAlaAlaAlaSerGlyProArg-----CysAsnArgPheVal 156
Db 15409 CAGCTCAGTGCAGCGCATGCAGACGAGCGGACGCGGACCGCTGCAGCGGTATCTG 15468
Qy 157 LeuLeuGlu-----AspMetGlnThr----- 163
Db 15469 ACCGAGACCGCACCGCGGCTGCTGCACACCGCCCATCGCCCGGATGCCGCTC 15528
Qy 164 -----LysIyCyGlnLeuValTrpThrPheSerHisAlaLeuValAsp 178
Db 15529 GCCCGCTGGGGCGCGACACAGTCCGGCTGGTGACGTTCCACATCTGCTGCTGAC 15588
Qy 179 ValThrPheGlnGlnArgValLeuSerArgValPheAlaAlaTrpIySerHisGlnIyAsp 198
Db 15589 GGGTGCAGCTCGTGCAGTGTCTGTCCGAGTGTCCGCGAGTACGCGCGCTGCGCGAC 15648
Qy 199 ThrHisArgProGluTrpProGlnIySerSerAspAlaThrAspThrAspSerGlnSerVal 218
Db 15649 ---GGCATCCCGTACCCCGCACTG-----CGCACACCTACCGCGAG 15690
Qy 219 SerValIySerMetSerCyGlnAspAsnAlaValSerAlaThrHisPheTrpGlnThr 238
Db 15691 TTGCTGGCCGACGTGGCGGGCGACAGACAC---ACCGCGCGAGAGTACTGCGCGCC 15747
Qy 239 HisLeuAsnAspLeuAsnAlaSerVal-----PheProHisLeuSerAsp 253
Db 15748 GCCCTCACCGGCGCTGCAGTGCACCCCGCTGCTGCATGCACCGCGCGCGCGCGACGCC 15807
Qy 254 HisLeuMetValProAsnProThrThrThrAlaGlnHisArgIleThrPheProLeuSer 273
Db 15808 CATCAGCGCGCGCGCGAC-----GCCGAGCTGAAGCTGCGCGCTGCGCGCGCG 15855
Qy 274 GlnIyLeuAlaLeuSerAsnSerAlaIleCysArgThrAlaLeu----- 287
Db 15856 GTGACCGGCGGACCTGGGACCGCGCGGAGCGCGCGGTGACAGATGAACCGTGGTG 15915
Qy 288 -----SerIleLeuLeuSerArgTrpThrHisSerAspGlnAlaLeuPheGly 303
Db 15916 CAGGGCTTGTGGGGCTGCTGCTGCGCGCGACGCGTGAAGCGGACGTACTGTCGCG 15975
Qy 304 AlaValThrGlnGlnSerLeuProPheAspIySerIyLeuAlaAsp----- 319
Db 15976 GCC---ACGGTGGCGCGCGCGCGACAT-----CTGGCGGCGCGCGGAATCGGTG 16023
Qy 320 ---GlyThrTrpGlnThrValAlaProLeuArgValHisCyGlnSerAsnLeuArgAla 338
Db 16024 ATCGGCTGTTCATCAACACCTTCGCGTGCCTC----- 16059
Qy 339 SerAspValIleAspAlaAlaIleSerSerTrpAspAspArgLeuGlnIyHisLeuAlaProPhe 358
Db 16060 ---GACGTC-----GATCCGAGCGCGCGGTGCTGCTGACG----- 16089
Qy 359 GlyLeuArgAspIleAsnThrThrIyAspAsnIySerAlaAlaCysIleAspPheGlnThr 378
Db 16090 TGGCTGCGCGGCGTGCAGAGAC-----GAGCAGGCGGAGCGCGCGCATGAGCAGGTC 16143

Qy 379 ValLeuLeuValIlnAspGlySerHisValAsnAsnGlyIleAngIyPheLeuGln 398
Db 16144 TCGCTGCCCGCAGGTGACGGCTGGCGCGGAGCGGCGGACCGGAGTGTTCGACAGC 16203
Qy 399 IleThrGlySerSerHisPheMet-----ProCysAsnAsnAlaLeuLeu 414
Db 16204 GTCTGGCGCTTCGAGAACTTCGCGCGGACCTTGCTCCGCGGGAATGACGGGCTGGCG 16263
Qy 415 LeuHisCysGlnMetGlySerGlyAla----- 424
Db 16264 CTGAGCGCC---ATCGAGCGCACCAACCTCCAACTACCGCGCTCAACCGCATCTTCAG 16320
Qy 425 -----LeuLeuValAlaTrpTrpAspHisAsnValIleAspSerLeuGln 439
Db 16321 CTCACAGAGAGCTGACCGTGTGCTGCGCTGACGACACCGCGGTTCGACGCGGACACC 16380
Qy 440 ThrThrArgLeuLeuGlnGlnPheGlnIyHisLeuIleIySerIyLeuGlnSerProLeuAsp 459
Db 16381 GTGGCGGCGCTGGCC-----GGCCATCTGCACACCTGTGTGAGAGAGACCGCGGAG 16431
Qy 460 LeuSerSer-----MetAlaGluValAsnLeuMetThrGluTrpAspArgAlaGluIle 477
Db 16432 AACCCGACCGCGCGGCTGGCGGAGCTGCCCTCTCTACCGCGCGCGGACGACACCATC 16491
Qy 478 ---GluSerTrpAsnSerGlnProLeuGlnValGln---AspThrLeuIleHisGln 495
Db 16492 GTGCACACCTGCAGCGACACCGCTCGAGTACTCGGTGCACCGCGCGTGCAGCGCGCTC 16551
Qy 496 MetLeuIyAlaValSerHisSerProThrIyThrAlaIleGlnAlaTrpAspGlyAsp 515
Db 16552 ATCGCGCAAGAGCGCGCGCGCGCGGACCGCATCGCTGTGCACCGGTGAACCGGACG 16611
Qy 516 TrpThrTrpSerGlnLeuAspAsnValIySerSerArgLeuAlaValHisIleIySerLeu 535
Db 16612 CTGAGTTACGCGCATGTTGACCGCGCGGACCAACAGCTGGCACACATCTGCCCGCGCG 16671
Qy 536 GlyLeuArgAlaGlnGlnAlaIleIleProValTrpPheGlnIySerIyTrpValIle 555
Db 16672 GGGCTG---GGCGGAGCGCGCTGTGCGGATGCGCTGCAGCGCGGAGGTGCTC 16728
Qy 556 AlSerMetLeuAlaValLeuIySerGlyAsnAlaPheThrIleuLeuAspProAsnAsp 575
Db 16729 GTGGCATCTTCGCGACGCTCAAGCGCGCGCGCGGTATGCGCGCTGCCCGGAATTC 16788
Qy 576 ProProAlaArgThrAlaGlnValIlnThrGlnThrArgAlaThrValAlaLeuThrSer 595
Db 16789 CCGCGGAGCGGCTCGCGACCATGCTGTCCGATCCCGCGCGCGCTCGCTCACCCAG 16848
Qy 596 LysLeuHisArgGlnThrValGlnIyLeuValGlyArgCysValAlaIleAspAspGlu 615
Db 16849 GAACACCTGTGGCGGGCTGCGCGGACGAGCGCGGGGTGTGTGCTGCAGCGGAGC 16908
Qy 616 Leu-----LeuGlnSerValSerIleAspAspPheSer 627
Db 16909 CTGGCGGCATCGAGCGGACCCACCGCGCGCGGTCTCCGCGCGGAC----- 16959
Qy 628 SerLeuThrIySerSerGlnAspLeuAlaTrpValIlePheThrSerGlySerThrGlyAsp 647
Db 16960 -----GCCGCGACCTGGCTATGTACCTACACCTCTGGCTCCACCGCGCGC 17007
Qy 648 ProIyAsGlyIleMetIleGlnIyHisArgAlaPheSerSerCysAlaLeuIyPheGlyAla 667
Db 17008 CCCAAGGGCGTCAATGTCGAGCACCGCTGCTGTCAACATCATCAACGAGCGGACGCG 17067
Qy 668 SerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAla 687
Db 17068 CTCTACGACGTGGCGCGCGACCGGATCTCAGTTCTTACCAATGACCTTCGACGCGC 17127
Qy 688 CysLeuLeuGlnIyLeuMetThrThrLeuIleAsnGlyGlyCysValCysIleProSerAsp 707
Db 17128 GGGCTGCGGAGGTCTTCTGACGCTTACCGCGCGGCGCACCTCTGTCATCGCGGACCC 17187

Qy 708 AspAspArgMetAen-----SerileProSerPheIleAsnArgTyRAsnValAsnTrp 725
Db 17188 GAGCGCCGCGAGAGCCCGCCCACTGCGGAGAGCTGGCGGAGTGCATGACCGCG 17247
Qy 726 MetMetAlaThrProSerTyRmetGlyThrPheSerProGluAspValProGlyLeuAla 745
Db 17248 CTCAGCGTCCGCGCGGTGGGCTCGGTCTGGACCGGCTCGCGCGGATACGC 17307
Qy 746 ThrLeuValLeuValGlyGluGlnMetSerSerValAsnAlaIleTPAlaProLys 765
Db 17308 AGCCTGGGGCTGCGCGGAGATGCTGCGCGGCACTCGCGGAGTGGCGCGGGG 17367
Qy 766 LeuGlnLeuLeuAsnGlyTyRgLyGlnSerGluSer---SerileCysPheAlaSer 784
Db 17368 CGCGCGGTGTTCACATCTACGCGCCCAAGAGCGCACCTGTCTCGTCCGCTG- 17421
Qy 785 AsnMetSerThrGluProAsnAsnMetGlyArgAlaVal----- 797
Db 17422 ---CACCGCGTGCACCGCGGGCGCGCGGCGCGAGTGCCTCGGACCGCGGTGCC 17478
Qy 798 GlyAlaHisSerTrpValIleAspProAsnAspIleAsnArgLeu-----ValProIle 815
Db 17479 AACACCGGTTTCATGTCATGCTGCAC-----GAGCGGCTGGCGGTGCTCGGCT 17526
Qy 816 GlyAlaValGlyLeuValIleGluSerProGlyIleAlaArgAspTyRileValPro 835
Db 17527 GGGGTGACCGGCGAGCTCTACATCGCGGTGGCGGCTGGCGCGGCTACCTGGG-CCG 17585
Qy 836 ProProGluLysSerPro-PhePheThrAspIleProSerTrpTyRProAlaAsnTh 855
Db 17586 CCGCGACCTGACCGCGGAGCGGCTGTCGCGGAC-----CCGTCGGA-- 17628
Qy 855 rPheProAspGlyValAlaLysLeuTyRArgThrGlyAspLeuAlaArgTyRAlaSerAspG 875
Db 17629 ---CCGCGCGGATCCCGCTCTACCGCACCGGAGCTGATCGCGGACCCCGCGAGG 17684
Qy 875 ySerIleValCysLeuGlyValArgIleAspSerGlnValIleArgGlyGlnArgValG 895
Db 17685 GCGGCTGAGATTCGCGCGGCGGCGGCGGACACAGTCAAGATCCGCGGCTACCTGCGA 17744
Qy 895 uLeuGlyAlaIleGluThrHisLeuArgGlnGlnMetProAspAspLeuThrIleValVa 915
Db 17745 GCCCGCGAGTGAAGAGCGCACCTGCTGGCGAG---CCGCGCGTCCGCGAGGCGGTGCT 17801
Qy 915 lGluAlaThrLysArgSerGlnSerAlaAsnSerThrSerLeuIleAlaPheLeuIle-- 934
Db 17802 GATCGCC---CGGAGCAGCAGCACCGGCGCACAGCGGTGCTGCTCATGTGCTGACC 17855
Qy 935 ---GlySerSerTyRArgIleAsnArgProSerAspAlaHisIleLeuAspHisAspAl 953
Db 17856 GAGCGGGAGC-----GGAACCGCGCGGAAACGCGCGCTGCTGCGC----- 17898
Qy 953 arThrLysAlaIleAsnIleLysLeuGlnGlnValLeuProArgHisSerIleProSerPh 973
Db 17899 -----GCCCTGGGCGGCGCACTCCGCGCTACATGGGCGGTGCGC 17939
Qy 973 eTyRlIleCysMetLeuGlnLeuProArgThrAlaThrGlyLysIleAspArgAlaGly 993
Db 17940 CCTGTACACCTGCGCGAGCTACCGCTGAGCACCGAGCGGCAAGGTGCATGTGCGGGGCT 17999
Qy 993 uArgIleMetGlyLysAspIleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAl 1013
Db 18000 G----- 18000
Qy 1013 aProAlaProIleProValPheAlaAspThrAlaAlaLys----- 1026
Db 18001 -CCGCGACCGGATCCGCGCGCGGCGGACCGCGAGCGATCCCGCGCGCACCCCGAC 18059
Qy 1027 -----LeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAs 1043
Db 18060 GGAAGAGCACTGGCCCTCATCTGGGTGAGCTGCTGGGTGCTGCA-----CACGTGCG 18113
Qy 1043 nValGlyAlaThrPheGluLeuGlyLysAsnSerIleThrAlaIleLysMetValAs 1063

Db 18114 CGTGAAGACAACTTCTTCACCTCGCGCGGAGCTCCATCAGACCGCTGGGTTGATGTC 18173
Qy 1063 n---MetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTyRglnHisProTh 1082
Db 18174 GCGGATGGGCGGCGCTTCGTTGAGACGTCTACACCGCGGACTTCTTGACGCCGCCAC 18233
Qy 1082 rLeuAlaGlyIleSer-----AlaVal 1089
Db 18234 CATCGCGCGCTTCCGAGCGCTAGAGAAAGATCTGGCGCATGTGGAAGAAGCGT 18293
Qy 1089 lValLysGlyAspProLeuSerTyRThr----- 1098
Db 18294 CGAGGGCGGCGC-CTATGACAGCTGTGAGCGGACACCGCGACAAACCGAACAC 18352
Qy 1098 ----- 1098
Db 18353 CACCGCGCTGCGCTGCGCGAGCGCACCGCGCGCTGCGGCGCATGTGAGAGAGCTGCT 18412
Qy 1099 -----LeuIleProLys 1103
Db 18413 GCGCGCGCGCTGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 18472
Qy 1103 rThrHisGluGlyProValGluGlnSerTyRserGlnGlyArgLeuTrpPheLeuAspG 1123
Db 18473 CGGCGACAGAGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCATGTA 18532
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Db 18533 GCTCGAACCGGAGAGCAACAGTACCAACCTGCGCGCTGCTGGGTGGCGCGGACCT 18592
Qy 1143 lAsnValAspAlaLeuAspArgAlaLeuAlaIleGluGlnArgHisGluThrLeuAs 1163
Db 18593 GAGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 18652
Qy 1163 gThrThrPheGluAspGlnAspGlnValGlyValGlnIleValHisGluLysLeuSerG 1183
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Qy 1183 uGluMetLysValIleAspLeuLysSerAspAspLeuAspProPheGlu----- 1199
Db 18713 ACCGCTGCCCTGTGCTGCTGCGCGGAGAGAGCGGAGCGGAGCGGAGCGGCTGCG 18772
Qy 1200 ---ValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTrpAr 1218
Db 18773 GACCTGTCTCAGTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCG 18832
Qy 1218 gAlaThrLeuLeuArgLeuGlyLysAspAspHisIleLeuThrIleValMetHisIle 1238
Db 18833 GGGCGAGCTGATCGCGCTGGCGGCGGCGAGCAACATGCTCGCGCTGCGCGCATCAT 18892
Qy 1238 eIleSerAspGlyTrpSerIleAspValLeuAspArgAspLeuAsnGlnLeuTyRserAl 1258
Db 18893 CGTACCGAGCGGCTGCTGATGGCGGTGCTCACCGGAGGACCGCGCACCTACAGCGCGC 18952
Qy 1258 aAlaLeuLysAspSerTyRAspProLeuSerAlaLeuThrProLeuProIleGlnTyRse 1278
Db 18953 GAGCGTGGCGGTGCGC-----GCCGTACTGCGGAACTTCGCGAGCTACCT 19003
Qy 1278 rAspPheAlaLysTrpGlnLysAspGlnPhe-----lLeuGlnGlnLysGlnLeuAs 1296
Db 19004 CGATGTGCGCGTCTGGAGAGGTACACAGCTGAGCTCGCGCGGTGCGGAGGGGCTGCA 19063
Qy 1296 nTyRTrpLysGlnLeuLysAspSerSerProAlaLysIleProThrAspPheAlaAr 1316
Db 19064 CCACTGGCGCGGAGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19123
Qy 1316 gProAlaLeuLeuSerGlyAspAlaGlyCysValHis---ValThrIleAspGlyLys 1335
Db 19124 GCGCGCGGTGCGGAC---AGCGCGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 19180
Qy 1335 uTyRglnSerLeuAspAlaPheCysAsnGlnHisAsnThrThrSerPheValValLeu 1355

| | | | |
|----|-------|---|-------|
| Dp | 19181 | CGCGGCACGCGCTTCGGAGCTGGGGCCGGGAACAGGGCCGACGCGCTTTCATGAGCGCTGGT | 19240 |
| Qy | 1355 | uAlaAlaPheArgAlaAlaHisIleTyrrArgLeuThrAlaValGluAspAlaValIleGlyTyr | 1375 |
| Dp | 19241 | CGCGCGCGATCCAGCTGCTGCTGCTGTCGCGCTGTGCGGGCAGCGGGAAATCGCGGTGGCAC | 19300 |
| Qy | 1375 | rProIleAlaAsnArgAsnArgProGluLeuGluAspIleIleGlyCysPheValAsnThr | 1395 |
| Dp | 19301 | CGCGCGGGCGGGGGCGGGCGGGACCGAGACCGAGAAATCGATGCGCTTTCGTTCACAA | 19360 |
| Qy | 1395 | rGlnCysMetCysArgIleAsnIleAspHisIleAspThrPheGlyTyrIleuIleAsnGlnVal | 1415 |
| Dp | 19361 | TCTGGATCTCTGGCTCCCGGATTCATGAGACCGCGGTGTTTCACCGACCTCTCGGGCGGT | 19420 |
| Qy | 1415 | lLysAlaThrThrThrAlaAlaPheGluAsnGluAspIleProPheGluArgValIleAsn | 1435 |
| Dp | 19421 | ACGGCGCAACGGTCTCTGGACGCGCTTCGCCACAGAGATGTCGCTTCACAGGGGTGTCGA | 19480 |
| Qy | 1435 | rAlaLeuGlnProGlySerArgPheLeuSerSerThrProLeuAlaGlnIleuIleAsnAl | 1455 |
| Dp | 19481 | GGCGCTCGATTCG---GAGCGGACCTCACCGCGCGCTGGCGGAGGTGCGGTGAA | 19537 |
| Qy | 1455 | aValHis-----SerGlnuAspLeuGlyArgPheGlyPheGlnGlyLeuGln | 1472 |
| Dp | 19538 | TCTCCACAACACCCCGCGGACCCGACAGAGAGCTGCCCGGGCTGG-----ATCGA | 19588 |
| Qy | 1471 | uSerValProValProSerIleuValTyrrThrArgPheAspMetGluPheHisIleuPheGln | 1491 |
| Dp | 19589 | GGAGATGCGCGCGCGCGGTGTTCGCG---TCCAGCATGAGACTCTGCTTGATTCACCGA | 19645 |
| Qy | 1491 | ngluThrAspSerIleuLeuGlySerValaAsnPheAlaAspGluLeuPheGlyMetGluThr | 1511 |
| Dp | 19646 | GCGGACGACGACCGGTGTCAAGAGGACCTTCACATCAACACCGAGATGTTGGCGGGACCGC | 19705 |
| Qy | 1511 | rValGluAsnValValArgValPhePheGluIleLeuArgAsnGlyLeuGlnuSerSerArg | 1531 |
| Dp | 19706 | CGCGCGCGGATGGCGCGGACGTCGTCACCTGCTCGAGAGACTACCGCGCGCGCGC | 19765 |
| Qy | 1531 | gThrProVal-----SerIleLeuProLeuThrAspGlyIleValThrLeuGlyLeu | 1548 |
| Dp | 19766 | GGTCCCGGTGGCCGGGCTGGCCGCTGCTGGCGCGCGCGGACGACCTCGGGGTGACCGAGGA | 19825 |
| Qy | 1548 | AlaAspValLeuAsnAlaIleuHisValAspTyrrProArgGluuSerSerLeuAla---As | 1567 |
| Dp | 19826 | GTGG-----CCGACCTCGGGGCGCGCGCGGGGACCGCGGATCCGACCGGGA | 19870 |
| Qy | 1567 | pValPheGlnThrGlnValSerAlaTyrrProAspSerLeuAlaValAlaAspSerSerCys | 1587 |
| Dp | 19871 | GTGTGTGGCGCGGAGGTCGGGAGACCTCGATGAGGAATGGCTGTGTCCGACGAGGA | 19930 |
| Qy | 1587 | sArgLeuThrTyrrThrGluLeuAspArgGlnuSerAspIleLeuAlaGlyTyrPheuArgArg | 1607 |
| Dp | 19931 | GACCTCAGCATGTCCAGAGCTGGACCGGCGGTATCAACCAAGTCGGCGCGCTGCTACTGGC | 19990 |
| Qy | 1607 | gArgSerMetProAlaGlnThrLeuValAlaValPheAlaProArgSerCysGluThrIle | 1627 |
| Dp | 19991 | CCGGGGTGGCGGGCGGAGACGCTGTGGGGGTGGCGGCTGCCCGCTCCGCGCAATGGT | 20050 |
| Qy | 1627 | evaAlaIlePhePheGlyValLeuIleuValaAsnLeuAlaTyrrLeuProLeuAspValArgSe | 1647 |
| Dp | 20051 | CACGGCGCATCTCTGGCGATCCAGAAAGACCGGATGGCGGCTATCTCCGCTGGAACCGAAGAG | 20110 |
| Qy | 1647 | rProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyProThrIleValLeuIle | 1667 |
| Dp | 20111 | CCCCGGGAACGCAACGGCTGATGATC----- | 20138 |
| Qy | 1667 | egLysIleAspThrAlaProProAspIleGluValThrAsnValGluPheValArgIleArg | 1687 |
| Dp | 20139 | -----GAGGACGCCCGCGCGCTGAGTGGTACCTCGCGGGGTTC----- | 20180 |
| Qy | 1687 | gAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluVal-----Ile | 1701 |
| Dp | 20181 | -----GCGACCGCGCGGAACTGGCGCGCCCGCACTGTTCT | 20218 |

[illegible]

| | | | |
|----|-------|---|-------|
| QY | 2032 | ucglttrpglnasphrisphnegluserglmettyrseraspile----- | 2046 |
| Db | 21254 | ggnetctcccgagcagatggtgctccctgcgtttctgctgacccgctgacccgctgcctgaa | 21313 |
| QY | 2047 | -----glglnuleaspproserthrillegltyseraspphetylgltyrthrserme | 2064 |
| Db | 21314 | cgccacagcgcaaggttcacccgggggctg----- | 21344 |
| QY | 2064 | ctyraspglyserglnlleasppheasppglumethlsglturpleu----- | 2079 |
| Db | 21345 | -----cccgacacccgacatccggcgccgacgagggacgagcccgatgcggcgacaccc | 21400 |
| QY | 2080 | -glglturthrthrarthrleuthlsapaaanaagserleuglyasnavalleuglnillegl | 2099 |
| Db | 21401 | ggcggagagacagctgtgcggcgcatctgtgtgagagtgctggcg--gtcacggacatccg | 21457 |
| QY | 2099 | yththglyserglymetlileuupheanleuaspserargleuglusertyrvalglyle | 2119 |
| Db | 21458 | cgctgagagacacattcttcacacctcgccggcgacattcatcttagccttagtggtggc | 21517 |
| QY | 2119 | ugluproserargseralaalaalaphavalanlyalyathr-----gluseril | 2136 |
| Db | 21518 | gcgggacccggagcgccgcatcgcgctgcgacccgacagacacattcttcggcgacacat | 21577 |
| QY | 2136 | epproserleuualaglyualyalaivsvalglnval-----glythrslah | 2151 |
| Db | 21578 | cgccgacatcttgcggcgccgacgcgctgcggcagacccgacccgscgacgctgcggcga | 21637 |
| QY | 2151 | raapllleglvglnvalasppheuthisproaspphevalvalleuanservalillegl | 2171 |
| Db | 21638 | cgac--ggcccggtcacccggcgagctggcg-- | 21665 |
| QY | 2171 | ntyrpheproserserglutyrleualaglnllealasppthrleuilehisleuproas | 2191 |
| Db | 21666 | -----ctcacccc | 21673 |
| QY | 2191 | nvalglnargllephethe-----glyasppvalargserglnalathrasnglni | 2208 |
| Db | 21674 | catccacacactgtgtttcttcaactccttcggcgacgctgacagcttcaacacatgcgt | 21733 |
| QY | 2208 | sphleuvalalalarglalallethsrleuaglylyasnaalaththlyaspparalr | 2228 |
| Db | 21734 | gtractctg----- | 21740 |
| QY | 2228 | gglntlymetalaglnleuaglnuaspmetglnuglnleuvalglnproalapheth | 2248 |
| Db | 21741 | -----gacgtgcggagggcgcccgacatcc-----ccggcg----- | 21770 |
| QY | 2248 | ethsrleuulyasppargpheproglyleuvalglnuhsvalglnlleuproluysas | 2268 |
| Db | 21771 | -----ctgcggcgcccgacactggtgcggcgctgacccgaacgacagcgactg-----cg | 21817 |
| QY | 2268 | nmetglnalvalasnuglnleuseralatyragtyrvalalavalvalhlsvalargl | 2288 |
| Db | 21818 | gcttcggcgccgtracccagagacgggacgtagcgagctgcacacacgcccggcgagacgg | 21877 |
| QY | 2288 | yserleuglyasppgluenuvalleuprovalglnlyaspparptrilleasppheglnal | 2308 |
| Db | 21878 | tcaactcttcgaacacactcatctgtctccggcgctgcggccgac----- | 21920 |
| QY | 2308 | aaenglnleuasnuglnlyserleuglyasppheuleuulysseraserapalalileme | 2328 |
| Db | 21921 | -----gaccacagacgcccgcgactgc-----gaccacagacgcccgcgactgc | 21940 |
| QY | 2328 | talavalserlyslleproheglnullethralaphnegluraglnvalvalaserie | 2348 |
| Db | 21941 | ggcgccg--g--gtcgacgcgcgcgacacgg----- | 21965 |
| QY | 2348 | uasnsersasnilleaspglturpglnleuserthrilleargssersalaglnlyaspe | 2368 |
| Db | 21966 | -gacttccggcgtgcgagggggcgcgctgcggggcgccgctttacacctgcggcaccc | 22022 |
| QY | 2368 | rserleuservalproaspphearglleargly----- | 2380 |

| | | | | |
|----|-------|--|---|-------|
| Db | 22025 | C-----CGGCGCGCCCGGCTGTA | CTTCGTCGGCGGACCACTCTGATGACGCGATGTC | 22077 |
| QY | 2381 | ----- | -GluValSerSerAlaArgLInTPSerGln----- | 2386 |
| Db | 22079 | CTGGCGGATCTCTGTCGGGACCTCGAGGACCGGCTACCGGCTGGCGGAGCGCGGCG | 22133 | |
| QY | 2387 | ----- | -GluValSerSerAlaArgLInTPSerGln----- | 2396 |
| Db | 22139 | GATGCACTGGGCGGCGGACCACTCTGTCGGCGACTGTCGGCGGCTTCGGCGCA | 22198 | |
| QY | 2397 | ----- | -AsnGluValLeuAspAlaValAlaPheHisSerCysCysSerGlnGlyArgThrLe | 2414 |
| Db | 22199 | TGTCGGGACCGCGCGCTTGACCGC | 22222 | |
| QY | 2414 | uValAsnPheProThrAspHisHisLeuArgGlySerAspLeuThrAsnArgProLe | 2434 | |
| Db | 22224 | -----GAACTGCGG----- | -TACTCGAAGGCG----- | 22244 |
| QY | 2434 | uGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeuArgSerLeuLe | 2454 | |
| Db | 22245 | ----- | -GTAACGAGCGCGCGCGCGCAAGCCCG | 22270 |
| QY | 2454 | uProSerTyrMetLeuProSerAsnIleValAlaLeuAspLeuMetProLeuAsnAlaAs | 2474 | |
| Db | 22271 | CCCG----- | -----CTCCCGGTGACACCGG | 22291 |
| QY | 2474 | nGlyLeuValAspArgIleGluLeuSerArgAlaAlaValValProLeysGlnLInTh | 2494 | |
| Db | 22292 | CGGCGTCCCGGACCGC----- | -CAGGCGCGCCGAGAGAGACCCCGCGAGAAAC | 22333 |
| QY | 2494 | rAlaAlaProLeuProThrPheProIleSerGluValGluValIleLeuCysGluGluAl | 2514 | |
| Db | 22340 | CGCGGGGTGCGGCCGCGAC----- | -GTCTCGGTACAGCTGTCGCGCGCGG | 22384 |
| QY | 2514 | aThrGluValPhe----- | -GlyMetLeuValAspIleThrAspHisPhe | 2528 |
| Db | 22385 | CACCGAGCGCTGTCGGGAGGTGTCGCGAGGCTTACCGACCCAGATCAACACTCTCT | 22444 | |
| QY | 2528 | ePheAsn----- | -LeuGlyGlnHisSerLeuLeuAlaTh | 2539 |
| Db | 22445 | GCTACGCGCGCTGGGCGGCGTGTGACCACTGGCGCGCGCGGAGCGGGTGTGATCCG | 22504 | |
| QY | 2539 | r----- | -LysLeuIleSerArgIleAspGlnArgLeuLysVal-- | 2551 |
| Db | 22505 | CCTGAGAGGACACGCGCGGAGAGCTCTTGACAGAGTGAACCTCACCGGCACCGTCGG | 22564 | |
| QY | 2552 | ----- | -ArgIleThrValLysAspValPheAspHis----- | 2561 |
| Db | 22565 | CTGGTTACCACTCTTCCCGTCCGCGCGCGGATGTCGGCGCGGACTGGGGAAAC | 22622 | |
| QY | 2562 | ----- | -ProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeu----- | 2575 |
| Db | 22625 | GGTCTCAAGAAGGCTCAAGAAACAGCTGCGGCGGGTGTCCCAACAGGACTCGGCATGG | 22688 | |
| QY | 2576 | ----- | -GlyLeuGlnGlnProValSerAspGly----- | 2584 |
| Db | 22685 | CGCGCTGGTCATCTGGCAGAGGCCAACCTCCCTTGAGAGACGTCGGAAGCCGAGGT | 22744 | |
| QY | 2584 | ----- | ----- | 2584 |
| Db | 22745 | CAGCTTCAACTACTCGGCGAGTGAAGTTCGCGCGACCGGACCGGCGCTGCGCGCGC | 22804 | |
| QY | 2585 | ----- | -GlnGlyGlnAspArgSerAla-----HisMetAlaProArgThrGln | 2598 |
| Db | 22805 | CATCTCAACAGGAGGCGCGCGAGCGCGCGCGCGCGACACCGTGGCAGCTGTGGA | 22866 | |
| QY | 2598 | uThrGluAlaIleLeuCysAspGlnPheAlaLysValLeuGlyPheGlnValGlyLeTh | 2618 | |
| Db | 22865 | GATCAACGCGGCGTGC----- | 22880 | |
| QY | 2618 | rAspAsnPhePheAspLeuGlnGlyGlnHisSerLeuMetAlaThrLysLeuAlaValArgIle | 2638 | |

Db 22881 -----ACGGCGCGCGCTGGAGTTCCTCACTGAGCACTCGGTGAAC-- 22922
Qy 2638 eglyHsArgLeuAphThr-----ValSerVallyAs 2650
Db 22923 -CGGACCGCGGAGAGACCGTCCAGACCGCTCGCGCGGCTTCATGACCGCGTGAAC 22981
Qy 2650 pValPheAphHs-----ProValLeuPheGlnLe 2660
Db 22982 GATCGTGGCCACATCGCGCGCGCGCTCGCGCGGCGGCAACCGCGTCCGACTCCGCGCT 23041
Qy 2660 uAlaIleAlaLeuAspMetLeuValGlnSerLeuThraGlnIleValGly---GlyAr 2679
Db 23042 GGGC---GGCTTCGAC-----CAGGCCACCGTGCACAGATCCCGCGACGCGCG 23089
Qy 2679 gGluMetAlaGluTyrSerProPheGlnLeuLeuPheThrcGluAapProGluGluPhe 2699
Db 23090 C----- 23090
Qy 2699 tAlaSerGluIleLysProGlnLeuGluLeuGlnIleIleGlnAapIleTyrProse 2719
Db 23091 -----ACGGTCGAGGACATCTACCGCGCT 23113
Qy 2719 rThrGlnMetGlnLysAlaPheLeuPheAphHsThrThraAlaArgProArg---Proh 2738
Db 23114 CACCGCGCATCGACGCGGACATGCTCTTCACGCGCTGAGCGAGTCCGAGCGCAACCGCTA 23173
Qy 2738 eVal---ProPheTyrIleAapPheProSerThrSerGluProAapAlaIleGlyLeuI 2757
Db 23174 CACCGGCGACTCGCGCGCTCGCGCGTGCAGCGCATCCGACCGCGGGGCA-----CTGGC 23227
Qy 2757 eLysAlaCysGluSerLeuValAenHsLysAapIlePheArgThryAlaPheAla---GI 2776
Db 23228 CGCGGCGCTGCAGCAGCGTCCGCGCACCGACCCCGCGCTGCGACCCGCACTCGTGGCA 23287
Qy 2776 uAlaSerGlyGluLeuTyrGlnValValLeuSerCysLeuAapLeuProIleGlnValI 2796
Db 23288 GAGCGTGCAGAACCCCTTCAGGTGGTGACGCGCGCGCGCTGCGCGGACCCATCA 23347
Qy 2796 eGlu-----ThrcGluAapAenIleAenThralaThraGlnLysPheLeuAapGI 2812
Db 23348 CGACCTGCGGCTCCCTGACCGAGCAGAACCGGACCGCGCTGAGCGGCGGCGGCG 23407
Qy 2812 uPheAlaLysGluProValArgLeuGly---HisProLeuIleArgPheThrIleIle 2831
Db 23408 GCGCGAGAGACCGTCACTCGATCTCGCGCTCGCGCGCGCTGCGCGTGAACCCCTGCG 23467
Qy 2831 sGlnThrLysSer---MetArgValIleMetArgIleSerHisAlaLeuTyrAapGlyLe 2850
Db 23468 GCTCAGCGACGCGCGCTCCAGATGTTCTGGAAGCTCCGACCACTCTGATGAGCGCTG 23527
Qy 2850 uSer-----LeuGlnHsValValArgLysLeuHsMetLeuTyrAenGlyAr 2866
Db 23528 GAGCTTGGCGGCGGTGCTGTCGAGGTGTGCGCGCCAGTATACCGCGGTGACCGCGGCC 23587
Qy 2866 gSerLeuLeuProPro-----HisGlnPheSerArgTyrMetGlnTyrThralaAap-- 2883
Db 23588 CCGGTGCGCGCGCGCGCGCGCGCGCTACCGGACTATGTCGCTGCGTGGCGGAGACA 23647
Qy 2884 -GlyArgGluSerCylHisGlyPheTArgAapValIleGlnAsn-----Th 2899
Db 23648 GAGACCGCGCGCGCGCGCGCGCGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGAC 23707
Qy 2899 rProMetThrIleuSerAapAapThryAlaAapGlyAenAapAlaThrcyLysAl 2919
Db 23708 CCGCGTCCGCG-----TACGACCGGACGCGCGGTGAGGAGGACACACG 23746
Qy 2919 aLeuHsLysSerLysIleValAenIleProSerGlnValLeuArgLysSer----- 2936
Db 23747 CACCGGCTCTCGGTGAGGTGCGGTGACAGTCTCGCGCGGCGGTGCGGCGGCTGTC 23806
Qy 2937 -----SerAenIleIleThrGlnAlaThryAlaPheAenAlaIaCysAlaLe 2952
Db 23807 CGAGGCGCGCGCGGTGCGCGGTGACCGTCAACACCTGTGTGAGGCGCGCTGGCGAT 23866

Qy 2952 uValLeuSerArgLysSerAapSerLysAapValValPheGlyArgIleValSerGlyAr 2972
Db 23867 CTGTCTGCGCGCTGACGCGCGGCGCGGCGCGAGCTGCTCTGCGACACCGCTCCGCGCG 23926
Qy 2972 gGlnGlyLeuProValGluTyrGlnIleAapIleValGlyProCysThraAapAlaProva 2992
Db 23927 TCCCGGACCGCTCGCGCGCGCGCGCGGTGAGCGCGGTGCTTCATGACACCGTCCGCGT 23986
Qy 2992 lArgAlaHsIleGluSerSerAapTyrAen-----GlnLe 3004
Db 23987 ACCGGGACCATGACAGCGTGCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 24046
Qy 3004 uLeuHsAapIleGlnAapGlnTyrLeuLeuSerLeuProHsGluThrIleGlyPhe 3024
Db 24047 GCTGCGCGCGCTGACAGCGAGCGAGCTGCACTCCGCGACAGACAGATGCTCGCTGCG 24106
Qy 3024 rAapLeuLysArgAenCysThraAapTyr-----ProGluAlaIleThraAapPhe 3041
Db 24107 GCAGATCCAGCGC-----TGAAGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCTTCGA 24154
Qy 3041 rCysCysIleThrTyrHsAenPheGluTyrHsProGluSer----- 3055
Db 24155 CAGCATGCTGCTTGCAGAACTACCTTCAGACAGAGGATGCGCGCGCGCGCGCGCGCT 24214
Qy 3056 -----GlnPheGluGlnArgValGluMetGlyValLeuThr----- 3068
Db 24215 GACCTCGGCGAGCTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 24274
Qy 3069 -----LysPheValAenIleGluMetAapGluProLeuTyrAapLeuAla 3083
Db 24275 CTGGCGCGACGAGCTGCATCTCAACCTCGCGGTACGACCGCGATGTTGACAGAGCG 24332

RESULT 6
US-10-282-122A-31388
Sequence 31388, Application US/10282122A
Publication No. US2004029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/269,308

[illegible]

Db 733 GCACAGTTGACGGTAAACACCTTGTCGACAGCCCTGGGACCTGTTACTGCAACGCTAC 792
 Oy 295 ThrHisSerAspGluAlaLeuPheGly--AlaValThrGluGlnSerLeuProPheAsp 313
 Db 793 AGCGCGACACCGGACGATGATGTTGGGGGACCGTGGCGCGCGCGCGGATTCGAAATTCGCC 852
 Oy 314 LysHisTrpLeuAlaAspGlyThrTrpGlnThrValAlaProLeuArgValHis----- 331
 Db 853 GAGATGACAGGCTACCGTCGGCTGTTCATCAACACATCCCGCTCCGGTCCGGTTGCCG 912
 Oy 332 ---CysGlnSerAspLeuArgAlaSerAspValMetAspAlaIleSerSerTrpAspAsp 350
 Db 913 GCGCGCGAAGCGCGGTACAGCGCCAAAGCGGTGCTCAAGTACATGCTTGACCAACAACCTC 972
 Oy 351 ArgLeuGlyHisValLeuAlaProPheGlyLeuArgAspIleArgAspThrGlyAspAspGly 370
 Db 973 AACCTGCGCGACGACGACGACATCTGCTTTGGTGGATATTCACGCGTGCAGCAGGTCGGT 1033
 Oy 371 SerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySerHisValAspAsn 390
 Db 1033 AGCGGTACAGCCCTGTGTGACAGC--CTGTTCGTGTTCCGAACGCGCGCTGGAGTCC 1088
 Oy 391 -----GlyIleAspGlyPheLeuGlnGlnIleThrGlnSerSerHisAspMetProCys 408
 Db 1090 AGCGTTGGCGCCGACGCTTCCACATGAAAGTCAAGCGTGGAGATTCGGCGACGACAC 1144
 Oy 409 AsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlnSerSerGlyValLeuLeuValAla 428
 Db 1150 AACCTACCGGCTCACCGGTGGTGTACCCGGGTGAGGTCTGGCG-----CTGACACTCG 1200
 Oy 429 TyrTrpAspHisAspValIleAspSerLeuGlnThrTrpArgLeuLeuGlnIlePheGly 448
 Db 1204 TCGTATGACCAACGCGCTGTTCGACAGCGGACCATCAAGGTCTGTGCTGCTGACTTCGCG 1266
 Oy 449 HisLeuIleLysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeu 468
 Db 1264 GCTTTGTTGTCGCGCTTAGCGACAGCTGACGCGGACTTCATGCTGTGGCCGCGCGCC 1322
 Oy 469 Met-----ThrGluTrpAspArgAlaGluIleGlnSerTrpAsnSerGlnPro 484
 Db 1324 CTTCCTGGCACTGCCCGGAGGTGCCGACCGCGCTGCCCGACGCTTACGACGACGAGCTAT 1386
 Oy 485 LeuGluValGlnAspThrLeuIleHisIleGluMetLeuValValSerHisSerPro 504
 Db 1384 GCGCGGCTGTTCGACGCC-----ACTGTGACGCTGTCGCGG 1411
 Oy 505 ThrTrpThrAlaIleGlnAlaTrpAspGlyAspTrpThrTrpSerGlyLeuAspAsnVal 524
 Db 1420 CAACGTGCGCGGCGCGCTTGCGACGAGGCGGTGAATGAGACTACGCGGAGTATCAACGG 1477
 Oy 525 SerSerArgLeuAlaValHisIleLysSerLeuGlyLeuArgAlaGlnIleAlaIleIle 544
 Db 1480 GCGCACACCGCTGGCGGATGTACTGACGAGGCAATGGTGTGAGCGTGCACAC--CTGGATC 1533
 Oy 545 ProValTrpPheGlnLysSerTrpAlaIleAlaSerMetLeuAlaValLeuLysSer 564
 Db 1537 GCTGTGCTCGGTAGACGCTGACTGTGCTGTGCTGGGACGATGTGTGGGTGTTCCAGCGG 1599
 Oy 565 GlyAsnAlaPheThrLeuIleAspProAsnAspProProIleArgThrAlaGlnValVal 584
 Db 1597 GGTGCGGATTTCTGCTCGGTGATCGTTCGCTTGGCGGTGCGCGCTGGCGATGTGCTG 1655
 Oy 585 ThrGlnThrArgAlaThrValAlaLeuHisSerLysValLeuHisArgGluThrValGlnLys 604
 Db 1657 CGCTTGACCCACGCGCGGTGTGTGTGCGATGAG----- 1697
 Oy 605 LeuValGlyArgCysValValValAspAspGlnLeuGlnSerValSerAlaSerAsp 624
 Db 1693 -----CATGTGCTGGGCTTGGCCCAAGGATGCTGAAAGGTTCCAAACGCGCGCG 1744
 Oy 625 AspPhe-----Ser 627

Dh 1744 ACCTTTGGTCTGGAGCAGGTGCAGCACCGCCGCGGACAGATGTCACCTG 1803
Qy 628 SerLeuThrIysSerGlnAAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAsp 647
Db 1804 CCGCATCAATCCGCGCAAGCTGCTGGCTTACCTATCTTCACTTGTGTTGACCGGGTGG 1863
Qy 648 ProIleGlyIleMetIleGluHisArgAlaPheSerSerCysAlaLeuLysPheGlyAla 667
Db 1864 CTTAAAGGCGTCAATGCTGCAACAGGCGGCATGCTCAACAAACAGCTGACGAAGCTACCG 1923
Qy 668 SerLeuGlyIleLeuSerAspThrArgAlaLeuGlnIleGlyThrHisAlaPheGlyAla 687
Db 1924 TACTTGGGCTGCGGGCAGCGAGCATGATCGCCCAAGCGGCTTGACAGAGCTTGATATC 1983
Qy 688 CysLeuLeuGluIleMetCThrThrLeuIleAsnGlyGlyCysVal----- 702
Db 1984 AGCGTCTGGCAATTGCTGACGGCGCCCTGTGTGTGGTCCGCGGTGAATCTTCCCGAC 2043
Qy 702 ----- 702
Db 2044 GCCGTGCGCAGATCCGACAGCGCTGTCACAGGTCGAGCGCACGGCGTGACCATC 2103
Qy 703 -----CysIleProSerAspAspAspArgMetAsnSerIleProSerPheIleAsnArg 720
Db 2104 CTGGAATGCGTACCGGC-GATGAT----- 2126
Qy 721 TyrAsnValAsnTrpMetMetAlaThrProSerTyrMetGlyThrPheSerProGluAsp 740
Db 2127 -----CAGCGCATGCTGMACTGCCAAGCCGG--CA 2157
Qy 741 ValProGlyLeuAlaThrLeuValLeuValGlyGluGlnMetSerSerSerValAsnAla 760
Db 2158 TTGCCACGCGCTGCTACCTGCTCACACCGCGCGCAACCATGTCAACCGCACTGCGCCGC 2217
Qy 761 IleThrAla-----ProLysLeuGlnLeuLeuAsnGlyTyrGlyGlnSerGluSer 777
Db 2218 CGCGTGGCGAGCGCTACCAACAGGTGMACTGTCAACCGCTACCGCGCGGAGAGTGT 2277
Qy 778 SerSerIleCysPheAlaSerAspMetSerThrGluProAsnAsnMetGlyArgAlaVal 797
Db 2278 TCCGACGACGTCGGCGCTGACCGGTCGTGATGATACCAACAGCTCCGTGCACCTGCCATC 2337
Qy 798 GlyAla-----HisSerTrpValIleAspProAsnAspIleAsnArgLeuValPro 814
Db 2338 GGTGTCGCCGACCGGACCAACCGCTCATGTCTCAACGACCTGCTGCAACCGCATCCG 2397
Qy 815 IleGlyAlaValGlyLeuValIleGluSerProGlyIleAlaArgAspTyrIleVal 834
Db 2398 GCCCGGGCCACCGCGGATGTCATGTGACCGCGGTAGGTGTCCGGCGCGGTTACCTTGGC 2457
Qy 835 ProProProProGluLysSerProPhePheThrAspIleProSerTyrTyrProAlaAsn 854
Db 2458 GATCCGGTGGCGACCGGATGAGCTTTGTCCCGAT-----CCGTTGCC 2502
Qy 855 ThrPheProAspGlyAlaLysLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAsp 874
Db 2503 AGCCGCGCGG---GGTGAAGCGCTGTACCGCAGTGGCGCACCTGGCGCACGTTGGCGCGAT 2559
Qy 875 Gly-----SerIleValCysLeuGlyArgIleAspSerGlnValIleArgGlyGlnArg 893
Db 2560 GGGGACAGCCCTGAGTATGTGGGGCGCGGCACTTCCAGGTGAAGATCCGGGGCTTACCG 2619
Qy 894 ValGluLeuGlyAlaIleGluThrHisLeuArgGlnGlnMetCProAspAspLeuThrIle 913
Db 2620 ATGAATCGGGGCAAAATCGAATCGCGCTGTGCGCATGAAGGTGACACAGCGCGGTG 2679
Qy 914 ValValGluAlaThrLysArgSerGlnSerAlaAsnSerThrSerLeuIleAlaPheLeu 933
Db 2680 GTGGTGGATCGG---CAGATGGCGCGGTGCAAGACGATGTGGGCTTACTCG 2727
Qy 934 IleGlySerSerTyrPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAlaAspAla 953
Db 2728 GTGGCC-----CGCATGCTCGGTCGCGCGGACCGCGAGATG 2763

Qy 954 ThrLysAlaIleAsnIleLysLeuGlnValLeuProArgHisSerIleProSerPhe 973
Db 2764 CGCAGCGCTGTGGCCGACATCTGTGCGGCGAGCTTCCGGGCTACATATGTCGCGGACATG 2823
Qy 974 TyrIleCysMetLeuGluLeuProArgThrAlaThrGlyLysIleAspArgAlaGlyLeu 993
Db 2824 TGGGTGGCTTCACAGCCCTGACCGCTGACCTGACCAATGGCAAGGTTCACCGCAAGCATTTG 2883
Qy 994 ArgIleMetGlyLysAspIleLeuAspLysGlnThrGlnIleAlaIleValGlnGlnAla 1013
Db 2883 ----- 2883
Qy 1014 ProAlaProIleProValPheAla-----AspThrAla 1024
Db 2884 CCGGACCGGACCCGAGCACCGCTTCAGCGACGCTACAGCGGTACCGACCGGAAACGTGTTCAG 2943
Qy 1025 AlaLysLeuHisSerIleTyrPValGlnSerLeuGlyIleAspProAlaThrValAsnVal 1044
Db 2944 CAGCAATTGGCGCAGGTCTGGAGCGAGGTCTGGGCGTCGAG---CGGATCAGTCTG 2997
Qy 1045 GlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLysMetVal---Asn 1063
Db 2998 GCGATGACTTCTTCAAGCTGGGTGGGCACTCCCTGCTGTGTGTCAGCTGTGGCGCT 3057
Qy 1064 MetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTyrGlnHisProThrLeu 1083
Db 3058 GTGGCGCGCAACTGGGCAATCGAAGTCAGCTCGATCGTGTTCGACACCGGACCTTG 3117
Qy 1084 AlaGlyLysSer-----AlaValValLysGly-----AspPro 1094
Db 3118 GAGAGCTTCAGCAGCGCGCTGCGAGTCGTCGAAAGGCGAGGCGCGCTGATTCAGAACGAG 3177
Qy 1095 LeuSerTyrThrLeuIle-Pro-----LysSerThr----- 1104
Db 3178 TTGGCTAAATCTTGGCGCGCTTGAAGACGTCTTACTGACAGAGATCGACGACTTGACC 3237
Qy 1104 ----- 1104
Db 3238 CAGTAGCGTCTGCGGCGCGGTATGACCGGCGCGGCTGTCAACTTCAGTACACCCAG 3297
Qy 1105 -----HisGlu----- 1106
Db 3298 AGCCGCGACCGTCCGCGCTCTTCATTGTTGGCAGCATCATGAGCTGTGCGGGCTG 3357
Qy 1106 ----- 1106
Db 3358 GCACGTTCCGACGCAAAAGACCGGTGCTGTGAGAGATGTTCAATGCAAGCATTTGCT 3417
Qy 1106 ----- 1106
Db 3418 CGATTCGAGATCACTGTGTCCGGAGCGCAAGCCCTGGCGCGCTTGCTCAAGCA 3477
Qy 1107 -----GlyProVal 1109
Db 3478 GCAAGGTGTCACCTTACGCGGTGACCGCATTTTCGCCGCGACCCGCGCAACCCGAC 3537
Qy 1109 IGlunIleTyrSerGlnGlyArgLeuTyrPheLeuAspGlnLeuAspValGlySerIle 1129
Db 3538 CCGGATCTTCAAGCGCGAGAGCGGACAGTGTCTTCTGCAATCGAACCCCGCCAGCGG 3597
Qy 1129 uTPTrpLeuIleProTyrAlaValArgMetArgGlyProValAsnValAspAlaLeuArg 1149
Db 3598 AGCCTACACATCGATGCGCGGCTGCGACGTGACAGGGCGGCTGGATATCAGAGGCTTGC 3657
Qy 1149 GATGAlaLeuAlaIleLeuGluGlnArgHisGlnThrLeuArgThrPhe---GluAs 1168
Db 3658 CCGTGCCTGCGACGCGTGTATCCAGCGCCACGAGTGTGCGACCACTGGCGACCAAGA 3717
Qy 1168 pGlnAspGlyValGlyValGlnIleValHisGlyLysLeuSerGluGluMetLysValIle 1188
Db 3718 CAGCGACCGGCTG---GTGCAATCATCAACCCGCAATGCGGTGAGTTCGCTCATCGA 3774

Db 5758 AGGGCATGTTGGAACTTACGAGCCGACCCAAACCATCTGCTGGGTTATCGAA 5817
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 Db 5818 GGTACCGACGACGGCCGAGGTGTGGTGGGCAAGCCGATCGGC-----AATAC 5865
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 Db 5866 CACTTCCACGCTCTCCAGCCGCCGATTGCGACGCGGTCCGCTGGCGCTGAGCGCGCAACT 5925
 QY 1911 uvalvalithrglyasrglyleuvalaargglytyrserasrlyp---alaleuargluas 1930
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 QY 1930 natrgheval-----hisilethrvalaamrprlnthrvallysalaty 1945
 Db 5986 GCGCTTCATCCCAACCGGACGCGGCAC-----GGCGCGCTGA 6024
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 Db 6181 ----- 6181
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 Db 6182 -----GACGTCAAGGCGG----- 6193
 QY 2045 pilleglyluileaprosethrilleglyserasrphelysglytrpthrsermetty 2065
 Db 6194 -----CCGCTGGCGACGACCTGCGGATATCGCGCTA 6231
 QY 2065 raarglyserglnleapheasrplumechisglutrpheuglyglutthrthargth 2085
 Db 6232 CGATGCCAGCTGCTGCAGGCTGAT----- 6256
 QY 2085 rleuHiasrpaamargserleuuglyaaenvalleuuglileglythrcllyserglymetil 2105
 Db 6256 ----- 6256
 QY 2105 eileupheasrleuamrserargleuglusertyrvalglyleuugluproserargseral 2125
 Db 6256 ----- 6256
 QY 2125 aalalaaarhevalaamlysalathrgluserlleproserleuualaglylualalyva 2145
 Db 6256 ----- 6256
 QY 2145 lglinalglythraltharprilleglylnvalasrprleuHiasrproasrleuvalva 2165
 Db 6256 ----- 6256
 QY 2165 lleuamrsevalilleglnlytrpheproserseglutryleuualagluileaalrth 2185
 Db 6257 -----GCCAGGTTCAGGAAC 6273
 QY 2185 rleuHiasrleuoproamvalglinarglylerphepheglyasrvalaargserglnalath 2205
 Db 6274 CCTG----- 6277
 QY 2205 raenglnHiasrheleuualaalarglalleHieThrleuuglyluyaaamlathtlyuav 2225
 Db 6277 ----- 6277

QY 2225 raervalaargglylwevalagluileuugluamrmetglugluleuvalglupr 2245
 Db 6277 ----- 6277
 QY 2245 calaphepethrserleuylasrparprpheproglyleuvalglunHiasvalglulle 2265
 Db 6277 ----- 6277
 QY 2265 uprolyasrmetglualavalanagluseseralatyratrgtyralaalavalalini 2285
 Db 6278 -----CGCTGGCATCAAGGCCA 6297
 QY 2285 valaarglyserleuglyasrpluleuvalleuprovalglulyleasrprilleas 2305
 Db 6298 CGCA----- 6301
 QY 2305 prheglnalaainglnleuamnglnlysserleuuglyasrleuuleuylseraseral 2325
 Db 6302 -----TTGAAGTCG----- 6310
 QY 2325 aalalilemeralavalserlyleleprophegluilethralthaphegluarglinalva 2345
 Db 6310 ----- 6310
 QY 2345 lalaserleuamrseamrleaprglutrplnleuserthrileargsereralagl 2365
 Db 6310 ----- 6310
 QY 2365 ugliaasrserseueralproamrillepheargllealglyglualaglyphear 2385
 Db 6310 ----- 6310
 QY 2385 gvalgluvalisersevalaarglnttrserglnaamglyalaleuamrallalapheni 2405
 Db 6310 ----- 6310
 QY 2405 shisCysSersegllyatrgthrleuvalaamrheprothrashrhisileuargl 2425
 Db 6310 ----- 6310
 QY 2425 yseramrleuThrasharprproleuglnaargleuinaamargargllealilegl 2445
 Db 6310 ----- 6310
 QY 2445 uvalaarggluargleuargserleuuproseptyrmetilleproseramrilevalva 2465
 Db 6311 -----ATGCCGACTCATGTGCGGACCCGACCTGGTGT 6345
 QY 2465 lleuamrplymerproleuamrallaainglyllyvalasrarglygluleuserargar 2485
 Db 6346 CATTCCACGATCCCTGCACCCCAACGCGCAAGCTGACCGGACGCGTGGCG----- 6400
 QY 2485 gglalyvalvalaiprolysglnlnthrallalaproleuprothrphroillesergl 2505
 Db 6401 -GGCGCTGACCTGGCGCGCCCGCCGCGCTGACGAGCGCCGACCGCGCTGACGA 6459
 QY 2505 uvalgluvalilleucyeglnlualathrgluvalaapheglymetlyeavalasrilleth 2525
 Db 6460 AGCGCTGGCGGCGATCGGCGCGATGCTGAAGCTC-----GGGACGTTGGCTGAG 6513
 QY 2525 raerphiepheasrleuuglyllyHiasrleuuleuualathlyleuuleileserargl 2545
 Db 6514 CGACAGCTTCTGCACTGGGTGGCATCTCTGCTGCGCGTCCGACATGATGTTGGCGCGCT 6573
 QY 2545 eaerglinaarglyleuvalaarglilethrvallyuavarvalaasrhisrprovalaheal 2565
 Db 6574 GCGCCAGCACTGGCGTGAAGTGGCGCTGCGGCTGCTGAGGCGCCGACGACTGGC 6633
 QY 2565 aasrleuualaser---Valillearglnlyleuglyleuglnlnprovalaserargl 2584
 Db 6634 GGGCTTGGCGGACGGGTGGCGGCTGCGGACGAGCGGCTGCGGCTGCGG----- 6682

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 Db 6683 -----GCATCGCTGTGTGCTCCACGGGAGAG----- 6709
 QY 2604 sAaRgLuPheAlaValLeuGlyPheGlnValGlyIleThrAspAsnPheAspLe 2624
 Db 6709 ----- 6709
 QY 2624 uGlyGlyHisSerLeuMetAlaThrIlybLeuAlaValArgIleGlyHisArgLeuAspTh 2644
 Db 6709 ----- 6709
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 Db 6709 ----- 6709
 QY 2664 uAaRAsnLeuValGlnSerIlybThrAsnGluIleValGlyGlyArgGluMetAlaGluTy 2684
 Db 6709 ----- 6709
 QY 2684 rSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAlaSerGluIleTy 2704
 Db 6710 -----CCCTGCGCTGTGTATGCCAGCAAGTCAATGGGTACTGTGG----- 6754
 QY 2704 sProGlnLeuGluLeuGlnGluIleIleGlnAspIleTyxProSerThrGlnMetGlnTy 2724
 Db 6755 -----CAACTGGAGCGCGACAGCGCGCTTACACATCGCGTCCGCTGACCTTGGCCGG 6810
 QY 2724 sAlaPheLeuPheAsnHisThrThrAlaArgProArgProValProPheTyIleAs 2744
 Db 6811 GGCGCTG----- 6817
 QY 2744 pHeProSerThrSerGluProAspAlaAlaGlyLeuIleValIaCySGIuserLeuVa 2764
 Db 6818 -----GATGTGGCGCGCTGTCCAGCGCTTCCAGCGCTTGT 6855
 QY 2764 lAaHisIleuAspIlePheArgThrValPheAlaGluAlaSerGlyGluLeuTyrgInVa 2784
 Db 6856 GGCACGGCAGAAAGCCTGCGCACCTTTCGTGCAGGTGCACGGCAAAGCGCCAGGT 6915
 QY 2784 lValLeu-----SerCyLeu-----AspLeuProIleGlnValIleG 2797
 Db 6916 GATTCAAGCGCGCGAGCGAGGTGCATGCTCGCCAGCGGATGTTCATGCTGTGCA 6975
 QY 2797 uThrGluAspAsnIleAsnThrAlaThrAsnGluPheLeuAspGluIleAlaIySGIuPr 2817
 Db 6976 ATTGCAAGCCACGGCTC-----GAGCATTTGGCGCGTGAACC 7011
 QY 2817 oValArgLeu-----GlyHisProLeuIleArgPheThrIleIleIyS-----GlnThrIySse 2835
 Db 7012 CTTCGACTGTGTCAACGGCCCATGATCCGGTGTGACTTTTGGCCCTTGAAGCCCAAGC 7071
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 Db 7072 GCATGTCTGTGTATGAACCTGCACCAATCATCAGCATGGGTGTGATGGCGGTGCT 7131
 QY 2855 lValArgIyLeuHisMetLeuTy-----AsnGlyArgSerLeuLeuProPr 2871
 Db 7132 GGTCAACAGCTCTGTGGCGGTGTACAGGGCTATCGTACGGGCGGTGCAACTGCC 7191
 QY 2871 oHisGlnPheSerArgTyMetGlnTyThrAlaAspGlyArgGluSerGlyHisGlyPh 2891
 Db 7192 CGGCGTGGCGGTGCATACCCGCACTACGGGCTTGGCAGCGCCAA----- 7237
 QY 2891 eTPArgAspValIleGlnAsnThr----- 2899
 Db 7238 -TGGCTGAGAGCGAGCAAGCGCGCACTGGCTTACTGGAGACAGATTGGCGG 7236
 QY 2900 -----PromethrIleLeuSerAspArgThrValValAspGlyAsnAspAlaThrCy 2917
 Db 7297 TGAACAGCCGCTGTGTGAATTGCGAACCGACTACCGCGCGCGAGCCACCGCGC 7356
 QY 2917 sLyAlaLeuHisLeuSerIySleValAsnIlePro-----SerGlnValLeuArgGlySe 2936

Db 7257 TGGCGGC-----CAATTGAGCCTGGCGCTGACGCGCCGCTGTGCAGACACTCAGCGCGCA 7413
 QY 2936 rSerAsnIle-----IleThrGlnAlaThrValPheAsnAlaAlaCyAlaLeuValIle 2954
 Db 7414 GGGCCAGCGCCAGAGCGCTACCTCTTCATGTGGCTGTGTGCGCTTCCAGACCTGTCT 7473
 QY 2954 uSerArgGluSerAspSerIyAspValValPheGlyArgIleValSerGlyArgGlnI 2974
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 QY 2974 yLeuProVal-----GlyTyrgInAspIleValGlyProCyThrAs 2988
 Db 7510 CGTCCGCTGGCCCAATGCCAGCGCGCGGCAAGAGGGGTGGTGGCTTCTTCGCA 7569
 QY 2988 nAlaValProValArgAla-----HisIleGluSerSerAspTyrgAsnGlnLeuHis 3006
 Db 7570 TACCCAGTGCACAAAGCCGAGTTTCACTGTGGCGCTGCTG----- 7626
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 Db 7627 CCAGTCCGCAACAGCGCGCTGTGATGCCAGGCCATCAGACCTGCCCTTCAACATG 7686
 QY 3026 uTyxArgAsnCySerThrAspTrpProGluAlaIleThrAsnPheSerCySileThrTy 3046
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 QY 3046 rHisAsnPheGluTyThrHisProGluSerGlnPheGluGlnArgValGluMetGlyVa 3066
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 Db 7855 CGCGACACACGTGAGCGGATGACAGCGGAGCTTTACTTC-----GCCACCGAAGCTGA 7908
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 Db 7969 TCGC 7972
 Db 7969 TCGC 7972
 RESULT 7
 US-10-282-122A-7449
 : Sequence 7449, Application US/10282122A
 : Publication No. US20040029129A1
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Hiansu
 : APPLICANT: Zamudio, Carlos
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 : APPLICANT: Trawick, John
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 : APPLICANT: Yamamoto, Robert
 : APPLICANT: Forsyth, R.
 : APPLICANT: Xu, H.
 : TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 : FILE REFERENCE: EPIRA.034A
 : CURRENT APPLICATION NUMBER: US/10/282,122A
 : CURRENT FILING DATE: 2003-02-20
 : PRIOR APPLICATION NUMBER: 60/191,078
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 : PRIOR APPLICATION NUMBER: 60/207,727

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PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR FILING DATE: 2001-02-16
Remainder of Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ. ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ. ID NO: 7449
LENGTH: 15450
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7449

Alignment Scores:

| Pred. No.: | 2,75e-148 | Length: | 15450 |
|------------------------|-----------|---------------|-------|
| Score: | 1867.50 | Matches: | 846 |
| Percent Similarity: | 41.22% | Conservative: | 521 |
| Best Local Similarity: | 25.51% | Mismatches: | 1328 |
| Query Match: | 11.58% | Indels: | 624 |
| DB: | 16 | Gaps: | 135 |

US-09-482-788-2 (1-3129) x US-10-282-122A-7449 (1-15450)

Qy 16 ThProLasePheSerHieGlyAspSerProLeu---AenSerSerTyGluGln 34
Db 4573 ACCGCGTCGCACTTC-----CCGCTGGCCGGGCTTTCCACAGCCAG 4614
Qy 35 LeuPheHieLeuTyGlyLeuAspSerSerArgIleGluAlaIleTyProCyThrPro 54
Db 4615 CTCGATGAATTG---TCCTTGATCTCGATTCGTCGGGACATCTACGCTGTGTCGG 4671
Qy 55 PheGlnLeuAspMetIleAspCyAsnAlaLeuAspIleGlnSerAlaIleGlyHieAla 74
Db 4672 ATCCAG-----CAGGCGCATGCTTTCACAGT 4698
Qy 75 ValTyAspValProThrAsp-----IleAsp 83
Db 4699 CTCATGGAACGGAAGCGACTATGTACACCATGGCCATGATTCGGCGCATTTGGAC 4758
Qy 84 IleSerArgPheAlaLeuAlaTPrLySgluIleValAsnGlnThrProAlaLeuArgAla 103
Db 4759 CCGGATCGCTTCGCGGACGTCGCGAGCCACCTCATGCCATGAGATCTGCGC--- 4815
Qy 104 PheAlaPheThrSerAspSerGlyLyThrSerGlnValIleLeuLyAspSerPhe--- 122
Db 4816 -----AGCGATTCCTCTGGAAGGACGCGTGCCT 4845
Qy 123 -----ValPhe-SerTrpMetCyTrpSerSerSerSerProAspG1 137
Db 4846 CAGCCGTCGACGAGTGATTCGACGACGACGCTGAGCTGCGGCTGCGCCCGCCAGGC 4905
Qy 137 uValAlaArgAsp-----GluAlaAlaAlaAlaAlaSerGlyPr 150
Db 4906 AGTGATCCGCAACGAGCGAGAGCTGAGCGGACCGGTTTCACCCGCGCAGGCGG 4965
Qy 150 oArgCyAsnArgPheValLeuLeuGluAspMetGlnThrLySgluLeuValTr 170
Db 4966 CCGCTTGCACGCG-TTGGTGTGGTG---CCGCTGCGCAATGGGCGGATGACCTCATCTA 5021
Qy 170 pThrPheSerHieAlaLeuValAspValThrPheGlnGlnArgValLeuSerArgValPh 190
Db 5022 TACTTATCACCACTCTCGATGAGCTGGAGCAAGCCCACTGCTCGCGAGGACT 5081

Qy 190 eAlaAlaTyLeuHieGluLy-----AerThrHieArgProGluThrPr 205
Db 5082 GCAGCGCTATCGGGCAGAGGATGACCGCTACCGCTTGGGCTTACCGCATATCCG 5141
Qy 205 o-----GluSerSerAspAlaThrAspThrAspSerGlnSerValSerAlaSerMe 223
Db 5142 TTGGTTCAGAGCGCGATCGAAGCGACCGAGCTCC----- 5178
Qy 223 tSerCyGluAspAsnAlaValSerAlaThrHiePheTrpGlnThrHieLeuAsnAspLe 243
Db 5179 -----TTCTGGCGGATCGCTGGCTCCCT 5204
Qy 243 uAsn-----AlaSerValPheProHieLeuSerAspHie 254
Db 5205 GGAATGCGCACAGCTGCGCGCGCGAGCGAGGACAGACACTTGGCCAGGATAGCA 5264
Qy 254 sLeuMetValProAsnProThrThrThrAlaGlnHieAlaGlnThrPheProLeuSerG1 274
Db 5265 TCTGGCGGAATGGAATCCGACAGACCGCGCA---CTGGCGTCTTCCGCCAAGCTCA 5321
Qy 274 pLyValAlaLeuSerAspSerAlaIleCyArgThrAlaLeuSerIleLeuLeuSerArgTy 294
Db 5322 GAAGTTCACCGCTACACCTTGGTG---CAAGCGCTGCGCGCTCTCTCGACGCGCA 5378
Qy 294 rThrHieSerAspGluAlaLeuPheGlyAlaValThr-----GluGlnSerLeuPr 311
Db 5379 CTCGCGGAGAGACAGTATCGATCTGCGCGCGCACCGTGGCGCGAGACTGCC 5438
Qy 311 oPheAspLyHieTyLeuAlaAspGlyThrGlnThrValAlaProLeuArgValHie 331
Db 5439 AGCATGAGCGCGAGTTC-----GATCTGTATCATACCTTCGCGTATCCGCC 5492
Qy 331 sCyGlnSerAspAlaLeuArgAlaSerAspValMetAspAlaIleSerSerTyAspAspAr 351
Db 5493 GCGCGACCGCACAGAGCGTCGCGGATCTCGACGGGATCAGCGCTCAACCTGCG 5552
Qy 351 gLeuGlyHieLeuAlaProPheGlyLeuArgAlaIle---ArgAsnThrGlyAspAsnG1 370
Db 5553 GCTGCGGACACAGAGATGAGCTCTGTACGACATCCAGCGCTGGCGCGGATGCGCG 5612
Qy 370 ySerAlaAlaCyAspPheGlnThrValLeuLeuValThrAspGlySerHieValAsnAs 390
Db 5613 CGAGCTCTGTTCAT-----AGCATCTGTGTTCGAAACTTCCCTGCGCGCA 5663
Qy 390 nGlyIleAsn-----GlyPheLeuGlnGlnIleThrGluSerSerHieAspMetPr 407
Db 5664 GCGTCTGCGCGAGGCTCCCGCGATCTGAGATCTGCAGCTTCACGCGCAACGACAGCAG 5721
Qy 407 oCyAsnAspArgAlaLeuLeuLeuHieCySgluMetGluSerSerGlyAlaLeuLeuVa 427
Db 5722 ---ACCAACTACCCCTGACGCTGGATGTCACCTGCGTGAACGCGCTGACGTA 5777
Qy 427 lAlaTy-----TyAspHieAsnValIleAspSerLeuGlnThrThrArgLeuGln 445
Db 5778 CGTCTATGCGCGCGCGGATTTGACAGCGGACATCGCCGATGAGCTGACCTG 5829
Qy 445 nGlnPheGlyHieLeuIleTyCySgluGlnSerProLeuAspLeu-----SerSerMe 463
Db 5830 -----CATCTGTGATCTGCTGCAGCGGAGTGGCGGACACCTCAGCGACGCT 5879
Qy 463 tAlaGluValAsnLeuMetThrGlyTyAspArgAlaGlu---IleGluSerTrpAsnSe 482
Db 5880 GGGCGAGCTGCGCTCTGCACCGCGGAGAACCGCAGAGCGCTCGGATTTGGAGCG 5939
Qy 482 rGlnProLeuGluValGlnAspThrLeuIleHieSgluMetLeuValAlaSerHie 502
Db 5940 A---CCGCTGAG-----GCGCTGCGCGCGCGCGCTCGCGCGGCTTCCGCGCA 5987
Qy 502 s-----SerProThrTyThrAlaIleGlnAlaTrpAspGlyAspTrpThrTy 518
Db 5988 TCAGGACGCTGCGCGCTGAGCGATCGCGCTGATGCGGAGGACAGATATCTACGTA 6047

QY 518 rsergltleuaspasnaValserArgleuAlaValhlelleysSerleuuglyleuAr 538
 Db 6048 TCGCGAACTGGATATGGCGCCGACGCTCTGGCCGCTGGCGCGCGCGCGCTG-- 6105
 QY 538 galagInglAlaIlelleProValTyrPhegluYserSerlystrValIleAlaSerMe 558
 Db 6106 -GCCGGGGAAGCCGTGGCGATCCGTCGCGGAGCGCTCCCTGACCTCGTCCGCGCT 6164
 QY 558 tleuAlaValleuYserSerlyleuAlaPheThrleuIleAspProAsnProProAl 578
 Db 6165 GCTGGGTATCTCAAGGCCGTCGCGCGGCTGCTGGCCGTGATCCGAATCCCGCGGA 6224
 QY 578 aArgThrAlaGlnValAlaThrGlnThrArgAlaThrValAlaIleuThrSerlyleuHI 598
 Db 6225 GCCCCTGGCTACATGTGGCGACAGCGCGCGCTGCTGATCTGC----- 6273
 QY 598 sArgGlnThrValGlnlyleuValGlyArgCysValValValAspAspGluLeuGlu 618
 Db 6274 -CAGGAACCCCTGGCGAGCGGCTGCGCCGCGACAGGTGAGCGGCTGCGCGTGA 6332
 QY 618 nserValser-----AlaSerAspAspPheSerSerleuThrlyle-----SerGlnAs 634
 Db 6333 GACCGCGCTGGCGCGCGGATGACGATACGCGCGCTCCGAGGTGACCTGGCGAGAC 6392
 QY 634 pleuAlaTyrValIlePheThrSerGlySerThrGlyAspProlyGlyIleMetIleG 654
 Db 6393 GCTGGCTTATGATCTATACGTCGCGCTGACCGCGACGCCAAGAGATGGCGGCTAG 6452
 QY 654 uhlAsArgAlaPheSerSerCysAlaLeuLyPheGlyAlaSerleuGlyIleAsnSerAs 674
 Db 6453 CCAGGCGCGCTGCTGGCGACGTCGCGAGCGGCGACGACCTTACGCGCGCTGG 6512
 QY 674 pThrAlaGlnAlaLeuGlnPheGlyThrhlAsAlaPheGlyAlaCysleuLeuGluIleMet 694
 Db 6513 CGACTGCCAATCACTGATTCGCTCGATCGATTCGATGCGCGACCAACCTTCCT 6572
 QY 694 rThrleuIleAsnGlyGlyCysValCysIleProSerAspAspAspArgMetAsnSer-- 713
 Db 6573 ACCTTGCTGGCAGAGCCCGCGGCTCTGCTC--GGGAGCGCTGGACAGTGGAGCGCGCA 6629
 QY 714 ----leProSerPheIleAsnArgTyrAsnValAsnTyrMetMetAlaThrProSerTyr 732
 Db 6630 ACATCTGGCGATGAGGTGAGCGGCGACGCGGTGATCTGATCTGATCCGCGGCTTA 6689
 QY 732 rMetGlyThrPheSerProGlu-----AspValProGlyleuAlaThrle 747
 Db 6690 TCTTTCAGCAACAGCGCGAGGATTCGCGACGCGCGCGCGATCCGCGTACCGCGCTG 6749
 QY 747 uValleuValGlyGlnGlnMetSerSerValAsnAlaIleThrAlaProlySleuG 767
 Db 6750 TATCTCTGGCGGAGAACCTGGGAGCGGACGCTGCTGACCCAGCAGCGGCTGAGCTGA 6809
 QY 767 nleu----LeuAsnGlyTyrGlyGlnSerGlySerSerIleCysPheAlaSerAsnMe 786
 Db 6810 AGCTGGTTCACAGCCCTACGCTCCACCGAGCGGTATCATCTCGCTGGCGCTGCACTG 6869
 QY 786 tSerThrGlnProAsnAsn-----MetGlyArgAlaValGlyAlaHisSerTyrPa 803
 Db 6870 TCGGAGCCAAAGAGCGCGCTCCGCTATCTGGCGCGCGCTCGCTCGCGCGCGCGCTG 6929
 QY 803 lIleAspProAsnAspIleAsnArgleuValProIleGlyAlaValGlyGlnleuValI 823
 Db 6930 CATACTGGACGACCGCTGACGCTGAGCGCG--GGATGATGAGCGAGAGCTGTACT 6986
 QY 823 egluSerProGlyIleAlaArgAspTyrIleValProProProGluYserSerProPh 843
 Db 6987 CGCGCGGAGATGCTGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCTT 7046
 QY 843 ePheThrAspIleProSerTyrTyrProAlaAsnThrPheProAspGlyAlaValSleu 863
 Db 7047 CGTGGCGGATCCGTTCTCA-----GTTTCGCGGAGCGCGCTGTA 7085
 QY 863 rArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIleValCysleuGlyArgG 883

Db 7086 TCGCACGGGAGACTGGCGGCTTATCGCGCTGACGCGGTCAAGGTCAATATCTCGCGCGCG 7145
 QY 883 eaAspSerGlnValLyIleArgGlyGlnArgValGlnleuGlyAlaIleGlnThrHsle 903
 Db 7146 CGATCAGCAGATAGATCCGTGCTTCCGATCGAGATCGGAGAAATCGAAGCCAACT 7205
 QY 903 uArgGlnGlnMetProAspAspLeuThrIleValGlnAlaThrlyAspSer--G 922
 Db 7206 GCTTGCACAC-----CCGATGTGGCGGAAGCAGCGGCTGCGCGCTGCA 7250
 QY 922 nserAlaAsnSerThrSerleuIleAlaPheleuIleGlySerSerTyrPheGlyAsnAr 942
 Db 7251 TGGCGTCGAGTCGCGCTGCTGGCGGCTACTCGTGGG-- 7290
 QY 942 gProSerAspAlaHslelleuAspHlsAspAlaThrlyAlaIleAsnIlelySleuG 962
 Db 7291 ----CGTGAAGCT--ATGGGGGTGAGACCTTGGCGGACCTGGCACCTGGCTGGC 7343
 QY 962 uGlnValleuProArgHlsSerIleProSerPheTyrIleCysMetleuGluProAr 982
 Db 7344 CGAGCGCTTGCCTGCTGCTACATGCAACCGACGCTGGCAGGTGCTGCCAGCTTGGCGCT 7403
 QY 982 gThrAlaThrGlyLyIleAspArgArgArgleuArgIleMetGlyLyAspIleleuAs 1002
 Db 7404 GAAAGCCAAAGCAGAGCTGATGCAAGGCGCTG----- 7437
 QY 1002 pLyGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAs 1022
 Db 7438 -CCGAAGGTGAGCGCGCTCCCGCGCGCGGAGGAGACCTCCGCGGAGGCGCTGA 7496
 QY 1022 pThrAlaAlaLyLeuHlsSerIleThrValGlnSerleuGlyIleAspProAlaThrVa 1042
 Db 7497 ACCTTGC-----GTGCAAGATCTGGAGGCGCTGCTGGTGTGAG-----GGCAT 7544
 QY 1042 laenValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIlelyMetVa 1062
 Db 7545 CGCGCGGAGAGACACTTCTTCAACTCGCGGCTGACTCCCTGACGCGCACCGCGGTGT 7604
 QY 1062 laenMetAlaArg--SerValGlyMetAspLeuLyValSerAsnIleTyrGlnHlsPr 1081
 Db 7605 CTCGCGCTGCGCGCAGGACCTGAGCTGAGCTGACCTTCCGATCTGTTCAAGCGGCT 7664
 QY 1081 cThrleuAlaGlyIleSerAlaValAlaVallyGlyAspProleuSer-----Tyr 1097
 Db 7665 GGTCTGCGAGACTTGCCTGCTTCCCTGAGTCCAGCGCGGAGCGGCTGCTGCTGCT 7724
 QY 1097 rThrleuIleProlySerThrHlsGlnGlyProValGlnGlnSerTyrSerGlnGlyAr 1117
 Db 7725 GCAAAATATCCCGCA--CTGCCAGAGCTGCTTTC-----TCGCATCTCAGCAAG 7775
 QY 1117 gLeuThrPheLeuAspGlnleuAspValGlySerleuTyrTyrleuIleProTyrAlaVa 1137
 Db 7776 CATGTGCTCTCTGGAACCTGAGCCTGAACCGCGCTTATCATCTCCCGACGCTACT 7835
 QY 1137 lArgMetArgGlyProValAsnValAspAlaAlaArgAlaAlaAlaIleuGluG 1157
 Db 7836 GCAAGTCTGGGTCTCTGAGCAAGCGCGGTGACAGAGGCTTGCATTTGGCTGGT 7895
 QY 1157 nArgHlsGlnThrleuArgThrThrPheGluAspGlnAspGlyValGlyValGlnIleVa 1177
 Db 7896 CGCGCGAGACACTTGGCGACCGGCTTCCAGAGAGTGAAGGTGACGCGCGCGCAAGAT 7955
 QY 1177 lHlsGlyLySerSerGlyIleMetCysValIleAspLeuCysGly--SerAspLeuAs 1196
 Db 7956 CTGGCGCAACATCCGTTGGCATTTGCTGCGAGATTTGGCGCGCGCGCGCAAGCAAC 8015
 QY 1196 pProPheGlnValLeuAsnGlnGlnGlnThrThrProPheAsnleuSerSerGlnAlaG 1216
 Db 8016 GTTGGCGCAGCGGTGGCGAGAAATCCGCAAGCCATTTGACCTGCTGCGCGGCT 8075
 QY 1216 YThrArgAlaThrleuLeuArgleuGlyGluAspAspHlsIleleuThrIleValMetH 1236

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| Dh | 8076 | GCTGGCGGCGTCTGCTGGCGCTGGCGGCGGAGGAGCATGTTGGTCATCAGCCAGCA | 8135 |
| Qy | 1236 | hNis1le1leSeraBrg1yTTPSerT1aBArVa1leuKrgArBleuBeng1leuTy | 1256 |
| Dh | 8136 | CCATGTCGTGTCGCGAGCGGTGGTGCATCAGATGTATGGTCGACAACTGCTCCAGGCTCA | 8195 |
| Qy | 1256 | rSerT1a1leuSuArBserT1yArBPrDleuSerT1a1leuThPrDleuPro1leG1 | 1276 |
| Dh | 8196 | TGCGCGGCGCGCGCGCGCGGCAACA-----CCAGCGTGGCGCCATTGAGCGTCCA | 8246 |
| Qy | 1276 | nTySerArBheAla1yTTrG1n1yArBPrD1ne1leG1uG1n1y-----LyG1 | 1294 |
| Dh | 8247 | GTAAGCGCATATGCTGGCTGGCATCGCGGCTCGCTGGACAGCGGCGAGGCGGCGGCGCA | 8306 |
| Qy | 1294 | nLeuAnTyTTr1yLyVg1leu1yArBserTserPro1a---LyV1leProThAr | 1313 |
| Dh | 8307 | GCTGATTAATCGCTCGTGAAGCGCTGGCGCGGCGGACGAGCGGCTCTCGTAATCGCGCGCA | 8366 |
| Qy | 1313 | rheAlaArPrD1a1leu1e1uSerG1yArBAr1aG1yArVAln1Va1ThPr1leArG1 | 1333 |
| Dh | 8367 | CCGGGTCGCGCGCGCGCGAGCGCGGAGCGCGGAGCGGCTGGACATGAGCGCTGCGGT | 8426 |
| Qy | 1333 | yG1leuTyTTr1n1e1leuArG1a1rheSuArBng1u1n1ArBThTTrSerPheAla | 1353 |
| Dh | 8427 | GTCATTAATCGAGAGAGCTGCTGGCTGGCGCGCGGAGAGGTGTCACTCCCTCATGCT | 8486 |
| Qy | 1353 | 1leu1e1u1a1ArheArG1a1a1n1e1TyTArG1e1uTh1r1a1Va1G1uAr1a1a11 | 1373 |
| Dh | 8487 | TCTATTGGCTGCTTCCAGATGCTGTTGAAGCGTATGAGCGGAGCGGAGTCCGATTCGCGT | 8546 |
| Qy | 1373 | eG1yThrPro1le1a1a1nArG1a1ArPrD1n1e1u1n1Ar1le1leG1yArPheVa | 1393 |
| Dh | 8547 | CGGGGTACTTTCGCGCAACCGGACCGGCGGAGGTTCAGCGCTCGATCGGCTTCTTCTGT | 8606 |
| Qy | 1393 | 1AsnThG1nCyBwEArG1leAen1leArBh1n1ArBh1rPheG1yThr1le1u1e1A | 1413 |
| Dh | 8607 | CATATCCAGAGTGTGCTGCTGGCAGATGATGCTGGCTGGCTTCCGCAATCTATCGG | 8666 |
| Qy | 1413 | nG1nVa1LyBa1ArTh1rTh1r1a1a1ArheG1uBng1uAr1leProPheG1uArG1a | 1433 |
| Dh | 8667 | CCGCGTCGCGAGCGCGGCGCTGGCGGACGCGCACGAGATCTGCGTTCAGACATTT | 8726 |
| Qy | 1433 | 1Va1Ser1a1e1nG1nProG1ySerTArBPrDleuSerTThPrDleu1a1G1n1e11 | 1453 |
| Dh | 8727 | GGTCCATGCTCTTGCAAGCC--GAACGCAATTCGACAGCCCGGTGTTCAGGTAT | 8783 |
| Qy | 1453 | ePhe1a1Va1n1h1Ser1n1yArB1e1nG1yArBhe1u1rPheG1nG1y1e1u1SerVa | 1473 |
| Dh | 8784 | GTAATACCAACCAAGC-----GGCAGCGGACAGATGCCCAAGTCGATGCTTT | 8831 |
| Qy | 1473 | 1ProVa1rProSer1yBa1ArT-----ThArGrPheArMetG1uPhe1a1e | 1489 |
| Dh | 8832 | GCAATCGCAGATTTTGGCTGGAGATGAGTGGCGGACAGATTCGATCTTGCGCTCGATAC | 8892 |
| Qy | 1489 | nPheG1nG1uThArBserT1e1u1yG1ySerVa1AnPheAlaArG1u1ePhe1yBwE | 1509 |
| Dh | 8892 | CTGGGAAACCCCGGACCGGCTTGGCGGCGGCTGTCAACCGGACGCACTGTTTCAGGC | 8951 |
| Qy | 1509 | TG1uThAr1a1G1uAnVa1ArG1Va1rPheBhe1u1le1uArG1nG1y1e1u1n1Se | 1529 |
| Dh | 8952 | GCGGACCGTCGAGCGCATCGCGGCGCATTTGGAGAACTGCTGCGCGGCGCATGTGGAATA | 9011 |
| Qy | 1529 | rSerArGrThPrDleu1Ser1le1e1nPro1e1uThArBPrG1y1leVa1ThPr1e1u1y1e | 1549 |
| Dh | 9012 | CCCGAGGCGCAGCTCGATCGCTGCCATTCGATTCGACAGAGCGTGGCGCACTTCT | 9071 |
| Qy | 1549 | nArPVa1leuAnVa1Lyh1n1Va1ArPrTyTProArG1u1SerTser1e1u1a1ArPAr1Ph | 1569 |
| Dh | 9072 | GGAAAGCTGAACGCGCATCGCGCGGAGATCCCGCTGCAACGCGGCGGCGCATGGTGT | 9131 |
| Qy | 1569 | eG1nThrG1nVa1Ser1a1TyTProArBserT1e1u1a1Va1ArBserTserCyBArG1e | 1589 |
| Dh | 9132 | CGAGGAGAGGTCGAGCGCACCGCGAGCGCGCGGCGCTTGCGTTCGCGAGAACTGCT | 9192 |

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| QY | 1589 | uThrTYrThcgluLeuAspArgInserAspIleuAlaGlyTYrPleuAspArgSe | 1609 |
| Db | 9192 | GGACTACGCCGACCTTAACCCCGGGCCCAACCGCCTGGCGCATGCCCTGATCGACCGCGG | 9251 |
| QY | 1609 | rMeProlAlaGluThrLeuValAlaValPheAlaProAspSerCysGluThrIleValAl | 1629 |
| Db | 9252 | GGTCGGTGGGAGACCGCGCTGGTGGCGCTGGCCATGAGAGCGTTCATCGATGATGTCGTGGC | 9311 |
| QY | 1629 | aphePheGlyValLeuValAlaAsnLeuAlaTYrIleuProlAspValArgSerProSe | 1649 |
| Db | 9312 | CTGATGCGCATCTTCAGAGCCCGCGCGCCCTACGTCGCGGTGAGACCCGAGTACCCCGA | 9371 |
| QY | 1649 | rAlaArgValGlnAspIleuAspSerGlyLeuSerGlyProThrIleValIleGlyHI | 1669 |
| Db | 9372 | GGAGCGCCAGGCGCTACATGCTGGAGGACACCGCGCTGACGCTGCTCAGCACTGCCA | 9431 |
| QY | 1669 | AspThrAlaProProlAspIleGluValThrAsnValGluPheValArgIleAspAl | 1689 |
| Db | 9432 | CCTGAAGCTCCCGCTGGCGGACAGCGCGATCGACCTGACACAG---GCCGATGC | 9488 |
| QY | 1689 | AlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGluHisAspSerThrIlyProSe | 1709 |
| Db | 9489 | CTGGCTGGAAACCATGCGCAGAAACAATCCGGGATCGAG-----CTGGA | 9533 |
| QY | 1709 | rAlaThrSerLeuAlaTYrValIleuTYrThrSerGlySerThrGlyArgProIyAsGlyVa | 1729 |
| Db | 9534 | CGCGAGAAATCTTGCGCATGTCACTTCAACAACCTCCGCTCACCGGAGACCCMAAGGTGC | 9593 |
| QY | 1729 | IleCilleGluHisArgValIleIleArgThrValThrSerGlyCysIle-----ProAs | 1747 |
| Db | 9594 | CGCGAACCGGCATTCGGCGCTGA--GCCAACCGCTGTGTGTGATGACGACGCGCTACGCG | 9651 |
| QY | 1747 | nTYrProSerGluThrArgMetAlaHisMetAlaThrIleAlaPheAspGlyAlaSerTY | 1767 |
| Db | 9652 | CTGGCGCTCGGCGACACACGCTTGACGAGAG--ACCCGCTCACCTTCGACGTGCGTGC | 9710 |
| QY | 1767 | rgIuIleTYrSerAlaLeuLeuPheGlyArgThrIleuValCysValAspTYrMetThrTh | 1787 |
| Db | 9711 | GGATCTTCTTCGCGCGGTGATGAGTGGGACAGTTTGATGGTGGCGCGCGCGGATGACCA | 9770 |
| QY | 1787 | rLeuAspAlaArgAlaLeuIlyAspAlaPhePheArgGluHisValAsnAlaAlaSerHI | 1807 |
| Db | 9771 | TCCGACCGCGGCGAAGCTGTGGCGCTGATCAACCGCGAAGGGGTGCACGCTGCACCT | 9830 |
| QY | 1807 | sValThrSer-----SerSerGlnAspValProlAspArgValProAr | 1821 |
| Db | 9831 | CGTCCGCTCATGCTCGACGCGCTTCCTCGACGAGCAGAACGATC----- | 9873 |
| QY | 1821 | gArgLeuSerArgThrIleuMetPhePheLeuValAlaThrAspSerThrAlaProAs | 1841 |
| Db | 9874 | ---GTCTCTGCACACCGCTGAACGCACTCTTGACGCGGCGAGCGCTGTCCGCGGA | 9929 |
| QY | 1841 | pAla-----LeuAspAlaGlnGlyLeuTYrGlnGlyValGlnCly | 1854 |
| Db | 9930 | CGCCACACACAGAGTTCGCCACAGCTGCCGCGACGCGCGCTC----- | 9972 |
| QY | 1854 | sTYrAsnGlyTYrGlyProThrGluAsnGlyValMetSerThrIleTYrProIleAspSe | 1874 |
| Db | 9973 | -TATTAACCTGATAGCGCCGACCGAGCGGCAATCGACGTCAACCACTG-----AGCTG | 10025 |
| QY | 1874 | rThrGluSerPheIleAsnGlyValProIleGlyArgAlaLeuAsnAsnSerGlyAlaTY | 1894 |
| Db | 10026 | CGTGGAGAGGAGGACGAGCGCGGTCCGATCGGCGCGCATCGCCMACTGGGCTGCTH | 10085 |
| QY | 1894 | rValIlyAspProlGlnGlnIleuValGlyIleGlyValMetGlyGluLeuValValTh | 1914 |
| Db | 10086 | CATCTCGATGCGACCTGACCTGAGCGCGGTGCGGCGGTGCTCGCGAGACTGTACTCGC | 10145 |
| QY | 1914 | rgIlyAspGlyLeuAlaArgIlyTYrSerAspIys---AlaLeuAspGluAsnArgPheVa | 1933 |
| Db | 10146 | CGGTGCGGCGCTGCTGTGGCTTACCAACGAGCGCTCCGGGCTGTACTGCCAGCGTTTGT | 10205 |

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| Qy | 1933 | l-----HisIeIethrValaIaMserGIInThrValVlaIaTyArgThGlyAspArgVa | 1951 |
| Db | 10206 | CGCCAGCCCGCTGTGGCTGGGG-----CGAGTGTACCGAGCGGCACCTGGC | 10256 |
| Qy | 1951 | lArgTyArgIleGIyAspGIyLeuIleGIuPhePhGIyArgMetAspThrGIInPheIy | 1971 |
| Db | 10257 | GCCTTACCGC---GCCATGGGGTGAATCGATACGCCGGCGGATGACCAACAGGTGA | 10313 |
| Qy | 1971 | slLeArgGIyAsnArgIleGIuSerAlaGIuIleGIuAlaIaLeuIleuArgAspSerse | 1991 |
| Db | 10314 | GCTCGCGGCGCTGGCATCGAGCTGGCGAGATCGAGCGCGCTCTGGAGCATCCGG | 10373 |
| Qy | 1991 | rValArgAspAlaIaIaValIaLeuGIInGIaInGIaAspGIInAlaProGIuIleuGI | 2011 |
| Db | 10374 | GGTCCGGAGCGCGGGTGGCTGGCGGTGACACACAG-----CAGTGGTCTGG | 10421 |
| Qy | 2011 | yPheValValAlaAspHisAspHisSerGIuAsnAspLyGIyGIuSerAlaInGIInVa | 2031 |
| Db | 10422 | CTAGCTGTGTCTGAGAGACGAGCGGCGGCACTGGCGCGAAAGCCTGGCCGACCTGGC | 10481 |
| Qy | 2031 | lGIuGIyTrpGIInAspHisPheGIuSerGIyMetTy----- | 2043 |
| Db | 10482 | GACAAAGCTCGCGGAAATACATGGTGGCGGCGAGTGGCTGGCGTGGAGCGATGCCGT | 10541 |
| Qy | 2044 | -SerAspIleGIyGIuIleAspProSerThrIleGIySerAspPheLyGIyTrpThre | 2063 |
| Db | 10542 | GAGTCCGAACGGCGCAAGCTGATCGCAAGCGCTCGCGCGACCGCAAGCTGTGGGGGA | 10601 |
| Qy | 2063 | rMetTyArgspGIySerGIuIleAspPheAspGIuMetHisGIuTrpLeuGIyGIuThrTh | 2083 |
| Db | 10602 | GACCCATGTGGCGCGGAGATGAATGAGCGACGTATCGCGCGCTGGCGGAGCCT | 10661 |
| Qy | 2083 | rArgThrLeuHisAspAsnArgSerIleuGIyGIuInValIeGIuIleGIyThrGIySerGI | 2103 |
| Db | 10662 | GCTGAACCTGGAGAGGTGGGGCGCCACCGCAACTCTTGGCCCTGGT---GGCATTC | 10718 |
| Qy | 2103 | yMetIleuPheAsnLeuAspSerArgLeuGIuSerTyValGIyLeuGIuProSerArg | 2123 |
| Db | 10719 | CATGTTTCATCCAGGTGGTGAATCGATCCCGTGG---GCGGGATATCAG----- | 10767 |
| Qy | 2123 | gSerAlaAlaIaPheValAsnLyAsIaThrGIuSerIleProSerLeuAlaGIyVal | 2143 |
| Db | 10768 | -----TTCACTCCGAAGGACCTGTTCACAAACAGACCGTACAGGGGTGGC | 10814 |
| Qy | 2143 | AlaVal-----GIInValGIyThrAlaThrAspIleGIyGIuInValAspAspLeuHisProAs | 2162 |
| Db | 10815 | GCGAGTGGCCCGCTACGAGCGCTGGCGTGGCAATGAGACAG----- | 10854 |
| Qy | 2162 | pLeuValIaIeAsnSerValIleGIuTyPheProSerSerGIuTyLeuAlaGIuI | 2182 |
| Db | 10855 | -----GCGCCTGT | 10862 |
| Qy | 2182 | eAlaAspThrLeuIleHisIleuProAsnValGIuArgIlePhePhGIyAspValArgse | 2202 |
| Db | 10863 | GAGCGGCGAGACGGTGTGTGGCG---TTCCAGCGGTGTCTTTC----- | 10905 |
| Qy | 2202 | rGIInAlaThrAsnGIuHisPheLeuAlaIaArgAlaIleHisIleThLeuGIyIuAsnAl | 2222 |
| Db | 10905 | ----- | 10905 |
| Qy | 2222 | aThrLyAspAspValArgGIuLyAsnValaGIuLeuGIuAspMetGIuGIuIleuLe | 2242 |
| Db | 10906 | -----GAAAGCGCATTTCCCAATCGCGACAGCATGGAAACAGCATTTGCT | 10949 |
| Qy | 2242 | vAlaGIuPro-----AlaPhePheThrSerLeuLyAspArgPheProGIyLeuVa | 2259 |
| Db | 10950 | GTTGAACCGCGCGAGCGCTCGAATGGAGAGCACTGAAGCGGCTTGACAGCGCTGTGT | 11009 |
| Qy | 2259 | lGIuHisValaGIuIleLeuProLyAsnMetGIuAlaValaAspGIuSerAlaTyArg | 2279 |
| Db | 11010 | TGAACATACAGACGCATTTGGCTGTGGCTTC-----CATGAACGAGCGAAACCTG | 11066 |
| Qy | 2279 | gTyAlaAlaValaValHisValaArgIySerIleuGIyAspGIuIleuValIeProValGI | 2299 |

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| Dd | 11061 | GCATGCCGGA-----CATGCCGAACCAAGCTGGGGCGGTGCCTGCTGCCTGCCCA | 11114 |
| Qy | 2299 | uLysAspAspTrpIleAspPheGlnAaenGlnLeu-----AsnGlnLysSe | 2315 |
| Dd | 11115 | GGCG-----GTGACCGCAACAAAGCGTGAAGTGCCTCTCGAGAGAGTCCGACGGCAG | 11165 |
| Qy | 2315 | rLeu-----GlyAspLeuLysSer-----SerPheAlaI | 2326 |
| Dd | 11166 | CCTGACCTGGCCGACCGCCACCTGTTGCGAGACCTGTGTGATATGACCGACGGCGG | 11225 |
| Qy | 2326 | allMeerAlaValSerLysIleProPheGlnIleTrpAlaPheGlnArgGlnAlaValAl | 2346 |
| Dd | 11226 | C-----CAGCGTCTGTGTGGT | 11245 |
| Qy | 2346 | AserLeuAsnSerAsnIleAsp-----GluTrpGlnLeu-----Se | 2358 |
| Dd | 11244 | GATCCACCATTCGTGGTGGTGAACGGGGTGTCTCTGGCGATTCCTGTGAGATTTGCAAG | 11300 |
| Qy | 2358 | rThrIleArgSerSerAlaGlnGlyAspSerSerLeuSerValProAspIlePheArgI1 | 2378 |
| Dd | 11304 | GGCTTACCACGACAGCGCTCCGTGGAGAACATCCG-----CGGCT | 11344 |
| Qy | 2378 | eAlaGlyGlnAlaGlyPheArgValGlnValSerSerAlaArgGlnTrpSerGlnAsnG1 | 2398 |
| Dd | 11343 | GCGTGGC-----AGACACACCCGTTCAAGCGCTGGGCGC----- | 11376 |
| Qy | 2398 | yAlaLeuAspAlaValPheHisHisCysCysSerGlnGlyArgThrLeuValAsnAspHePr | 2418 |
| Dd | 11377 | -----GCGCGA----- | 11385 |
| Qy | 2418 | oThrAspHisIleLeuArgGlySer-----AspLe | 2428 |
| Dd | 11383 | -GTGAGCGAGCATGCCGTGTGTGATGATGATGAAGCGCAATTGCATTTGGCGCGAGCT | 11445 |
| Qy | 2428 | uLeuThrAsnArgProLeu-----GlnArgLeuGlnAsnArgTr | 2441 |
| Dd | 11442 | GCTGAAGAGTGGCGCGCGCCAGCTTCCGTGCGAGCATCCGCAAGGCGCTCTGAGCAGCG | 11501 |
| Qy | 2441 | gIleAlaIleGlnValArgGlnArgLeu---ArgSerLeuLeuProSerTyMetIlePr | 2460 |
| Dd | 11502 | TTTGGCTACCTCCGTGACAGAGTGCCTTCACCCGACGTTGACCGAAGC----- | 11555 |
| Qy | 2460 | oSerAsnIleValValLeuAspLysMetProLeuAsnAlaAsnGlyLysValAspArgLy | 2480 |
| Dd | 11551 | -----TTGCTGAAGCAGGGCGCGGACGCTACCGACCGACGATCAACGATCT | 11597 |
| Qy | 2480 | sgIuLeuSerArgArgAlaLysValAlProLysGlnGlnThrAlaAlaProLeuProth | 2500 |
| Dd | 11598 | TCTGTACACCGCCCTGGCGCGAGTGGCTTCCGTTGAGCGCGCTCT----- | 11646 |
| Qy | 2500 | rPheProIleSerGlnValGlnValIleLeuCysgIuGlnAlaThrGlnValPheGlyMe | 2520 |
| Dd | 11647 | -----TCAG | 11655 |
| Qy | 2520 | tLysValAspIleThrAspHisPhePheAsnLeuGlyGlnHisSerLeuLeuAlaThrLy | 2540 |
| Dd | 11652 | CCTGTACAGTGGTGAAGGCGAT-----GGGCGGAGAGACTGTGTGCCGATAT | 11692 |
| Qy | 2540 | sLeuIleSerArg-----IleAspGlnArgLeuLysValArgTleThrValLy | 2556 |
| Dd | 11700 | CGACCTGATGTCGACCGTGGGTTGGTTCACACAGTTTGTCCCGTGCCTGAGC----- | 11755 |
| Qy | 2556 | AspValPheAspHisProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuG1 | 2576 |
| Dd | 11755 | -----CCGGTC-----GGGAGATCTGGCGAGCTCCCTGAAGCGCATCAAGA | 11799 |
| Qy | 2576 | yLeuGlnGlnProValSerAsp---GlyGlnGlyGlnAspArgSerAlaHisMeerAlaPr | 2595 |
| Dd | 11796 | ACAGTTGGCGTGCATTCGCAACAAAGGCGTGGGTATAGCTTGTCTGCGGATATGCTGG | 11855 |
| Qy | 2595 | oArgThrGluThrGlnAlaIleLeuCysAspArgGlnPheAlaLysValLeuGlyPhe----- | 2613 |

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|----|-------|--|--------------------------------------|-------|
| Db | 11856 | A----- | -----GAGGAAAGGCCGGGATCTGGCGGGGATTGCC | 11888 |
| Qy | 2614 | -GlnValGlyLeuThrAspAsnPhePheAspLeuGlyGlnHisSerLeuMetAlaThrIty | 2633 | |
| Db | 11889 | GCAGCGCGCGATTCATTCTTCAATTAC-----CTGGCGCAATTGAGCACTCATGTTGCAGCA | 11942 | ::: |
| Qy | 2633 | AlaLeuAlaVal-----ArgIleGlyHisArgLeuAspThrThrValIse | 2647 | ::: |
| Db | 11943 | GATGGCTCTGCTGGACCCCGGCTGGCGAAAGCGGGGGGAGAGATGGACCC----- | 11994 | ::: |
| Qy | 2647 | rValIysAspValPheAspHisProValLeuPheGlnLeuAlaIleAlaLeuAspAsnIle | 2667 | |
| Db | 11995 | -----GGGCGTCCGCTGGACAACTG | 12014 | |
| Qy | 2667 | uValGlnSerIysThrAsnGlnIleValIleGlyIleArgLeuMetAlaGlnItySerProh | 2687 | |
| Db | 12015 | GCTG---AGTCTCAATGCGCGCGGATTGTCGACCGGTGAACAGATGATGACTGAGCGTTTCAG | 12071 | ::: |
| Qy | 2687 | ecGlnLeuLeuPheThrGlnAspProGlnIuphMetAlaSerGlnIleLysAspGlnIle | 2707 | |
| Db | 12072 | CTCGCAAGATTTCGGCGAGGACCAAGGTGCGCTCGCTGGCCGATGACTATGTGGCTGAGCT | 12131 | |
| Qy | 2707 | u----- | 2707 | ----- |
| Db | 12132 | GAGCGCGCTGGTCGACTTCTGCTGCATTTGGCCACGCGCATGGGCGACGCGCTTCGATTT | 12191 | ----- |
| Qy | 2708 | -----GlnLeuGlnGlnIle | 2712 | |
| Db | 12192 | CCCGCTGCGCGGATTGGACCAAGCGCGCTGTGATGCCCTGCGGTCGCGCTGGAGAAAG-- | 12249 | |
| Qy | 2712 | eIleGlnAspIleItyrProSerThrGlnMetGlnIlyValAlaPheLeuPheAspHisThrth | 2732 | |
| Db | 12250 | -GTGAGGACATCTTATCCGCTGATCCCAACGACAGCGGCGATCTGTC--CATTCGCT | 12305 | |
| Qy | 2732 | rAlaArgProArgProPheValProPheItyrIleAspPheProSerThrsSerGlnProAs | 2752 | |
| Db | 12306 | G-----TACGACGACGAGATGAGGAGCATATCAATCAATGATGCTGTGGA | 12356 | |
| Qy | 2752 | pAlaAlaGlyLeu-----IleValAlaCysGlnSerIleValAsnHisIle | 2767 | |
| Db | 12351 | TGTGTCCGGCTTCGATCTCCCGCGCTTCGCGCGCATGCGCTGGACCGGCA | 12410 | |
| Qy | 2767 | uAspIlePheArgThrValPheAlaGlnAlaSerGlyGlnIleItyrGlnValValIeuse | 2787 | |
| Db | 12411 | CGCGATCTCGCGAGTGGATTTCGCG--TGGCAGGGGAGACTGCACAG-- | 12456 | |
| Qy | 2787 | rCysLeuAspLeuProIleGlnIlyIleGlnI-----ThrGlnIus | 2800 | |
| Db | 12457 | -----CCCTTCGACATGCTGTATCGACAGCGCGCAATGCCCTTCGCGCGAAACA | 12503 | |
| Qy | 2800 | pAsnIleAsnThrAlaThrAsnGlnI-----PheLeuAspGlnPheAlaLysGlnIur | 2817 | |
| Db | 12504 | GGACTGAGCGGAGCGGAGATCGGAGCGCGCGCGCTGCGGCTGAGCTGGCGGCGAGCG | 12563 | |
| Qy | 2817 | oValArg-----LeuGlnIleProLeuIleArgPheThrIleIleLysGlnIth | 2833 | |
| Db | 12564 | CGAACCGCGGTTTCGAACTGCAAGCGCTGCGCGCACTGGTCGCGCTGTGGTGAAGCTCC | 12623 | |
| Qy | 2833 | rLys-----SerMetArgValIleMetArgIleSerHisAlaLeuItyrAspGlyLeuSerIe | 2852 | |
| Db | 12624 | CGAAGGTGAGCATCACTGATCTTACACCCATCATCAATCTCTCTGGACGAGTGAAGCA | 12683 | |
| Qy | 2852 | uGlnHisValValArgIlyLeuHisMetLeuItyrAsnGlyItyrSerIleLeuProhI | 2872 | |
| Db | 12684 | TGCCCAAGTGTCTACGAGAGGTCGAGAGTCTGTATGCCGAGCGCTCG-----CCGGA | 12734 | |
| Qy | 2872 | gGlnPhe-----SerArgItyrMetGlnItyrThrAla-----AspGlyArgG | 2886 | |
| Db | 12735 | GCACCTCCGGGATGGCGGCTATAGCGACTACATCGCTGTTCACAGCGGACGACGCGCG | 12794 | |
| Qy | 2886 | uSerGlyHisGlyPheThrArgAspValIleGlnAsnThrProMetThrIleLeuSerAs | 2906 | |
| Db | 12795 | AGCTACCGAGGCACTTGGCGCGAG-----CAGATGCGGCTCTGGACGA | 12839 | |

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|--|--|-------|---|--------|
| Oy | | 2906 | pAerThr---ValValAspAlly-----AmAAspAlaThrCylValyl | 2919 |
| Dd | | 12840 | GCGGACCCCAATTGGTGTGAAGGACAATGGCTACGCCGGGACATGCAGACTGCGCCAAAGCGGCTGG | 128939 |
| Oy | | 2919 | aLeuHieLauSerLySalleValAnilIleProSerGlnValLeuArg----GlySerSe | 2937 |
| Dd | | 12900 | AGAACAACCTCGTAGAGTGAGACCAACAGGCTAACCGCGGCGCTCCGGAGATTTCGCCCGGCG | 129559 |
| Oy | | 2937 | rAnellillelThGlmlaIeThryValIheAnaIlalacySAIaleuValLeuSerArgGI | 2957 |
| Dd | | 12960 | CCACGAGTCACTCTCATATCCCTGTGCACAGCGGCGGCTGAGCGCTCTTCCAACGCTA | 13019 |
| Oy | | 2957 | uSerApsSerLyAAspValValPheglYargIleValISergIYargGIngly---Leupr | 2976 |
| Dd | | 13020 | TACCAGAACACACACCGTGGTCTTTCCGGCGGCAACCGCTCCGGCGGCGCCCGGATCTGCC | 13079 |
| Oy | | 2976 | O---ValGluTyrgLnAspIleValGlpProCyvrThraAlaValProvalArgAlani | 2995 |
| Dd | | 13080 | GGGGTGTGAAACACAG-----GTCCGGTGTTCATCAATACCTTCCGGTGGTGGTAAC | 13133 |
| Oy | | 2995 | eIle---GluSerSerApyTrAnslInleuHieIsapRIegInAspGlnTyIleue | 3014 |
| Dd | | 13134 | GCTGGCTCCACAATGACCTTCGACCAACTGTCTGCAAGGAGCTGCACACGCAACACTGGC | 131939 |
| Oy | | 3014 | uSerIePrOnIeGlUthrIleGlyPheSerApleuLyArGAsnCyThrAAspITpr | 3034 |
| Dd | | 13194 | GTTGCGGGAACAGAGAGACACGCGCTGTGTCAGACTGCAGCGC-----TGC-- | 132329 |
| Oy | | 3034 | oGUlaIlelThraSnPheserCySylelThrTYrhIsan-----PheGluTy | 3051 |
| Dd | | 13240 | -----GCGGAGGTTCGCGCGGACGAGCGGTTTGCACAACTGTGTGTTCGAAAA | 13289 |
| Oy | | 3051 | rHisProGluSerGlnPheglUGlnIgrValIGluMetGlyValIleuthrtyrPheVea | 3071 |
| Dd | | 13290 | CtAcCCGCTGAGAGAGGTGCTGCACAGCTCTCCGCTGGAGGCGTs-----GTTTTGG | 13343 |
| Oy | | 3071 | IaSlIleGluMeAspGluProLeu---TYrAAspLeuAlaIleala | 3085 |
| Dd | | 13344 | TGCCGTAGCGATGCAGAGCACCAACTATCCGCTGGCGCTGGCGG | 13389 |
| RESULT 8 | | | | |
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|----|-------|---|----------------|--------------------------------|-------|
| Db | 13579 | CCGGGAGACAGACT--- | GTGGACACTGCTGT | TTTCCGGATCCGCGAGCGGATCGCGGCATC | 13635 |
| OY | 559 | LeuAlaValLeuLysSerGlyValMetAlaPheThrLeuIleAspProAsnAspProAla | 578 | | |
| Db | 13636 | CTCGGGGTCTCAAGACGGGGGGCGGGCTTACCTCCATCCATCCACCCGTCGCCCGGACACC | 13695 | | |
| OY | 579 | ArgThrAlaGlnValAlaThrGlnThrAlaAlaThrValAlaLeuThrSerLysLeuHis | 598 | | |
| Db | 13686 | CGCGTCGAGTTTCATGCTCTCGCGGACGGGAAACCGATGCCGCGCTCCACACC----- | 13746 | | |
| OY | 599 | ArgGluThrValGlnLysLeuValGlyArgCysValVal-----ValAspArgLys | 615 | | |
| Db | 13747 | GCCGAGCGCGGCGAGCGCGCTGCGCGCGCGCGCGCGCGTGCATCGATCGACATCCG | 13806 | | |
| OY | 616 | LeuLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrLysSerGlnAspLeu | 635 | | |
| Db | 13807 | GGCATCTGCATCCCTG-----CCGGACACCGCGCTGCGCTGCGCGACCGGACCGGACATC | 13860 | | |
| OY | 636 | AlaIleValAlaIlePheThrSerGlySerThrGlyAspProLysGlyLysMetIleGlnHis | 655 | | |
| Db | 13861 | GCGTACCTGCATCTACACTCTCGGACACACCGAGTGGCGCCCAAGCGATCGGCTACAC | 13920 | | |
| OY | 656 | ArgAlaPheSerSerCysAlaLeuLysPheGlyAlaSerLeu-----GlyIleAsn | 672 | | |
| Db | 13921 | CACAAACGACACCAACGCTGCTGCGCTGCTGAGACGCGCGCTGCGCTGCGCGGGGAGTGG | 13980 | | |
| OY | 673 | SerAspThrAlaGalaLeuGlnPheGlyThrIleAlaPheGlyAlaCysLeuLeuGlnIle | 692 | | |
| Db | 13981 | TCCGCAATGTCACTGCTG-----GCCTTGCAGCTGTGCGGTGGAGATCC | 14025 | | |
| OY | 693 | MetThrThrLeuIleAsnGlyGlyCysValCysIleAspSerLysAspAspArgMetAsn | 712 | | |
| Db | 14026 | TTCCGCGCGCTGCTGCGCGGAGACGCGTGTGTGTG----- | 14061 | | |
| OY | 713 | SerIleProSerPheIleAsnArg-----Tyr | 721 | | |
| Db | 14062 | ---ATGCCCGAGGGGGTGGCGCCGCTACACGACGACTGACACGACCGCTGATCCGCGCG | 14118 | | |
| OY | 722 | AsnValAsnThrMetMetAlaThrProSerTyrMetGlyThrPheSerProGlnAspVal | 741 | | |
| Db | 14119 | CACGTCACCGGTGACCCAAACCCGCTGCGCGCTGGCGATGCTCTCCCGCAGGGGTGG | 14178 | | |
| OY | 742 | ProGlyLeuAlaThrLeuValAlaValGlyGlnGlnMetSerSerLysAlaAlaIle | 761 | | |
| Db | 14179 | GAGTCGGTGG---TCGCTGTGTCTGGCGCGGAGAGCTGCCCGCGCAGGTGTGACCAA | 14235 | | |
| OY | 762 | TyrAlaProLysLeuGlnLeuLeuAsnGlyTyrGlyGlnSerGlnSerSerIleCys | 781 | | |
| Db | 14236 | TGGCGCGCCCGGACCGGGTGAATGTGAAGCTTACGCGCCACCCAA---ACCAAGATGTCC | 14292 | | |
| OY | 782 | PheAlaSerAsnMetSerThrGlnProAsnAsnMetGlyArgAlaVal----- | 797 | | |
| Db | 14293 | GTGAGC-----ATCAGGCGCCCGCTGACCGCGGAGATCTGGATACCGCGCATCGGG | 14343 | | |
| OY | 798 | -----GlyAlaHisSerTyrValIleAspProAsnAspIleAsnArgLeuVal | 813 | | |
| Db | 14344 | TCGCGCGATCGATGGGGGGCGCGCTGTGTGTCTGAC-----GAATCGCTGGCGCGGATG | 14397 | | |
| OY | 814 | ProIleGlyAlaValGlyGlnLeuValIleGlnSerProGlyIleAlaArgAspTyrIle | 833 | | |
| Db | 14398 | CCGCGCGCGCGTGGGGGAACTTACGTACCGCGCGATCCGATGCGCGCGAGATATTC | 14457 | | |
| OY | 834 | ValProProProGlnLysSerProPhePheThrAspIleProSerTyrTyrProAla | 853 | | |
| Db | 14458 | GGGGGGCGGTC---CTGAACCGGGCGGC---TTGTCGCGCGTGGCGCTGGGGGGCGCCAC | 14514 | | |
| OY | 854 | AsnThrPheProAspGlyAlaLysLeuLysTyrArgThrGlyAspLeuAlaArgTyrAlaSer | 873 | | |
| Db | 14515 | -----GCGCGGATGTATTCGACACCGGAGCACTGGTGTGCGCTGCGCTGCC | 14556 | | |
| OY | 874 | AspGlySerIleValCysLeuGlyArgIleAspSerGlnValLysIleArgGlyGlnArg | 893 | | |
| Db | 14557 | GACGGGCGACGAGCTACCTGGGGCGCGGCGGACGACGAGGTCAAGGTGCGCGCTTACCGC | 14616 | | |

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|----|-------|--|-------|
| QY | 694 | ValGluIuEnuGIyAlaIleGIuThrHisIleuAArgInGInMePProAerAerIleuThrIle | 913 |
| Db | 14617 | ATCGAGCTGGGCGAGATCTCAGCGCGCGCTCTCGGCGCTGACCGGGGTGAGCAGCGCCCTC | 14676 |
| QY | 914 | ValValGIuAlaIaThrIlybAArgSerGIuSerSerIaAaSerThrSerIleuIleAlaPheIeu | 933 |
| Db | 14677 | GTGCTC-----GCCCGCAGAGACAAATCCCGGGGACAAAGCGCTGGCTGGCATATC | 14727 |
| QY | 934 | IleIlySerSerIyRheGIuAaAaPProSerAerAlaHisIleIleuAerHisAerAla | 953 |
| Db | 14728 | ACCGCGACCGCC-----GACCGCGCGGAGGCC----- | 14754 |
| QY | 954 | ThryIaIaIleAaenIleuIleuGIuGIuValIleProAArgHisSerIleProSerPhe | 973 |
| Db | 14755 | -----CGCGCGCGCTGGCGAGCGGCTGCCCGCTACATGATCCCGCGCGCC | 14802 |
| QY | 974 | TyrIleCyMeIleuGIuIeuPProAArgThrAlaThrGIyIlyValIleAerAArgAArgIeu | 993 |
| Db | 14803 | GTGCTGGGCTGCGACGCATCCCGTTGACCCCGCAAGGAAATCTGACCCCGCGCGCTG | 14862 |
| QY | 994 | ArgIleMetGIyIyAerIleuAerIlyGIuThrGIuGIyAlaIleValGIuInAla | 1013 |
| Db | 14862 | ----- | 14862 |
| QY | 1014 | ProAlaProIleProAlaPheAla-----AsPThrAla | 1024 |
| Db | 14863 | -----CCGCGACCGCGACTACGCGCGCGGAGTACCGCGCCACAGACCCACCGAG | 14916 |
| QY | 1025 | AlaIyIleuHisSerIleTPrValGIuSerIeGIyIleAerProAlaThrAlaSerVal | 1044 |
| Db | 14917 | GAGATCTGTGGCGGACATCTACGCCGAGAGCTGTGGGTGAG-----CGGCTGGCGCT | 14970 |
| QY | 1045 | GIyAlaThrPhePheGIuIeGIyGIyAaSerIleThrAlaIleIySerMetValAaMet | 1064 |
| Db | 14971 | GAGCATCTTCTTTGCACCTGGCGGGAGACAGCATCTCGGCGCATGTGGCTTACGGCGGC | 15030 |
| QY | 1065 | AlAArg---SerValGIyMetAerIlyValSerAaMetIyGIuHisIleProThrIleu | 1083 |
| Db | 15031 | GTCACACCGCCCGCTGACGCCGACCTGCCGTCCGACCGGTGTCAAGCGCCACAGCTC | 15090 |
| QY | 1084 | AlaGIyIleSerAlaValIyValGIyAerProIleuSerIyThrIleIleProIySer | 1103 |
| Db | 15091 | GCCCGCGTACCGCCCGCGGATC---GGGAGCGGGGAGC---GACATCGACCGCTTGAGC | 15144 |
| QY | 1104 | ThrHisGIuGIyPro-----ValGIuGIuSerIySerGIyAArgIeuTPrPheIeu | 1121 |
| Db | 15145 | GCCCGTATGAGCGCGCGCGGTGTGGCGCGCTGTCTGCGCAGAAACGCGCTGTGTCTTG | 15204 |
| QY | 1122 | AspGIuIleuAerValGIySerIleuTPrIyIleIleProTyrAlaValAArgMetAArgIy | 1141 |
| Db | 15205 | GATCAATGTGAGGGGCCCTTACCGGTTTAAACATGGCGCGCGCTGGCGGTGAGCGC | 15264 |
| QY | 1142 | ProValAaSerAlaAerAlaAArgAlaIleuAlaIleuGIuGIuAArgHisGIuThr | 1161 |
| Db | 15265 | CCGCTGGACACCGAGGCGCTGGCGGGCGGCGCTGGGAGAGGTGGCCCGGACGAGAC | 15324 |
| QY | 1162 | IeuAArgThrThrPheGIuAerGIuAerGIyValGIyAlaGIuIleVal-----HisGIu | 1179 |
| Db | 15325 | CTGGCGACCTGTGTTCGCGCGCCCGGAGGGCGACCCACAGGTGTGTGCTGCCCGCGAG | 15384 |
| QY | 1180 | IyIleuSerGIuGIuMetIyValIleAerIyCyGIySerAerIyAerProPhe--- | 1198 |
| Db | 15385 | CGGCGCAATCTGGGTGGAGGTCTGTGACCGCACGCGCTGTGTGGCAGCAACATCTGAC | 15444 |
| QY | 1199 | GIuValIleuAaGIuGIuInThrThrProPheAaIleuSerSerGIuAlaGIyTPrArg | 1218 |
| Db | 15445 | GAGCGCATCGCGCACCGCGCGCTACACCTTGACCTTGGCGGCCAAATCCCGCTGCAC | 15504 |
| QY | 1219 | AlaThrIleuAArgIeuGIyGIyAaAerHisIleIleuThrIleValMetHisIle | 1238 |
| Db | 15505 | GCAAGAGCTTTTGGTCTTCCAGACGACCGGACGTGTGTGTGTGGCGGTGGTGGACCAATC | 15564 |

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|----|-------|--|------|
| QY | 1239 | lAserspGlyTrpSerIleAspValLeuArgAspIleuAnGlnIleuTyrsAla | 1250 |
| Dp | 15655 | GGCGGCGAGCATGTCATTCACCCCGCTGGGTGATCTTCGGTGGCCCTTAGCC-- | 1562 |
| QY | 1259 | AlaLeuLysAspSerLysAspProIleuSerAlaLeuThrProLeuProIleGlnTySer | 1278 |
| Dp | 15622 | -----CGGGGGTGGCGGGGACAGCCCGGGGCTGGGAGCGCGTGGGAGTACGTC | 1567 |
| QY | 1279 | AspPheAlaLysTrpGlnLysAspGlnPheIleGlnGlnLys----- | 1292 |
| Dp | 15676 | GACTACACCGCTGTGGCAGCGCGCCAAATCGATGATCCACGATCCCGGACGCCGATC | 1573 |
| QY | 1293 | ---LysGlnLeuAnTyTrpLysLysGlnLeuLysAspSerProAlaLys----- | 1309 |
| Dp | 15736 | GGCGCCAGCGCTGAGCTTGGAGAGACGGCTGGCC--GGCATGCCGAGCGCTGGCG | 1579 |
| QY | 1310 | IlleProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGlyCysValIleVal | 1329 |
| Dp | 15793 | CTGGCCACCGAC-----CGCCCTATCCGCTGTGGCCGACACAGCGGGCGCACCGTGG | 1584 |
| QY | 1330 | ThrIleAsp-----GlyGlnLeuTyTrpLysSerLeuArgAlaPheCysAsnGlnHisAsn | 1347 |
| Dp | 15847 | GAAATGCACTGGCGCGCGAGCTGCACAGAGATCGGACATCGCCCGCCGACACAC | 1590 |
| QY | 1348 | ThrThrSerPheValIleLeuLeuAlaAlaPheArgAlaAlaHisTyArgLysLeuThrAla | 1367 |
| Dp | 15907 | GCCACCGAGCTTCAGTGAATGCACAGCCGCTTGACCGCTGCTGGCCAAAGCTTGGCGCC | 1596 |
| QY | 1368 | ValGlnAspAlaValIleGlyTyThrProIleAlaAsnArgAsnArgProGlnLeuGlnAsp | 1387 |
| Dp | 15967 | AATCCCGATGGCGGGGCTTCCCATCGCGGGGGCGCGCCACCCGGCGCTGAGACAC | 1602 |
| QY | 1388 | IleIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHisAspThr | 1407 |
| Dp | 16027 | CTGGTCGGATTCCTGTCACACACCTGATGCTGGGGTGGACGGCGCGGAGATCCGACG | 1608 |
| QY | 1408 | PheGlyThrLeuIleAsnGlnValLysAlaThrThrThrAlaAlaPheGlnAsnGlnAsp | 1427 |
| Dp | 16087 | TTCCACCGAGCTGCAGCGCGGCTCGGACCCGCGAGCTTGAGAGCTTCGAGCACAGAT | 1614 |
| QY | 1428 | IlleProPheGlnArgValIleValSerAlaLeuGlnProGlySerArgAspLeuSerSerThr | 1447 |
| Dp | 16147 | GTGCCGTTTCAGAGCTGTGTGTGAGCGGCTCAACCG--ACCCGAGCTCACCCATCAC | 1620 |
| QY | 1448 | ProLeuAlaGlnLeuIle-----PheAlaValHisSerGlnLysAspLeu | 1462 |
| Dp | 16204 | CCGCTGTGAGCGATGATGCTGGCGCTGGAGAACTTCGCGGGGACGACACCGGCGCGCC | 1626 |
| QY | 1463 | GlyArgPheLysPheGlnGlyLeuGlnSerValProValProSerLysAlaTyTrh-- | 1481 |
| Dp | 16264 | GCGGGGCTGTCCCTCGCGGATGTGGAATACGCGCATTCGGTGGACACCCACACCGCG | 1632 |
| QY | 1482 | ArgPheAspMetGlnPheHisAlaLeuPheGln-----GlnThrAspSer | 1495 |
| Dp | 16324 | CGAGTGAACCTGCACCTTCTCCGCTGGCGGACGCTGAGCGAGCGGCGGCGGCGG | 1638 |
| QY | 1496 | LeuLysGlySerValAsnPheAlaAspGlyLeuPheLysMetGlnThrValGlnAsnVal | 1515 |
| Dp | 16384 | ATCGGCGGACAGTGGAAATTCGCGACCGACGACTTTCACCCGACACACATTCGACAGCTG | 1644 |
| QY | 1516 | ValArgValPhePheGlnIleLeuArgAsnGlyLeuGlnSerSerArgThrProValSer | 1535 |
| Dp | 16444 | ATCGGGCGGCTGCGCGCGGTGCTGGAAGCGATGACCGCCGACCGACACAATCCGTGTGG | 1650 |
| QY | 1536 | IlleLeuProLeuThrAspGlyIleValThrLeuGln-----LysLeuAspVal | 1551 |
| Dp | 16504 | TGCGGTGACCTGCTGCAC-----GAGCGGAGACAGCCCGGCTTCGACACC | 1654 |
| QY | 1552 | LeuAsnValLysHisVal-----AspTyTrpArgGlnSerSerLeuAlaAspVal | 1568 |
| Dp | 16549 | CTGGGCAACCGGGGGGCTGACCGGACCTCCGCGCTTCGATTCCTCCCAACACTT | 1660 |
| QY | 1569 | PheGlnThrGlnValSerAlaTyTrpAspSerLeuAlaValAlaAspSerSerCysArg | 1588 |

Db 16609 TTCCGCCAGCAGCGCCGCCGACCCCGGACCGCCCTCCGCTGGCTCTGGCGCGCGCGCGG 1666

Qy 1589 LeuThrTyrrThrgIuLeuAspArgGlnSerAspIleLeuAlaGlyIrrPleuArg--Arg 1607

Db 16669 ATGACCTACCGGGAGCTGACAGAGCGCGCCAAACCGGTGGCGGACCTGTCGCGGTGCGG 16722

Qy 1608 ArgSerMetProAlaGluThrLeuValAlaValPheAlaProArgSerCysGluThrIle 1627

Db 16729 GGGCGCGCGCCGGGACACCGGTGGCGACTGCTGTTTTC--CGGTGGCGCGAGCGCATC 1678

Qy 1628 ValAlaPhePheGlyValIleuValAlaAsnLeuAlaTyrLeuProLeuAspValArgSer 1647

Db 16786 GTCCGCATCTCTGGGGGCTCTCAAGTCCGGGGCGGCTTACTGCGCATTCGACCCGCGCTG 1684

Qy 1648 ProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyProThrIleValLeuIle 1667

Db 16846 CCGGCGCAGCGGATCGGGTTCATCTGAGCGAC--GCCGCGCGCTGGTCCGATACG 1690

Qy 1668 GlyHisAspThrAlaPro-----ProAspIleGluValThrAsnValGlu 1682

Db 16903 ACCGCCAGCTGGGCGCGCGCTGCACCGCCAGCAGCAGCAGCGCCAGTCTGCAGCTCAC 1696

Qy 1683 PheValArgIleArgAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGlu 1702

Db 16963 GACCCCGCGATCGAGCGCGCGCTCTCAAGCGC-----1699

Qy 1703 HisAspSerThrLysProSerAlaThrSerLeuAlaTyrValLeuTyrrThrSerGlySer 1722

Db 16996 -----CTGCCGCGCGCGGGGGGAGCAGACATCGCTCACTGATCTACACTCGCGGACCC 1704

Qy 1723 ThrGlyArgProLysGlyValMetIleGluHisArgValIleIleArgThrValThrSer 1742

Db 17050 ACCGCGCTGCCCAAGCGGTTCGCGTGGCAGCCACCGTACAGCGCGCCAGTTCGTAAGGCG 1710

Qy 1743 GlyCysIleProAsnTyrrProSerGluThrArgMetAlaHisMetAlaThrIleAlaPhe 1762

Db 17110 GAG-----TCGGGGGCTGCGCGCGGAGGCGCTGGTGCAGTGGCATTCGCTGGCTTC 1716

Qy 1763 AspGlyAlaSerTyrGluIleTyrrSerAlaLeuLeuPheGlyArgThrLeuValCysVal 1782

Db 17164 GACGTGTGCGGTGGAGATCTTCTGGGCGCCAGCTGACAGCGCGGGCGGTGTGTGATC 1722

Qy 1783 AspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGluHisVal 1802

Db 17224 CCCGCAATCCGTGGCGCGCTTCACCGGAAGACTCGACGCGCTGATTAACGGAACAGATC 1728

Qy 1803 AsnAlaAlaSerHisValThrSerSerSerGlnAspValProLeuArgValProArgArg 1822

Db 17284 AGCGTCTCAACCAAGCCCGTGGCGGCGCGCGCGCTGTCA-----CCCGAGGCG 1733

Qy 1823 LeuSerArgThrLeuMetPhePhePheLeuValValThrAspSerThrAlaProAspAla 1842

Db 17335 CTCAAGAGAC-----CTCAACCTGTGTGTGGCCCGCGCAGGCGCTGCGAGGAG 1738

Qy 1843 LeuAspAlaGlnGlyLeuTyrrGlnGlyValGlnCysTyrrAsnGlyTyrrGlyProThrGlu 1862

Db 17383 CTG---GTCACCGCTGGGCGCGCGGGCGGACGATGATCAACGCTACGGGCCCAACGAG 1743

Qy 1863 AsnGlyValMetSerThrIleTyrrProIleAspSerThr-----GluSerPheIle 1879

Db 17440 -----GCCACGCGTTAAGCGGCGATCGACGCGCGCGCTGGCGCGCGGAGCGCTG 1748

Qy 1880 AsnGlyValProIleGlyArgAlaLeuAsnAsnSerGlyAlaTyrValAlaAspProGlu 1899

Db 17488 GGTGTGTGCGCATCGCTCCCGCGTCCCGGCGCGGCGCGGTTCGTGTCTGAAGAAGTCG 1754

Qy 1900 GlnGlnLeuValGlyIleGlyValMetCylGluLeuValValThrGlyAspGlyLeuAla 1919

Db 17548 CTGCGCGCGGAGCGCGCGGGTGTGTGTGGGAGCTTATGTCGCGGCGCGCGGGGTGACC 1760

Qy 1920 ArgGlyTyrrSerAspLys--AlaLeuAspGluAsnArgPheValHisIleThrValAsn 1938

| | | | |
|----|-------|--|-------|
| Db | 17608 | TGCGGCTATTGGGGGGGGGGGGTTCACCGCGCTCGCGGTTCTGGGCGTGTCCGTTCCGGG | 17667 |
| Oy | 1939 | AspGlnThrValIyValaIyTyrGThGlyAspArgValArgTyrArgIleGlyAspGly | 1958 |
| Db | 17668 | GCGCCCGGGGGCGGGATGTATCGCACCGGGACCTGGTGGCGTGGCGCC--GGCGACGGC | 17724 |
| Oy | 1959 | LeuIleGlnPhePheGlyArgMetAspThrGlnPheValIleArgGlyValAspArgIleGly | 1978 |
| Db | 17725 | CAACTGGACTATCTGGGCGCGGCTGCAGAAACAGTCAAGATCCGGAGCTTACCGCATCGAA | 17784 |
| Oy | 1979 | SerAlaIleGlnIleAlaIleLeuLeuArgAspSerSerAlaIleArgAspAlaIleVal | 1998 |
| Db | 17785 | CTCGGCGAGTGGCGGGCGCGCCCTGGCTGGGTGGACGGTGTCCACACAGCGCGTGGTGC | 17844 |
| Oy | 1999 | LeuGlnGlnMetGlnAspGlnAlaProGlnIleLeuGlyPheValIleAlaPheHisAsp | 2018 |
| Db | 17845 | GCCGCGAGACCGGGCGCGGGACAAAGCGGCTGGTGGCTTACATCACCC-- | 17892 |
| Oy | 2019 | HisSerGlnMetAspLeuGlyGlnSerAlaAsnGlnValIleGlnGlyTyrGlnMetHisPhe | 2038 |
| Db | 17892 | ----- | 17892 |
| Oy | 2039 | GluSerGlnMetTyrSerAspIleGlyGlnIleAspProSerThrIleGlySerAspPhe | 2058 |
| Db | 17893 | -----GGACCGCGGACCGGGCGCGCGGTGGCGCGCC-- | 17922 |
| Oy | 2059 | LeuGlyTyrThrSerMetTyrAspGlySerGlnIleAspPheAspGlnMetHisGlnTyr | 2078 |
| Db | 17922 | ----- | 17922 |
| Oy | 2079 | LeuGlyGlnThrThrAlaGlnThrLeuHisAspAsnArgSerLeuGlyValMetValLeuGlnIle | 2098 |
| Db | 17922 | ----- | 17922 |
| Oy | 2099 | GlyThrGlySerGlnMetIleLeuPheAsnLeuAspSerArgLeuGlnGlySerTyrValGly | 2118 |
| Db | 17923 | -----GGCTGGCGGACACGGCTGCCCGCGCTTACATG-- | 17952 |
| Oy | 2119 | LeuGlnProSerArgSerAlaAlaPheValAsnValAspIleThrGlySerIlePro-- | 2137 |
| Db | 17953 | -----GTCCGGCGGGCGGTGTC--ACGGTCGACGGAAATCCGTTG | 17991 |
| Oy | 2138 | SerLeuAlaGlyValValValGlnValGlyThrAlaThrAspIleGlyGlnValAsp | 2157 |
| Db | 17992 | ACGGCCAAACGGAAATCTGCACACCGCGCGCTGGCCGACCCGAATCTCCGACGCGGAC | 18051 |
| Oy | 2158 | AspLeuHis--ProAspLeuValValLeuAsnSerValIleGlnTyrPheProSerSer | 2176 |
| Db | 18052 | CGGTATGCGCGCCCGGAC-----AACCGCTGCT--GAG | 18081 |
| Oy | 2177 | GlyTyrLeuAlaGlnIleAlaAspThrLeuIleHisLeuProAsnValGlnArgIle-- | 2195 |
| Db | 18082 | GAGATCCCTGGCGGGCATCTATGCCAGGTGTCG-----GGCGTGCAGCGGGTGGG | 18122 |
| Oy | 2196 | -----PhePhe-----GlyAspValArgSerGlnAlaThrAsnGlnHis | 2208 |
| Db | 18133 | GTCCGACGACTGCTTCTGCACCTGGCGGGGAC-----AGCATCTCTCGATGACAGTGG | 18166 |
| Oy | 2209 | PheLeuAlaAlaArgAlaIleHisThrLeuGlyValAsnAlaThrIleAsp--AspVal | 2227 |
| Db | 18187 | GTGACCGGGCGCGCGCGCGCGCGCTGTGTGCAAG-----ACCGGACATCTTGGTC | 18240 |
| Oy | 2228 | ArgGlnValMetAlaGlnLeuGlnAspMetGlnGlnLeuLeuValGlnProAlaPhe | 2247 |
| Db | 18241 | GAGCAGACGCGTCCCGCGGTGGCGGGGTGCAGAGTGGCCAGCCGACGCGCGG-- | 18297 |
| Oy | 2248 | PheThrSerLeuLysAspArgPheProGlyLeuValGlnHisValGlnIleLeuProLys | 2267 |
| Db | 18297 | ----- | 18297 |
| Oy | 2268 | AsnMetGlnAlaValAsnGlnLeuSerAla-----TyrArgTyrAlaAlaVal | 2284 |
| Db | 18298 | GCCGACGAGGTGTCTGGGAGATACCGGACCCCGCATCTCCGCTGCGACGAGCGTG | 18357 |

| | | | |
|----|-------|---|-------|
| QY | 2285 | HisValArgIysLeuLeuGlyAspGluLeuValLeuProValGluIlyAspAspTrpIle | 2304 |
| Db | 18358 | GAAGCCCGCCGCGC | 18372 |
| QY | 2305 | AspPheGlnIlaAsnGlnLeuAsnGlnIlySerLeuGlyAspLeuLeuIysSerSerAsp | 2324 |
| Db | 18373 | -----CAAGTCATCTACGTTCAACCAAGCCATCTC----- | 18402 |
| QY | 2325 | AlaAlaIleMetAlaValSerIlySIIeProPheGluIleThrAlaPheGluArgGlnVal | 2344 |
| Db | 18403 | -----GTGCGGGCGCGCGCGGTCAACC-----GAGCGCAGCGT | 18438 |
| QY | 2345 | ValAlaSerLeuAsnSerAsnIleAspGlu-----TrpGlnLeuSerThrIleArg | 2361 |
| Db | 18439 | GTCAACGGTGTTCAGAGCCCTCTGTGACCGGACAGCCATCTGCGGTGCGGTCCAGCC | 18478 |
| QY | 2362 | SerSerAlaGluGlyAspSerSerLeuSerValProAspIlePheArgIle--AlaGly | 2380 |
| Db | 18499 | GACGACGCCACCGGCGAGTGTCGTGCTGACAGTCCCGAACCCGGCGGTGACCCGCG | 18558 |
| QY | 2381 | -----GluAlaGlyPheArg | 2385 |
| Db | 18559 | GCTGCGCTGCATGCGGTGACGAGCTGTCCAGCGCGCGCTCATCCAGGCGCGGTGCGG | 18618 |
| QY | 2386 | ValGlu-----ValSerSerAlaArgGlnTrpSerGln--AsnGlyAlaLeu | 2400 |
| Db | 18619 | CTGAACCCCGCGCGCGCGGTGATGCTCAGCGCGGTGTGGCGAAGCCACCGCGGAGCTG | 18678 |
| QY | 2401 | AspAlaValPheHisIleCysCysSerGlnGly-----ArgThrLeu----- | 2414 |
| Db | 18679 | GTGTGTATCTTCCACCACTGCGCGGTGACGAGTGTCTATGGCGAATCTGTGTGACAGAC | 18738 |
| QY | 2415 | ValAsnPhePro--ThraPheHisIle-----LeuArgIlySerAsp | 2427 |
| Db | 18739 | TTGAACATCGCGCTGTGGCGGACATCACCGCGGCGACCGGTGCGTTACCGCGCGCGG | 18798 |
| QY | 2428 | LeuLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgIleAlaIleGluValArg | 2447 |
| Db | 18799 | ACCTGTTTCGCGCGCGGTGAGCGTCAACGCGCTGGCGCGGACGCCACCCAGCGGAGTGGCG | 18858 |
| QY | 2448 | GluArgLeuArgSerLeuLeuProSerIlyrMetIleProSerAsnIle----- | 2463 |
| Db | 18859 | GACCGGCG--CGGCGCTGTGGCGGCGGTGGCGGCGGACCCGCGCGCTGCCGCGGTGCG | 18917 |
| QY | 2464 | -----ValIleLeuAspIlyMetProLeuAsnAlaAsnGlyIlyValAsp | 2478 |
| Db | 18918 | TCCGAGCGTGAACACTTTCGCTCCGCGGCGCACTCTGACGAGCTGGACACCGAAAC | 18977 |
| QY | 2479 | ArgIlySerGluLeuSerArg--ArgAlaIlyValValProIlyGlnGlnIleThrAlaAlaPro | 2497 |
| Db | 18978 | CACCGCCATGCTGTGCTGTAGAGTGGCGCGGCGCATTCACGCGGCGTGTCAAGACATCTT | 19037 |
| QY | 2498 | LeuProThrPheProIleSerGlnValGluValIleLeuCysGluGluI-----AlaIle | 2515 |
| Db | 19038 | GCTATATGCGGTGCGCGGTGCG-----TGCGCGAGATTTTGGCGGAC | 19079 |
| QY | 2515 | rGluValPheGlyMetIlyValAspIleThrAspHisPhePheAsnLeuGly----- | 2532 |
| Db | 19080 | CCGCGGCGACCGCCATTCGATCCAGCTCGGCGGCGAC-----GGCGGCGCGGA | 19127 |
| QY | 2533 | -----GlyHisSerLeuLeuAlaThrIlyIleuIleSerArgIleAspGlnArgLeuIly | 2550 |
| Db | 19128 | GGAACGTGGCGCGGACATTCACCTGTCCACACCGTGGGCTGTTCACACCAATACCC | 19187 |
| QY | 2550 | sValArgIleThrVal-----IlyAspValPheAspHisProValPhe | 2564 |
| Db | 19188 | GGTGCGCTGACCGTGTGGCGCGCTGTGATTTGGGCGGAGTCTGTGCGCGCGCGCGGACT | 19247 |
| QY | 2564 | eAlaAspLeuAlaSerValIleArgGlnGlyLeu-----GlyLeuGlnGlnProValSerHis | 2583 |
| Db | 19248 | GGGGACATCTCTCAAGCGCGCCAGAGAACATCTTCGCTGCGTCCGCGGACCGCTGAGCTA | 19307 |

QY 2583 pgljnglmglnaspargseralahlsmetalaproargthrgluthrglualalle 2603
DB 19308 cggg-----ctgtgtgctgactaataatccggcggtgagactgacggagcga 19355
QY 2603 ucysabpgluphualylvalleuglypheglnvalglylletthraspaphpheas 2623
DB 19356 cccggcgatcgaggttaactactctgggcccgcagggggggccacagatgtaacggcga 19415
QY 2623 pleu-----glylyhiserleumetalamthrylsleualargllegly-- 2639
DB 19416 catgtgcccggcccgacccggacggctggagcggcaccggcgccgacatcccat 19475
QY 2640 -----hisargyleuaspthrthryalservalysaspvalpheasphiprova 2656
DB 19476 gccactgatacgacaccttgagactcaacggcggtacacgtgacgtccggccggcg 19535
QY 2656 lleuphegln-----leualalaleuaspasleuvalglnserlysth 2672
DB 19536 gctgcacggccacatgacactggcgccctgcgcgtgacatcagacgagatcccgccgt 19595
QY 2672 rhangluile-----valgl 2677
DB 19596 gagccggctgtgtccagacgctgacggcgatctgcgcgcacgtgcggcgccggcg 19655
QY 2677 ygljarglumevalaglutyzserpophglnleuelpheglnuaspproglnu 2697
DB 19656 cggcgtagacggcctcgacatccggcgccgctc----- 19692
QY 2697 uphemetalasergluleybrpoglnleuglnleuglnleuglnleuglnleuglnle 2717
DB 19693 -----accacgacacagctcagctgacgtggcgccacacggcgtccacgctgct 19745
QY 2717 rproserthnglmeaglnlysalaphleupheaphrthethrthralarg---proar 2736
DB 19746 ggcgctgacggcgctgacgaggtgtgctgttcacggcgaacacggcgacggcgacga 19805
QY 2736 gprophevalprophethrytleasphepserthsergluprophalalaglyle 2756
DB 19806 cgaactctatggcgggcagctgcacatccgcatcgccggcgccgtcagccggcgct 19865
QY 2756 uilelysalacysegluserleuvalenhiyleuaspillepheargthryalphealag 2776
DB 19866 ggcgcgacggcggtgcacggcgctgctgacacggcgaacacgtgagccggcttgcga 19925
QY 2776 ualasergljnglueytrglvalvalleusercysleuaspuleuproileglnval 2796
DB 19926 cgcgctgacgacggcggtccagatcattccggcgacggcgacggcgctgagcgctgt 19985
QY 2796 egluthr-----gluasphaniileanthrathrhangluupheleuaspglupheal 2814
DB 19986 cagagctgcacggcgagagagacatccggcagctggcg-----gccgacagcgccgc 20036
QY 2814 alysgluprovalargyleuglyhis--proleuileargphethrillelyys--gl 2832
DB 20037 cgcgctgtgacggcgatctcagagctcggcgctcggcggtgagcgacggcgacggcg 20096
QY 2832 nthrlysermetargvalilemetarglieserhisaleuayrargelyleuserle 2852
DB 20097 gacccgacggcgacggcgctgctgacacacacacatgctgacggcgctgagat 20156
QY 2852 ugiuhsvalarglyleuhsmetleuyrhanglyargserleuuproproh 2872
DB 20157 gccgactctgttgaggagatcttccggcgctactacggcgacggcgcttccggcgccgc 20216
QY 2872 eglupheserarglyrmeaglntrthralaasp--glyarggluserglyhsqlyph 2891
DB 20217 gccctaccccgcgctgtgctgacgtgacggcgacacggcgacacggcgccggcgccgc 20276
QY 2891 etprargasprvalilegln-----asnthrpromethrilleuserasphartha 2909
DB 20277 gtagggcgagaggtgtgacggcgcttgcacacacggcgacggcgccggcgacggcgct 20336
QY 2909 lvalaspgllyasnapralathrcysylsalaleuhsleuserlylevalasnllepr 2929

DB 20337 cgaactcgggccggcgaacagctc-----gagacgttccacccctggcc 20375
QY 2929 oserglnvalileuargglyseraseranile-----lletthrglnlath 2944
DB 20376 cgcgcgactgacccggcgccgttcacacgttgccggcgctgctgacacacacgtgacac 20435
QY 2944 rvalpheasnalalacysalaleuvalleuserargluseraspherylsaspval 2964
DB 20436 ctgtgctgacggcgccgctgttcggcgctgctgtgctgacacggcgacacggcgacgtgct 20495
QY 2964 lphgilyargilevalserglyarglmglyleuprovalglutryrclnappileval 2984
DB 20496 ctgcgacacacggcgctgacggcgccggcgacggcgacggcgacggcgacggcgacggcg 20555
QY 2984 yprocystrhasnalavalprovalarglahlalileguseraseraspharythn--gl 3003
DB 20556 cctgtgatacagacggcgctgacggcgccggcgacacgtgacacggcgacacggcgac 20615
QY 3003 nleuhsleuaspilleglnaspglntyrleuhsleuserleuprohlegluthrilleglyph 3023
DB 20616 cctgtgacacacggcgctgacggcgccgttcacacacacacacacacacacacacacacac 20675
QY 3023 eseraspuleuylargasncysethrtrpproglnalalethrasn----- 3039
DB 20676 caacgagatccacga-----atcacggcgccagacgaacagct 20711
QY 3040 -phesercyscallethrythrihsenpneglutrythihsenpneglutrythihsenp 3059
DB 20712 ttctgcacacggcgctgacggcgccgttcacacacacacacacacacacacacacacac 20771
QY 3059 nglnargvalglumecglyvalleuhyrlysphevalasnlleglumeaspgluprole 3079
DB 20772 cagagactggcgctgac 20816
QY 3079 utyraspuleuvalalealaglyvalgluproaspglvalaglyleuylasphartha 3099
DB 20817 ctacccgctgacggcg-----cagcgccagacggcg-----gggtgcagctgacggcgcccaat 20867
QY 3099 lilealalystrglneuphegluyarglyvalgluhsleuhsleuhsleuhsleuhsle 3119
DB 20868 cgaatgcgcacacggcggttttcacacacacacacacacacacacacacacacacac 20927
QY 3119 rlystrpnegluglyleuhsnsr 3127
DB 20928 ggcgctgactgctgacatgacggcg 20952

RESULT 9
US-10-282-122A-33351
; Sequence 33351. Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

QY 558 MetLeuAlaValLeuIleuYSerGlyAAsnAlaPheThrIleuLeuAspProMetAspProPro 577
 DB 1564 ATGCTGGCCATCTCAAGCGCGGGCGCTAGCTGCGGATTCACCGGATTCACCGCAG 1623
 QY 578 AlaArgThrAlaGlnValValThrGlnThrArgAlaThrValAlaLeuThrSerLysLeu 597
 DB 1624 GATCGCTGAGCTTCTGATGAGCAGACGCGATTCGATTCGATTCGATTCGATTCGATTC 1677
 QY 598 HisArgGlnThrValGlnIleuValGlyArgCys---ValValAlaAspArgIleu 616
 DB 1678 -----ACGAGTTCGCGGCGGCGGATTCCTGACAGCTTCGACAGCTTCGACAGC 1722
 QY 617 LeuGlnSerValSerAlaSerAspPheSer-----SerLeuThrLys 631
 DB 1723 CTGAGTCTGCGGATCGCTGATGCTGCTACAGCAGCAAAACCGGATTCACAGACCTCG 1782
 QY 632 SerGlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspProLysGlyIle 651
 DB 1783 CCAGACAACTCGGCTACGATTCATACCTCAGGTTCCAGCGCAAAACCAAGGCGACC 1842
 QY 652 MetIleGlnHis-----ArgAlaPheSerSerCysAla-----LeuLysPhe 665
 DB 1843 TTGCTGCTCATCAACACTGATGCGCTGCTGCGGCTACGACGAGCTGTTCAAGTTC 1902
 QY 666 GlyAlaSerIleuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPhe 685
 DB 1903 AAC-----GAAAAAGAGCTGCGAGCTG---TTCCATCTCTTCGCTTC 1944
 QY 686 GlyAlaCysLeuLeuGlnIleMetThrThrIleuIleAsnGlyIle---CysValCysIle 704
 DB 1945 GACTTCTCGGCTGAGATTTTCGCGCGCTGCTGACGCTGACGCTGACGCTGATATGCTG 2004
 QY 705 ProSerAspAspAspArgMet---AsnSerIleProSerPheIleAsnArgIleAsnVal 723
 DB 2005 CCTTGGAGGTAAACCGCTTCGCGGAGAGTTCATCGCTGCTGTTGACAGCAGCTC 2064
 QY 724 AsnThrMetMetAlaThrProSerTyrMetGlyThrPhe-----SerPro 738
 DB 2065 ACGGTCTTACACAGACGCGATTCGCTTCAGCAATTCATGCGCGCTTCGATTC 2124
 QY 739 GlnAspValProGlyLeuAlaThrIleuValIleValGlyGlnIleMetSerSerSerVal 758
 DB 2125 ACTTCGTGTATTCGCTGAGAACATATATCTTGGCGGAGAGCGCTGACGCTTCGACG 2184
 QY 759 AsnAlaIleThrAlaProLysLeu-----GlnLeuLeuAsnGlyTyrGly 773
 DB 2185 CTGAAACCGCTGCTGCGACGCTTCGCGGATCAGACGCGACTGATCAATGATGCGC 2244
 QY 774 GlnSerGlnSerSer---SerIleCysPheAlaSerAsnMetSerThrGlnProAsnAsn 792
 DB 2245 ATTACCGAAACCGCTGATGACCTTACAGACCCATCACCTGCGCGGACAGCAGCACAC 2304
 QY 793 -----MetGlyArgAlaValGlyAlaHisSerTyrValIleAspProAsnAsp 808
 DB 2305 CCGGACGCGCGATTCGCGAGCGATTCGCGACCTGTCGTATGACGTCGACGCGCAT 2364
 QY 809 IleAsnArgLeuValProIleGlyAlaValGlyIleValIleGlnSerProGlyIle 828
 DB 2365 TTCAC---ACGGTTCGCGAGGTTGCGAGCGGAACTGCACACGCGCGGCTTC 2421
 QY 829 AlaArgAspTyr-----IleValProProProPro 838
 DB 2422 GCGCGGCTTATCACAACGCGCTGACCTACGCGCTGACGCTTCGCTTCGCA----- 2472
 QY 839 GlnLysSerProPhePheThrAspIleProSerTyrProAlaAsnThrPheProAsp 858
 DB 2473 -----GACCGCTTC-----GCCAAC-----GAC 2490
 QY 859 GlyAlaValLeuValTyrGlnThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIleVal 878
 DB 2491 GGGGCGGCTTGTTCACGCGACGCGGATTCGCGCGCTATTAACCGCAGCAACCATCGAA 2550
 QY 879 CysLeuGlyArgIleAspSerGlnValIleArgGlyGlnArgValGlnLeuGlyAla 898

DB 2551 TACCGCGCGGCTTTCAGCATTAAGTAAGATCGCTTCGCGCATTCAGACGCGGAA 2610
 QY 899 IleGlnThrHisLeuArgGlnGlnMetProAspAspLeuThrIleValIleGlnAlaThr 918
 DB 2611 ATCGACCGCGGCTGACAGGCACTTCGCTGCGCGGAACTGATTCGCTGCGC----- 2661
 QY 919 LysArgSerGlnSerIleAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyr 938
 DB 2662 -----GCATGACGCGGCAACTGCGCGGCTGATTCGCTGCGCGCT----- 2700
 QY 939 PheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrLys---AlaIle 957
 DB 2701 -----CAGCTGACGCG-----GATCAACAGCGCTACGTAACCTG 2739
 QY 958 AsnIleLysLeuGlnGlnValLeuProArgHisSerIleProSerPheTyrIleCysMet 977
 DB 2740 AAAGCGGAGCTTCGTGCAACCTGCGGATTCATGCTGCGGACCCACTTCATCTTCCTC 2799
 QY 978 LeuGlnLeuProArgThrAlaThrGlyLysIleAspArgArgLysArgIleMetGly 997
 DB 2800 GACAGCTGCGCTGACGCGCAATGCGACAGCTGACCGCAAGCGCTGCGCGCGGAC 2859
 QY 998 LysAspIleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIle 1017
 DB 2860 GCGCGT-----CAGTTGCAAGCGGCTTACGCTG-----GCGCGCAA----- 2895
 QY 1018 ProValPheAlaAspThrAlaAlaLysLeuHisSerIleTyrValGlnSerLeuGlyIle 1037
 DB 2896 -----GCGAGCTGGAAGAACATTCGCTGCGTTCGAGCGCGCTTCMAAGTTC 2946
 QY 1038 AspProAlaThrValAsnValGlyAlaThrPhePheGlnLeuGlyGlyAsnSerIleThr 1057
 DB 2947 GAG-----CAATGCGAGCGCAGCAGCACTTCCTGAGCTGCGGCGGCTTCGCTTCG 3000
 QY 1058 AlaIleLysMetVal-----AsnMetAlaArgSerValGlyMetAspLeu 1072
 DB 3001 GCGGTGAGATGCTGCTGCGCGGCTTCGAGACATTCACAGCGGAGCGGCGCTC----- 3054
 QY 1073 LysValSerAsnIleTyrGlnHisProThrLeuAlaGlyIleSerAlaValLysGly 1092
 DB 3055 -----AAGCACTGTTCCGAACAGCGGCTGCTGCTGCTGCGCGCGCTGCAAGAA 3108
 QY 1093 -----AspProLeuSerTyrThrIleuIleProLysSer 1103
 DB 3109 AAAAATGCGAAATGATCATGCACTGAGCAATTCATTAATCATCTGCA-GGCATCTCAA 3167
 QY 1104 ThrHis-----GlnGlyProValGln 1110
 DB 3168 ACGTTTATCAGCGGAGGAATGATTAATTGATTGCTTACAGAGAGACCCAGCTCAA 3227
 QY 1111 Gln----- 1111
 DB 3228 CAGTTCCTGACTCCGTTAATGCTGCTGCGCGGTGAACGCAAGCGCTGCGATCTG 3287
 QY 1112 ----- 1111
 DB 3288 CTCAGCGCGGAGGCTGAATCTTCACGCGGCTCACCGCATTCGACAGAGACGCGC 3347
 QY 1112 -----SerTyrSerGlnGlyArgLeuThrPheLeuAspGlnLeuAspVal 1126
 DB 3348 GCACCGCTGCGCTGCTGCTGCGAGCGGCAATGATCATCTGCGCAACTGGAACCG 3407
 QY 1127 GlySerLeuTyrIleuIleProTyrAlaValArgMetArgGlyProValAsnValAsp 1146
 DB 3408 CACAGCGCGGCTTACCAATTCGCTGCTGCTGCTGCTGATGATGCGCGCTGAGTTCGAG 3467
 QY 1147 AlaLeuArgArgAlaLeuAlaLeuGlnGlnArgHisGlnThrLeuArgThrPhe 1166
 DB 3468 GCGTTCGCGCGCGCTTGAACAGCTGATGACGCTGACCAAAACCTTCGCGACCACTTC 3527
 QY 1167 GlnAspGlnAspGlyValGlyValGlnIleValHisGlnLysLeuSerGlnGlnMetLys 1186

| | | | |
|----|------|--|------|
| Qy | 1873 | AhpserthrgIuserPheIleasnGlyValProIlegIyAArgAlaleuAnaAsnSerGly | 1892 |
| Db | 5634 | ACCCCTGGCCGATACGCACAAACCCGAGCCCGCATTTGGACGGAGGATTCGGACCTGTGC | 5693 |
| Qy | 1893 | AlaTyrValValAspProGluGlnGlnIleuValGlyIlegIyValImetGlyGlyLeuVal | 1912 |
| Db | 5694 | TGGTAACGGCTGCAGACCGCATTTTCAACCCGGTCCGCCAGGGTTTCACCGCGGAATGCAC | 5753 |
| Qy | 1913 | ValThrGlyAspGlyLeuAlaArgGlyTyrSerAspLys--AlaLeuAspGlyAsnArg | 1931 |
| Db | 5754 | ATTGGCCCATGCCGGCTGTGGCCGGGGTTATACACACCGTGTGCATGCACCGCTGCAGCGC | 5813 |
| Qy | 1932 | PheValHisIleThrValAsnAspGlnThrValIlyAlaTyrArgThrGlyAspArgVal | 1951 |
| Db | 5814 | TTTTTGGCCAGATCCGCTTCTCCAAACGACGCGCGGCTTTGATTCACACCGGAGATCTGACC | 5873 |
| Qy | 1952 | ArgTyrArgAlIlegIyAspGlyLeuIlegIyPhePheGlyArgMetAspThrGlnPheLys | 1971 |
| Db | 5874 | CGTTATTAACCCGCA--GGAACCATGCATACACCGCGGCGGCTATTCGACCATCAAGTGA | 5930 |
| Qy | 1972 | IleArgGlyAsnArgIlegIyUserAlaGluIlegIyAlaAlaLeuLeuAspSerSer | 1991 |
| Db | 5931 | ATCCGTGGCTCCCGATCGAATCGGCGCAATTCGAAGCGCGCTGCAGAACGCATTCGGCT | 5990 |
| Qy | 1992 | ValArgAspAlaAlaValValLeuGlnGlnAsnGluAspGlnAlaProGluIleLeuGly | 2011 |
| Db | 5991 | GTGGCGCGAATGCATTTGCTGCTG-- | 6011 |
| Qy | 2012 | PheValValAlaAspHisAspHisSerGlyAsnAspLysGlyGlnSerAlaAsnGlnVal | 2031 |
| Db | 6012 | -----GCCGTG | 6017 |
| Qy | 2032 | GluGlyTyrGlnAspHisAspHisSerGlyMetTyrSerAspIlegIyGluIleAspPro | 2051 |
| Db | 6018 | GACCGG----- | 6023 |
| Qy | 2052 | SerThrIlegIySerAspPheLysGlyTyrThrSerMetTyrAspGlySerGlnIleAsp | 2071 |
| Db | 6023 | ----- | 6023 |
| Qy | 2072 | PheAspGlyMetHisGlyTyrPheLysGlyLysThrArgThrLeuHisAspAsnArgSer | 2091 |
| Db | 6023 | ----- | 6023 |
| Qy | 2092 | LeuGlyAsnValLeuGluIlegIyThrGlySerGlyMetIleLeuPheAsnIleuAspSer | 2111 |
| Db | 6023 | ----- | 6023 |
| Qy | 2112 | ArgLeuGlyUserTyrValGlyLeuGluProSerArgSerAlaAlaAspValAsnLys | 2131 |
| Db | 6023 | ----- | 6023 |
| Qy | 2132 | AlaThrGlyUserIleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAlaThr | 2151 |
| Db | 6023 | ----- | 6023 |
| Qy | 2152 | AspIlegIyGlnValAspAspLeuHisProAspLeuValValLeuAsnSerValIlegI | 2171 |
| Db | 6023 | ----- | 6023 |
| Qy | 2172 | TyrPheProSerSerGluTyrLeuAlaGluIleAlaAspThrLeuIleHisLeuProAsn | 2191 |
| Db | 6023 | ----- | 6023 |
| Qy | 2192 | ValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGluHisPheLeuAla | 2211 |
| Db | 6023 | ----- | 6023 |
| Qy | 2212 | AlaArgAlaIleHisThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLysMet | 2231 |
| Db | 6023 | ----- | 6023 |
| Qy | 2232 | AlaGluLeuGlyAspMetGluGluIleuLeuValGluProAlaPhePheThrSerLeu | 2251 |

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|----|------|--|------|
| Db | 6023 | ----- | 6023 |
| Qy | 2252 | LysAspArgPheProGlyLeuValGluHisValGluIleLeuProLysAsnMetGluAla | 2271 |
| Db | 6023 | ----- | 6023 |
| Qy | 2272 | ValAsnGluLeuSerAlaTyrArgTyrAlaAlaValAlaHisValArgGlySerLeuGly | 2291 |
| Db | 6024 | -----CAACTGGCGCGCTAT- ::: ::: | 6038 |
| Qy | 2292 | AspGluLeuValLeuProValGluLysAspAspTrrPileAspPheGlnAlaAsnGlnLeu | 2311 |
| Db | 6039 | -----CTGCTGCGCGCGCTCACCCCTGACAG- ::: ::: | 6062 |
| Qy | 2312 | AsnGlnLysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValSer | 2331 |
| Db | 6063 | GATCAACACAGCGCTACGTAACCTGAAACCTGAAACCC- ::: ::: ::: | 6095 |
| Qy | 2332 | LysIleProPheGlnIleThrAlaPheGluArgGlnValValAlaSerLeuAsnSerAsn | 2351 |
| Db | 6095 | ----- | 6095 |
| Qy | 2352 | IleAspGluTrrGlnLeuSerThrIleArgSerSerAlaGlnGlyAspSerSerLeuSer | 2371 |
| Db | 6095 | ----- | 6095 |
| Qy | 2372 | ValProAspIlePheArgIleAlaGlyGluAlaGlyPheArgValGluValSerSerAla | 2391 |
| Db | 6095 | ----- | 6095 |
| Qy | 2392 | ArgGlnTrrSerGlnAsnGlyAlaLeuAspAlaValPheHisHisCysCysSerGlnGly | 2411 |
| Db | 6095 | ----- | 6095 |
| Qy | 2412 | ArgThrLeuValAsnPheProThrAspHisHisLeuArgGlySerAspLeuLeuThrAsn | 2431 |
| Db | 6095 | ----- | 6095 |
| Qy | 2432 | ArgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeuArg | 2451 |
| Db | 6096 | -----GACCTCCGT | 6104 |
| Qy | 2452 | SerLeuLeuProSerTyrMetIleProSerAsnIleValIleAspLysMetProLeu | 2471 |
| Db | 6105 | GCGAACCCTGCCGATACATGCTGCCACCCACCTTATCTTCTCTCGACAACTGCCGTG ::: ::: ::: ::: ::: | 6166 |
| Qy | 2472 | AsnAlaAsnGlyLysValAspArgLysGluLeuSerArgArgAlaLysValAlaProLys | 2491 |
| Db | 6165 | ACCGCAACGGCAAGCTGACCGCACGACGCGCTG- ::: ::: | 6197 |
| Qy | 2492 | GlnGlnTrrAlaAlaProLeuProThrPheProIleSerGluValGluValIleLeuCys | 2511 |
| Db | 6197 | ----- | 6197 |
| Qy | 2512 | GluGluAlaThrGluValPheGlyMetLysValAspIleThrTrpAsnAspPheAsnLeu | 2531 |
| Db | 6197 | ----- | 6197 |
| Qy | 2532 | GlyGlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnArgLeuLysVal | 2551 |
| Db | 6197 | ----- | 6197 |
| Qy | 2552 | ArgIleThrValLysAspValPheAspHisProValPheAlaAspLeuAlaSerValIle | 2571 |
| Db | 6197 | ----- | 6197 |
| Qy | 2572 | ArgGlnGlyLeuGlyLeuGlnGlnProValSerAspGlyGlnGlyGlnAspArgSerAla | 2591 |
| Db | 6198 | -----CCAACGCGCGACCGCG--AGCCACTTGCACAGCGCGC | 6230 |
| Qy | 2592 | HisMetAlaProArgThrGluThrGluAlaIleLeuCysAspGluPheAlaLysValLeu | 2611 |
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Db 6231 TACGTGGCCGCGAGGTGAATTGAGACAGACAGTGGACAGTCTGCGCCGCAATGTCCTG 6290
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Db 6291 AAGGTGGGAGGTCGGTGGCAGGACAAATTTCTTCAACTCGCGGCCCATTTGCTGCTG 6350
Qy 2631 AlaThrLeuLeuAlaValGlyIleGlyIleAspLeuAspThrThrValSerValIleAsp 2650
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Qy 2651 ValPheAspHisProValIlePheGlnLeuAlaIleLea----- 2663
Db 6411 CTGTTTGAAGCCCGCATCTGGCAGCCTTTGCCCAAGCGCGCGCGGCGGCGGCGGCAAT 6470
Qy 2664 ---LeuAspAsnLeuValGlnSerLysThrAsnGluIleValGlyIleArgIleMetAla 2682
Db 6471 GACGCGCAGCGCTTCATCAAGCGCGACCGGACAGCGCGCTGGCTGTGTTACGGCGAG 6530
Qy 2683 GluTyrSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAlaSerGlu 2702
Db 6531 CAGCGTCAGTGTGTT-----CTCTGGCAGCTCGACCTGAAAGC--ACCGCTTACAGC 6581
Qy 2703 IleLysProGlnLeuGluGlnGluIleIleGlnAspIleTyrProSerThrGlnMet 2722
Db 6582 ATTCCTGACAGCCCTCGCGCTG----- 6602
Qy 2723 GlnLysAlaPheLeuPheAspHisThrThrAlaArgProArgProPheValProPheTyr 2742
Db 6602 ----- 6602
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Qy 2763 LeuValAsnHisLeuAspIlePheArgThrValPheAlaGlnAlaSerGlyGluLeuTyr 2782
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Qy 2783 GlnValValLeuSer-----CysLeuAspLeuProIleGlnValIleGluThrGluAsp 2800
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Qy 2801 AsnIleAsnThrIleThrAsnGluPheLeuAspGluPheAlaLysGluProValArgLeu 2820
Db 6768 ACCCTTGAGGCTGT-----GTGAGAGAGGAAATGACGCCCGCTTCGATCTG 6815
Qy 2821 GlyHis---ProLeuIleArgPheThrIleIleLysGlnThrLysSerMetArgVal--- 2838
Db 6816 GAACAGAGGTCGCTGCTGCGCTGCGCTGCGCTGATGTCGCGCGCATGAAACAGTCTG 6875
Qy 2839 IleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGlnHisValIleArgLys 2858
Db 6876 ATCTGACCCAGACAGCATGCTCGATGCGGTGCGTGCATGCCGATCATGTCGATGAA 6935
Qy 2859 LeuHisMetLeuTyrAsnGlyArgSer-----LeuLeuPro-----Pro 2871
Db 6936 CTGGTGCGCTGTACGAAGGCTACAGCAGGCGCGGAGGTCGCTGCTGTAATCGAC 6995
Qy 2872 HisGlnPheSerArgTyrMetGlnTyrThrAlaAspGlyArgGlnSerGlyHis----- 2889
Db 6996 ATGCAATGACCCGACATAGCGCTGTGGCAACGACGCTGATGACGCGCGGTGACGAGCA 7055
Qy 2890 -----GlyPheTyrArgAspValIle---GlnAsnThrProMetThrIleLeuSer 2905
Db 7056 CGGCAATGCGGATCGAATGGAAGCAACATGGGAGACAGACAGCGGATTCGAGCTGCT 7115
Qy 2906 AspAsp-----ThrValValAspGlyAsnAspAlaThrCysValValAlaLeuHisLeu 2922
Db 7116 GCGGATCATTCAGACCGCGCTGTGCAAGGACGCTCGGTCGCGGCTGCGGTCGAACTG 7175
Qy 2923 Ser---LysIleValAsnIleProSerGlnValLeuArgLysSerAsnIleIleThr 2941
Db 7176 GCGCCAGCGCTTGATCGACGACTTGAAACAGGTGCGCGGCAACAGGCT-----GTCA 7229

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Qy 2942 GlnAlaThrValPheAsnAlaAlaCysAlaLeuValLeuSerArgGlnSerAspSerLys 2961
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Qy 2962 AspValValPheGlyArgIleValSerGlyArgGlnGlyLeuProVal----- 2977
Db 7290 GACATT-----CGTGTGGTGTGCGATGTCGCAACCGGACCC 7325
Qy 2978 -----GluTyrGlnAspIleValGlyProCysThrAsnAlaValProValArgAlaHis 2995
Db 7326 CGCGCGGAAACCGAAGCTTGATGCGCTTTTGTGTAACCAACCAAGTGTGCGCGGAA 7385
Qy 2996 IleGlu---SerSerAspTyrAsnGlnLeuLeuHisAspIleGlnAspGlnTyrLeuLeu 3014
Db 7386 TTGACTTGACACAACTTCACGGAACCTGTCGAACAGGTCAAAACACACCGCGCTGCA 7445
Qy 3015 SerLeuProIleGluThrIleGlyPheSerAspLeu-----LysArg 3028
Db 7446 GCGCGAGCGCATGAGAGCTGCGCTGGAACAACTGTGCAAGCTTGCAGCCCAACAGC 7505
Qy 3029 AsnCysThrAspTyrProGluAlaIleThrAsnPheSerCysCysIleThrTyrHisAsn 3048
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Qy 3049 PheGluTyrHisProGlnSerGlnPheGluGlnAlaArgValAlaMetGlyValLeuThr 3068
Db 7545 -----CACGAGACCGAGCGGCGGAGGTCGCGGCTGTCGCGGCTTTCAGGTT 7595
Qy 3069 LysPheValAsnIleGluMetAspGluProLeuTyrAspLeuAlaIleGlyGluVal 3088
Db 7596 GAAGCGTGTGCTGGAGAGCTACCGCGCGAGCTGACCTGACCTGCTG---AACACCGCC 7652
Qy 3089 GluProAspGlyAlaGlyLeuLysValThrValIleAlaLysThrGlnLeuPheGlyArg 3108
Db 7653 GAACAGAGCGC---GACCTGAGCGGAGCGCTGACCTGACGCGACCGGCTTTCAGGCGC 7709
Qy 3109 LysArgValGlnHisLeu 3114
Db 7710 AGCACTATTGMACGCATG 7727

RESULT 10
US-09-976-059-1
; Sequence 1, Application US/09976059
; Patent No. US20020164747A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Stafla, Alfredo
; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
; FILE REFERENCE: 3019-PCR
; CURRENT APPLICATION NUMBER: US/09/976,059
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (3118)..(4032)
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; NAME/KEY: misc_feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature

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| OTHER INFORMATION: ORF 5; | negative strandedness |
| NAME/KEY: misc feature | |
| LOCATION: (9464) .. (8110) | |
| OTHER INFORMATION: ORF 6; | negative strandedness |
| NAME/KEY: misc feature | |
| LOCATION: (9691) .. (10761) | |
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| LOCATION: (13617) .. (12802) | |
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| LOCATION: (15203) .. (11614) | |
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| LOCATION: (75535) .. (76464) | |
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| LOCATION: (78110) .. (76449) | |
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| LOCATION: (79864) .. (78107) | |
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| NAME/KEY: misc feature | |
| LOCATION: (81624) .. (79861) | |
| OTHER INFORMATION: ORF 26; | negative strandedness |
| NAME/KEY: misc feature | |
| LOCATION: (81909) .. (81682) | |
| OTHER INFORMATION: ORF 27; | negative strandedness |
| NAME/KEY: misc feature | |
| LOCATION: (82346) .. (82062) | |

| DB | Seq1 | Seq2 | Score | Length | Matches | Conservative | Mismatches | Gaps |
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| Qy | 88 AAlaLeuAlaTrpLysGluLeu---ValAsnGlnThrProAlaLeuArgAla---PheAla | 105 | | | | | | |
| Db | 29037 GCCGCCGCCGCCGAGAGAGTTCGACCTGACCCCGGCCGCCGTATCCGGCGGACGCGCG | 29096 | | | | | | |
| Qy | 106 PheThrSerAspSerGlyLysTrpThrSerGlnVal-----IleLeuLysAspSer | 121 | | | | | | |
| Db | 29097 GCCGATCCGAGACGCGCGCGCGCTGCTGCTGCTGCATCCACACACTCGTGACGACGAC | 29156 | | | | | | |
| Qy | 122 PheValPhe-SerTrpMetCysTrpThrSerSerSerSerSerProAspGlnValValArgAs | 141 | | | | | | |
| Db | 29157 ACGACGTTTCGACGCTGG---TGCCTGGCGCGACTCGCGGCGCT-----TC | 29195 | | | | | | |
| Qy | 141 PGLAlaAlaAlaAlaAlaAlaSerGlyPro-----ArgCysAsnArgPheValLeuLe | 158 | | | | | | |
| Db | 29196 CTCGAGGCGCGCGCGCGCGCGCGAGCTTCGCCAGAGCTTCGCGCGA | 29255 | | | | | | |
| Qy | 158 uGluAspMetGlnThrLysLysCysGlnLeuValTrpThrPheSerHisAlaLeuValAs | 178 | | | | | | |
| Db | 29255 GCGCGCGCTCGGATGTCGCGCGGAGGACGACGAGCGATTTTCGCGAGTGTCTCGCGA | 29314 | | | | | | |
| Qy | 178 PValThrPheGlnGlnArgValLeuSerArgValPheAlaAlaTyrLysHisGluLysAs | 198 | | | | | | |
| Db | 29315 CGTCAAC----- | 29321 | | | | | | |
| Qy | 198 rThnHisArgProGlnThrProGluSerSerSerAlaThrArgThrAspSerGlnSerVa | 218 | | | | | | |
| Db | 29322 -----GAGACCAACCGCGCGCGCTGACCGAGCTGACCGAGCGCGCTC | 29368 | | | | | | |
| Qy | 218 lSerValValSerMetSer-CysGluAsp-----AsnAlaValSerAlaThrHisPheT | 236 | | | | | | |
| Db | 29369 CCGGCGCGCTCGAGGTCTCGCTCGCGGTCCGCGAGCGCGCTCGCGGTCCGCGAGGT | 29422 | | | | | | |
| Qy | 236 TrpGlnThrHisLeuAsnAspLeuAsnAlaSerValPheProHisLeuSerAspHisLeuM | 256 | | | | | | |
| Db | 29429 GCGCGCGACCTCGCGCTCGCGCGCGG---GCCACCGCTTCTC---CACCTGGCC | 29474 | | | | | | |
| Qy | 256 etValProAspProThrThrThrAlaGlnHisArgIleHisPhePheProLeuSerGlnLysA | 276 | | | | | | |
| Db | 29474 ----- | 29474 | | | | | | |
| Qy | 276 lAlaSerAsnSerAlaAlaCysArgThrAlaLeuSerIleLeuLeuSerArgTyrThrN | 296 | | | | | | |
| Db | 29475 -----TGGCGCGCGCTGTAGCGGTATCGCGGCGCG----- | 29507 | | | | | | |
| Qy | 296 lAspArgGlnAlaLeuPheGlyAlaVal-----ThrG | 307 | | | | | | |

| | | | |
|----|-------|--|-------|
| Dd | 29508 | -----GACGACGTGGTGTGGAAACAATCTCTTCGAGCGAATGAACTGGGCGCGCG | 29562 |
| Qy | 307 | luginSerLeuProPheAspIyuehIeTyLeuAlaAspGlyThrTyrgInThrValAlaP | 327 |
| Dd | 29563 | CCGAACGGGTGCC-----GGCGTGTTCATCAACAGCTTC | 29598 |
| Qy | 327 | roleuAlaGValAlaHicGyGInSerAenLeuAlaArgAlaSerAValMetAspAlaIleSers | 347 |
| Dd | 29599 | CGGTGCGGGT-----CGACTGAACGGCACAGACCTGGGGAGGGCGGTGACCG | 29646 |
| Qy | 347 | eTyTAAspAAspArgLeuGlyHicIleu-----AlaProPheGlyLeuArgA | 362 |
| Dd | 29647 | CCCTGGCGGACCAATAGCGGAGTGTATGGCGGACGACGCGCGCTCGCGCTGGCGC | 29706 |
| Qy | 362 | spIeArgAenThrGlyAAspAenGlySerAlaAlaCysAAspPheInThrValLeuIy | 382 |
| Dd | 29707 | AGCGGCGCGGCGGGTCCGCGGGGAGT-----CGCGTTCACGTGCGTGTTC | 29757 |
| Qy | 382 | AlThrAspGlySerHisValaAenAnGlyIleAnGlyPheLeuGInGInIleThrGus | 402 |
| Dd | 29758 | ACTATCGGACACATGTGCGGGCGCGGACGACGCGGAGCGCTCGAGGCGCTACGCGCG | 29817 |
| Qy | 402 | eSerHisAAspMetProCysAenAenArgAlaLeuLeuLeuHicGyGInMetGInSers | 422 |
| Dd | 29818 | TGCTGCACCGGACACACAGAACTATCCGTGGTGC-----TCGGTGCAGACG | 29868 |
| Qy | 422 | erGlyAlaLeuIleu-----ValAlaTyTyTAAspAlaAenAlIleA | 436 |
| Dd | 29869 | ACGGCAGAGCTTGACCTGGTGTGAAGCGGTGCGCGCGGAGGGCGGGTGGTGG | 29928 |
| Qy | 436 | spSerLeuGInThrThArgLeuLeuGInGInPheGlyHicIleuIleTyCysLeuGInS | 456 |
| Dd | 29929 | GCGCGCTCATGCAGAAATGCTTGGCCGACGTGGTGGCGCGCTTGGCGCGGTCGCGGAA | 29988 |
| Qy | 456 | eProIeAspLeuSerSerMetAlaGlyAlaAenMetThrGlyTyTAAspArgAlaG | 476 |
| Dd | 29989 | CGCCCTG-----TCCGCGGTGGGGGATC-----GACGAGCGG | 30024 |
| Qy | 476 | IuIleGly-----SerTPAAsnSerGInProLeuGInGInAlaAspThrLeuI | 492 |
| Dd | 30025 | AGATTCGAACGGGTGCTTACAGCTGGAACAGACAGCGTGCSCCGGTAAGTGAAGTGTGG | 30084 |
| Qy | 492 | leHicHicGInMetLeuAlaValaSerHisSerProThTyVThrAlaIleGInAlaT | 512 |
| Dd | 30085 | TGCCGCGCTTGTTCGCGGACGAGGTGGCGGCTCGCGCGATGCGAGCGGTGGCGG | 30144 |
| Qy | 512 | rPAAspGlyAspThrThTySerGInLeuAAspAenAlaSerSerAArgLeuAlaValaHicI | 532 |
| Dd | 30145 | AGGGTGTCTCGTGTCTTATCGCAGGCTTATGCGCGATGCGATGCGATGCGTGGCGCGGAGCC | 30204 |
| Qy | 532 | IeTySerLeuGlyLeuAlaArgAlaGInGInAlaIleIleProValTyPheGInTySerL | 552 |
| Dd | 30205 | TGGTGGCGCGCGGTGTGGGTGTGAAGTCCGCGGTGG---GTGGCGTTCGAGCGGTTC | 30261 |
| Qy | 552 | ySTPValIleAlaSerMetLeuAlaValaLeuTySerGlyAenAlaPheThrLeuIleA | 572 |
| Dd | 30262 | CCGAGAGTCTGTCCGCGTCTCTGGCGGTGGCGAAAGCGGGGCGGTGTTCGCGTGG | 30321 |
| Qy | 572 | spProAAspProProAlaArgThxAlaGInAlaValAlaThrGInThrArgAlaThrValA | 592 |
| Dd | 30322 | ACCTTTCGTGGCCCGCAGCGCGGTATCGATGCGGTGTTCGTACTGGCGCGCGGTGG | 30381 |
| Qy | 592 | IaIeuThrSerTyLeuHicHicArgGlyInThrValGInTyLeuValGlyArgCysValaIy | 612 |
| Dd | 30382 | CGGTGGCTGACCGG-----CCGATGACCGGAGTGCAGCGTGTGC | 30420 |
| Qy | 612 | AlaAspArgGlyLeuLeuGInSerVal-----SerAlaS | 623 |
| Dd | 30421 | CGGCGACACAGATGGGGATTTCGGCTGTGCGTCCGCGCGCGGTGGCGGGGCGG | 30480 |
| Qy | 623 | eAspAAspPheSerSerLeuThTySerGInAAspLeuAlaTyTyValIlePheThrSer | 643 |

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| Qy | 643 | lyserThrglyAaPrClyGlyIleMeclleGluHlaArgAlaPheSerSerCysAlaL | 663 | |
| Db | 30505 | GCTTCACGGGCGCGGCCCAAGGGTGTGTGACCCACCCACAGAACCTGTGATTGGCGC- | 30563 | |
| Qy | 663 | eulysPheGlyAlaSerLeuGlyIleAsnSerAthr-----ArgA | 677 | |
| Db | 30564 | -----ACCACACGCTGTGGGCTCCGACCCCGCGG | 30594 | |
| Qy | 677 | laleuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGluIleMetThrThrLeuI | 697 | |
| Db | 30595 | TGTTGTTCCATGCCCCCGCCACGCGCTTGAATGCGTGCATGATGATCTGGAGCGCTGT | 30654 | |
| Qy | 697 | lealenglyGlyCysValCysIle---ProSerAaPheAaPheArgMetAsnSerIleProS | 716 | |
| Db | 30655 | TGAATGCGCGCACGGTGTGTGTGCTGCTCCGACGGCAGCATGACCGGACGATCTTGAAGG | 30714 | |
| Qy | 716 | erPheIleAsnArgTyrAsnValAsnThrMetMetAlaThrProSerTyrMetGlyThrP | 736 | |
| Db | 30715 | ACCTGATCCCGGGGACATGATGACGACCTGATGATGACCCCGGCTCTGTTCGGGCTCC | 30774 | |
| Qy | 736 | heserProGluAspValProGlyLeuAlaThrLeuValLeuValGlyGluGlnMetSerS | 756 | |
| Db | 30775 | TGCAACCGGTGTGTTCGGGGGCTACACGAGTTTGACACCGCGGGAGATGGCGTGTGCG | 30834 | |
| Qy | 756 | er---SerValAsnAlaIleTrpAla-----ProLysLeuGlnLeuLeuAsnGlyTyrG | 773 | |
| Db | 30835 | CGAGGCGGGTGC CGCGCGGACCGAAGACGAAACCCGGGCTGTGCGGTCGGCAGCTTTTATG | 30894 | |
| Qy | 773 | lyGlnSerGlyuSerSerSerIleCysPheAlaSerAsnMetSerThrGluProAsnAsnM | 793 | |
| Db | 30895 | GCCCCAGCCGAG--GTGACCTTGTGGCGACGACGACATCTGCTGTGACGGGGTGCAG | 30951 | |
| Qy | 793 | etGlyAArgAlaVal---GlyAlaHiserTyrValIleAspProAsnAspIleAsnArgL | 812 | |
| Db | 30952 | TCCGGCGCGCGTTGGACAAACCCCGCGTGAATCTCTGGAT-----GACTTGTGTGCAC | 31005 | |
| Qy | 812 | eulValProIleGlyAlaValaGlyGluLeuValIleGluSerProGlyIleAlaArgMetP | 832 | |
| Db | 31006 | CGGTCCCGTCCGCTGACTGTGGACCTGATGTGGCCCGGCGCGCTTGGCGCGTGCCT | 31065 | |
| Qy | 832 | yrIleValProProProProGluLysSerProPheMetThrAplleProSerTyrTrpP | 852 | |
| Db | 31066 | ATGCGGGCATGCCCGGTTGACGCGCGACGCGGTTCGTCCCGAC----- | 31109 | |
| Qy | 852 | roAlaAsnThrPheProAspGlyAlaIleuLeuYrAArgThrGlyAaPheLeuAlaArgTyrA | 872 | |
| Db | 31110 | -----CGTTCTCGCGTGTGTGTGTGCGCTCTACCGCACGGGTATCTGTGCTCGGTGA | 31161 | |
| Qy | 872 | laserAspGlySerIleValaCysLeuGlyAArgIleAspSerGlnValaIleArgGlyG | 892 | |
| Db | 31162 | CTGACGACGCGGGGTGCTCATTTGCGCGGGCGCGCATGATACGGGAAGATTCCGAGCT | 31221 | |
| Qy | 892 | lnaArgValGluLeuGlyAlaIleGluThrHisIleuAArgGlnMetProAsp-----A | 910 | |
| Db | 31222 | ATCCGGGTGAGACCGGGGAGAGTTGAAGCGGTCTCTGGCTCAACAC--CCCGACGTCAACC | 31278 | |
| Qy | 910 | spLeuThrIleValaIleGluAlaThrLysArgSerGlnSerAlaAsnSerThrIleProS | 930 | |
| Db | 31279 | AGGTGGCAGTGTGTGTGCT-----CGCAGACACACCGCAGGGATTAAGCGGCTGG | 31326 | |
| Qy | 930 | leAlaPheLeuIleGlySerSerTyrPheGlyAsnArgProSerAaPheAlaIleLeuA | 950 | |
| Db | 31327 | TCCGCTATGTCTGCGCGGTGAC----- | 31349 | |
| Qy | 950 | spHisAaPheAlaThrLysAlaAlaIleAsnIleLysLeuGluGlnValLeuProArgHiserT | 970 | |
| Db | 31350 | -----GTGAGGCGCATATCCGACGAGAGCGCCTTCGCGGCTCACTGG | 31389 | |
| Qy | 970 | leProSerPheTyrIleCysMetLeuGlnLeuProArgThrAlaThrGlyLysValLeuArgA | 990 | |
| Db | 31390 | TCCGTTGGCGCATCTGTGAATGCGTGTGCGCTGTGACACAGAACCAAGAGGTGACC | 31449 | |

| | | | | |
|----|-------|---|------------------|-------|
| Oy | 990 | ggaagaaglaaaglllmemcyllylaasprlleuueaurysglnthngllyalailev | 1010 | |
| Db | 31450 | ggggccgacagc----- | 31460 | |
| Oy | 1010 | alnglnlnalaproalaPro----- | 11eProValphealaA | 1022 |
| Db | 31461 | -----ccggcccgctccgttgagacgcggcgccggcgagcc----- | gccc | 31503 |
| Oy | 1022 | erhrralalaalybleuhie---SerletrValglnserleuglylleaProalaT | 1041 | |
| Db | 31504 | ACGGCGGTGAAGACTATGTGTGCGCCGCTTCCCTAGGTGTCCGACCTGGAT-----C | 31557 | |
| Oy | 1041 | hrValaenValaGlyAlaThrPhegheulueuglyglaenSerlelthrralalaileym | 1061 | |
| Db | 31558 | GGGTCGGTGTCCAGACGACGACTCTTCGCTTGGGTGGGACATTGCGTGTGGTGGCGGT | 31617 | |
| Oy | 1061 | evValaenMetalaatgSerVal---GlyMetaspleuValSerlaenleTyrglnH | 1080 | |
| Db | 31618 | TGGTGAGCGCGTATTCGGACAGGTGTTCGGGTGGAGGTTCGCGTCCGCTCCGATG | 31677 | |
| Oy | 1080 | leProthrrleuAlaGlylleserAlaValValyuglyasrProleuSerTyrrhileuI | 1100 | |
| Db | 31678 | CGCGGACTCCGGCGCGGTGTGTGGCCGCTTGTCCAGGCGGACGCGCGCGAGCGCG | 31737 | |
| Oy | 1100 | leProlySerThrHniglulGlyProValglnlnSerTyserglnGlyArgleuTrp | 1120 | |
| Db | 31738 | TACGGCGCGGGGTGCGTCCGGCGCGGTGCGCGTGTGCTGTTCGGACACCGCGTGTGT | 31797 | |
| Oy | 1120 | heleuaerGlnleuaerValGlySerleuTrpTyrrleuIleProTyralaValaMetra | 1140 | |
| Db | 31798 | TCCGTGTCCACGTGAGAGGTCCAGCGCGCACCTCAACAATCCCGGGGGCGCTGGCGCTGG | 31857 | |
| Oy | 1140 | rgGlyProValaenValaAspAlaleuayrgrAlaaleuAlaaleuglnlnaTgrHnlg | 1160 | |
| Db | 31858 | ACGGTCTCTTGATCCGGATCTCTTAACGGCGCGCTTGACATGTGTGGCCCGGACG | 31917 | |
| Oy | 1160 | luthrleuaTgrThrPheglnuaerGlnuaerGlyValGlyAlglnleValHnsgln | 1180 | |
| Db | 31918 | AGGTGTGCGTACCGTCTTCAACGCTGCACGCGCGACGCGGTGGCAACAGATCTCGACG | 31977 | |
| Oy | 1180 | ybleuSerGlnGlnmetLeuValIleasrleuTygIysrleuaerleuaerProheglnuV | 1200 | |
| Db | 31978 | ATCCGCAAGTCTCCGTCGCGTGTCTCAAGGTTCAGCCCGCACCGCGGTGCCC----- | GAAG | 32031 |
| Oy | 1200 | alleuaenGlnGlnlnThThrProPhealnuSerSerGlnAlaGlyTrpArgalaT | 1220 | |
| Db | 32032 | CGGTGGCGCGTCCCGCGGGGACACCGGTTCGACTCGGCGGGAACTCGCGTGGCGCGG | 32091 | |
| Oy | 1220 | hrleuLeuaTgrleuGlyGlnuaerAspHsileleuThrIleValHmetHnshlles | 1240 | |
| Db | 32092 | TCCGTGCTGGGACCGCGGACGACGTGCACGTGTGGTCTCGTGTGACATCAATTGGCGG | 32151 | |
| Oy | 1240 | erAspGlyTrpSerIleAspValleuayrgrAsrleuaynGlnleuTyrsrAlaAlaL | 1260 | |
| Db | 32152 | CCGACGGCTGTGCATCGCGCGCTCGCCCGGGACTTGGCGCGCGCTACCGCGCCAGGA | 32211 | |
| Oy | 1260 | eulyaasrSerTyasrProleuSerAlaleuThrProleuProIleGlnTyserAsp | 1280 | |
| Db | 32212 | TC---GACGCGACGCGCGCG---GCCCTCGCGCGGTGCGCGGTGACGTACGCGACT | 32262 | |
| Oy | 1280 | heAlaalyTrpGlnlnlyAsrplnHelIeuln----- | GlnL | 1293 |
| Db | 32263 | ACGCGCTCTGGACGCGGACGTGCTCGGTTCGAGACGACCCGGACAGCTCATCTCC | 32322 | |
| Oy | 1293 | ysglnleuaenTyrrTrpLylysglnleuTyasr---SerSerProAlaTyIleProT | 1312 | |
| Db | 32323 | AACAGGTGTGCTATTTGGCGCGGACGTGGCGCGCGACCGAGGAATTGATCTGGCGG | 32382 | |
| Oy | 1312 | hrAsprrleuAlaayrProAlaleuSerGlyAspAlaGlyCyValHnleValThrIleA | 1332 | |
| Db | 32383 | TGACACGGGCGCGCGCGCGGACGATCGGATCGCGGACACACCGTGGAGTTTCGCGCTG | 32442 | |

| | | | |
|----|-------|---|------|
| QY | 1332 | spgIygluLeuTYrGlnSerLeuNrgAlaPheCysAsnGlnHisAsnThrSerPheV | 1332 |
| Db | 32443 | CCCCGGCGGCGACCCACCACCACTCGCCGAATCGCCCGCCGACGGCGTCACTTCA | 3250 |
| QY | 1352 | aIValLeuLeuAlaAlaPheArgAlaAlaHisTYrArgLeuThrAlaValGluAspAlaV | 1372 |
| Db | 32503 | TGACCGTGCMAACCGCCCTCGCTCTCTGTCCAAACTCGGGCGCGGACCGGACATCC | 3256 |
| QY | 1372 | allIegIyThrProIleAlaAsnArgAsnArgProGluLeuGluAspIleIleGlyCysP | 1392 |
| Db | 32563 | CCATCGGGCGTGGCGGTGGCGGACCGACCCGACCTTCGACAACTCATCGGCTTCT | 3262 |
| QY | 1392 | heValAsnThrGlnCysMetArgIleAsnIleAspHisHisAspThrPheGlyThrLeuI | 1412 |
| Db | 32623 | TGGTCACACCTCGTCTGTACGACCGACCTGACCGGCAACCCACATCACTGACCTGC | 3268 |
| QY | 1412 | IeAsnGlnValIleValAlaThrThrThrAlaAlaPheGluAsnGluAspIleProPheGluA | 1432 |
| Db | 32683 | TGCACCGGACCCGGACACCACTCTGCACGCTTTCACCCACCAAGAGTCTCCCTTCCAAA | 3274 |
| QY | 1432 | rgValValSerAlaLeuGlnProGlySerArgAspLeuSerSerThrProLeuAlaGlnI | 1452 |
| Db | 32743 | AACTCGTGCAGACCTGACACCC---ACCGCTCTCTGCGCCGACCCCTCTTCCAGG | 3279 |
| QY | 1452 | eulIlePheAlaValHisSer---GlnIysAspLeuGlyArgPheIysPheGlnGlyLeuG | 1471 |
| Db | 32800 | TCATGATGATGACCTCGACAGCGCGTCCGGCGGCGAAGACCGCTGCGTCCCGGCGTGC | 3285 |
| QY | 1471 | IuservAlaProValPro-----SerIysAlaTYrThrArgPheAspMetGluPheN | 1488 |
| Db | 32860 | GGGTCAACGACCTCCGCGCCGGGAGACACCCGGCAAGTGGACCTGACCTGACGCTGC | 3291 |
| QY | 1488 | IstleuPheGlnGluThrAspSerLeuIysGlySerValAsnPheAlaAspGluIlePheI | 1508 |
| Db | 32920 | ACGAGGTGGCGGGCGGAGACGGCATGCACGCGACGCTCTCGGGCGGCGGACCTTTCG | 3297 |
| QY | 1508 | ysMetGluThrValGluAsnValValArgValPhePheGluIleLeuArgAsnGlyLeuG | 1528 |
| Db | 32980 | AGCAGGAGACGGTGGCGGCGCTCCCGCAC-----CGTTCTCTGCMAACCTCGAAG | 3303 |
| QY | 1528 | InservSerArgThrProValSerIleLeuProLeuThrAspGlyIleValThrLeuGluI | 1548 |
| Db | 33031 | CCATGGCGGGCGCCCGGACGAC-----CGCTCGACCC | 3306 |
| QY | 1548 | ysLeuAspValIleuAsn-----ValIysHisValAspTYrP | 1560 |
| Db | 33064 | GGATCGAGGTCTGTCTCGCGGGGAGCGGCTCGCGCTGTGTGAGTGCAGACGACGACG | 3312 |
| QY | 1560 | roArg-----GlnSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTYrP | 1577 |
| Db | 33124 | CTCGTCGGTGTGTGAGT | 3318 |
| QY | 1577 | roAspSerLeuAlaValAlaAspSerSerCysArgLeuThrTYrTYrGlnLeuAspArgG | 1597 |
| Db | 33184 | CGAGCGCGGTTCGGT | 3324 |
| QY | 1597 | InservAspIleLeuAlaGlyTYrPheuArgArgArgSerMetProAlaGluThrLeuValA | 1617 |
| Db | 33244 | GGTGGAGTGCCTTGTGGCGGACCTGTGGCGCGCGGTGTGGGTGTGTGTGTGTGTGTGT | 3330 |
| QY | 1617 | IaValPheAlaProArgSerCysGluThrIleValAlaPhePheGlyValIleuIysAlaA | 1637 |
| Db | 33304 | TGTGTGGGTGTGAGCGGTCTCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 3336 |
| QY | 1637 | snLeuAlaTYrLeuProLeuAspValArgSerProSerAlaArgValGlnAspIleLeuS | 1657 |
| Db | 33364 | GGGGCGT | 3342 |
| QY | 1657 | erGly-----LeuSerGlyProThrIleValI | 1666 |
| Db | 33424 | CGAAGTGGCGGCGCGGATTCGGGTGCTGACCGCGCGATGAGCGGGGTGACGGTCTGT | 3348 |
| QY | 1666 | eu-----IleGlyHisAspThrAlaProProAspIleGluValThrAsnValGluPheV | 1684 |

33484 CCGCGCGCTGGCGGGGATTCGCGCTC----- 33512
QY 1684 aAArgIleAArgAPAlaLeuAAspSerAAspAlaArgGlyPheGluValIleGluHisA 1704
Db 33513 -----GTCCTCGGCGACCTTGACCGCGGATCGGGCGCTTGTG----- 33551
QY 1704 spSerThrIlyProSerAlaThrSerLeuAlaTyValLeuTyThrSerGlySerThrg 1724
Db 33552 --CCGGCGCGGTCCGGTCCGGCGCGGTCTACCCGATGTACACTCGGGTTCACCGG 33609
QY 1724 IyArgProGlyValMetIleGluHisArgValIleIleArgThrValThrSerGlyC 1744
Db 33610 GTCGGCGCAAGGAGTGTGTACCAACCAACCAACCTCGGATTTGGCCACCAACAGT 33669
QY 1744 YalIleProAenTyProSerGluThrArgMetAlaHisMetAlaThrIleAlaPheAsp 1764
Db 33670 GTTGGGGTCCGACCC-----CGGGTCTTTTCCACGCGCGCGCGCTTCGACG 33720
QY 1764 IyAlaSerTyArgIleTySerAlaLeuLeuPheGlyArgThrLeuValCysValAspT 1784
Db 33721 CGTCGTGTATGATTTGGGTGCGTGTGATGAGCGGACGCGTGTG---GTGGCTC 33777
QY 1784 yMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGluHisValAsnA 1804
Db 33778 CGCGCGCACATCGACGCAACGCTTGTAGGGAGCTG---ATCGCGCGCATGATGTA 33834
QY 1804 IaAlaSerHisValThrSerSerGlnAspValProLeuArgValProArgArgLeuS 1824
Db 33835 CGCACGTCGATGTGACCGCGGC-----TTGT 33861
QY 1824 exArgThrLeu-----MetPhePhePheLeuValIleThrAspSerThrAlaProAspA 1842
Db 33862 TGGCGGGTGTGACCCGCTGCTTCGCGGCGCTGACCGAGTCTCACGGGCGGGATG 33921
QY 1842 IaLeuAspAlaGlnGlyLeuTyGln-----GlyValGlnCysTyra 1856
Db 33922 CGGTGTGCGCGGAGCGGTGCGCGCTCAAGACGGGAATCCGGGTCTCGGGTGGCG 33981
QY 1856 smGlyTyArgIlyProThrGluAsnGlyValMetSerThrIleTyProIleAspSerThrg 1876
Db 33982 AGCTGTACGCGCGACCGAGGTACCTTGTGCGCACGACATCTGTGAT----- 34034
QY 1876 IuSerPheIleAsnGlyValProIleGlyArgAlaLeuAsnAspSerGlyValaTyraIv 1896
Db 34035 -----GACGGGGTCCGATCGGGCGCGCTTGACAAACACCGCGTACGCTTC 34083
QY 1896 alAspProGluGlnGlnLeuValGlyIleGlyValMetGlyGluLeuValaThrGlyA 1916
Db 34084 TCAGACGACTCTGCGCGCGCTCCGACAGGTGTGTGGGGAGACTGTATGTGCGCGGT 34143
QY 1916 spGlyLeuAlaArgGlyTySerAsp---LysAlaLeuAspGluAsnArgPheValHisI 1935
Db 34144 CGGGTCTGGCGCGGCTTATGCGGCGATGCCCGGGTGTGACCGCGACGATCTGCCCG 34203
QY 1935 LeThrValaAsnAspGlnThrValIyAlaTyArgThrGlyAspArgValaArgTyArgI 1955
Db 34204 ACCCATTCACACCGCGGT---CGCTCTACCGCACGGGTGATCTGTGCGGGT---G 34257
QY 1955 IeGlyAspGlyLeuIleGluPhePheGlyArgMetAspThrGlnPheValIleArgGlyA 1975
Db 34258 CCGACGATGTGTGCTGCTCATTTGCTGTGGCGGCGCGATGATCAGGTAAATTCGTGGCT 34317
QY 1975 smArgIleGluSerAlaGluIleGluAlaLeuLeuAspSerSerValaArgAspA 1995
Db 34318 ATCGGGTGGAGCGCGGCGAGGTGAAGCGTCTGCTCAACACCCGACGCTCGCCAGG 34377
QY 1995 IaAlaValaValLeuGlnGlnAsnGluAspGlnAlaProGluIleLeuGlyPheValaValA 2015
Db 34378 TACGACGTGTGCTGCGCGAGGACCCCAAGCGCAAGCGCTGTGCTCGCTACGCTGC 34436
QY 2015 IaAspHisAspHisSerGluAsnAspIyGlyGlnSerAlaAsnGlnValGlnGlyTTP- 2034

34437 -----GGCGGGGATGTCGACGCTATG 34458
QY 2035 --GlnAspHisPheGluSerGlyMetTy---SerAspIleGlyIleAspProSerT 2053
Db 34459 CGGAGAGAGCGCTTCGGGCGTACATGTTCCGCTTCGTCGAGATTGGATGCGCTGC 34518
QY 2053 hrIleGlySerAspPheIyGlyTyTrpThrSerMetTyArgGlySerGlnIleAspPheA 2073
Db 34519 CGCTGACCAAGCAACAGAG-----GTGACCGCGCGCTCTCCGCGCGC 34563
QY 2073 spGluMetHisGluTyPheGluGlyGluThrThrArgThrIleuHisAspAsn-----A 2090
Db 2090 rGserLeuGlyAsnValLeuGluIleGlyThr----- 2100
QY 34624 CCGCGTTCGCGGAGATGTGCTGACCTGGATCGGGTGGGTGCGACGACATCTTGCGCC 34683
Db 2101 -----GlySerGlyMetIleLeuPheAsnLeuAspSerArgLeuGluSerTyValGlyL 2119
QY 34684 TCGCGCGGCATTCGCTGCTCGCGCTCTCCCTGTGAGATCTGCGCGCGCAC---GGCG 34740
Db 2119 euGluProSerArgSerAlaAlaPheValAsnLysAlaThrGluSerIleProSerI 2139
QY 34741 TTCACATCTTCGTTCCGGGCTCTTC-----GCCACCCCGACCGCGCGCGC 34788
Db 2139 euAlaGlyIyAlaIyValGlnValGlyTyThrIaThr---AspIle----- 2153
QY 34789 TGGCGCGCTCGCGG-----GMAACGCGCGCGCGGACGTCGCGCCCAACCTCA 34836
Db 2154 -----GlyGlnValaAspAspLeuHisProAspLeuValIleLeuAsnSerValIleG 2171
QY 34837 TCCCGACGCGCGCGCGCGCCAGAACTGACCCCGACATGCTGCCCTGTGACCTG--- 34892
Db 2171 IuTyPheProSerSerGluTyLeuAla----- 2180
QY 34893 -----ACCGGAGAACTGACCACTCGTGGCGCGCGCGCGCGCTC 34941
Db 2181 --GluIleAlaAspThrLeuIleHisLeuProAsnValGlnArgIlePhePheGlyAspV 2200
QY 34942 CCAACATCGCGCACTACCTACCCCTAGCCCGGTGCAAGAGGCACTTCTTCACACAC 35001
Db 2200 alArgSerGlnAla---ThrAsnGluHisPheLeuAlaAlaGlyAlaIleHisThrLeuG 2219
QY 35002 TCATGTACGAGGCGGATGACCAACGAGTCACTCTGCGCGCGGATTTCTGCGCTCGCG 35061
Db 2219 IyLysAsnIleThrIyAspAspValArgGlnIyMetAlaGluLeuGluAspMetGluG 2239
QY 35062 GCGGT-----C 35067
Db 2239 IuGluLeuLeuValaGluProAlaPhePheThrSerLeuIyAspArgPheProGlyLeuV 2259
QY 35068 CCGAGCTG-----GACGCTTCTCTCGGGGCC 35094
Db 2259 alGluHisValGluIleLeuProLysAsnMetGluAlaValaAsnGluLeuSerAlaTyra 2279
QY 35095 TGCAGCAGGTG-----GTGACCGCGCACAGCTCATTC 35127
Db 2279 rGtyTyra-----AlaValIleHisValaArgGlyS 2289
QY 35128 GACAGGCGCATCGCTGCGACAACTGCGCGAGCGCGCTCGACAGTGTGTCACCGCACGCA 35187
Db 2289 exLeuGlyAspGluLeuValLeuProValaGluLysAspAspTrpIleAspPheGlnAlaA 2309
QY 35188 CCGTGCCTGCACCGAAGTCAACCC-----G 35214
Db 2309 smGluLeuAsnGlnLysSerLeuGlyAspLeuLysSerSerAspAlaAlaIleMetA 2329
QY 35215 ACCAGCTGACGCGCGCGCGCACCGCGCGCTCCGCTCGACCAACCGCTCTCTCA 35274
Db 2329 IaValSerIySilePro----- 2334
QY 35275 GCGTTCACATCGACCCGAAACCGACGCGCGGTGCTGCGCTCGCTCCGATGCAACCA 35334

QY 2335 -----PheGluIleThrAlaPheGlu---ArgGlnValAlaAs 2347
 Db 35335 TCGTGAAGACACACACCGCCCTGCACATCTCTCCAGACAGATCCGACCATCTCCCGC 35394
 QY 2347 LeuLeuAsnAsn-----IleAspGluTrpGlnL 2357
 Db 35395 GCGCAACCGACACCTCCCGCCCGGTACCGTTCCCGGACTTCGTGGCCGACGAGCCGCGC 35454
 QY 2357 euserThrIleAspSerSerAlaGlu-----GlyAsp----- 2367
 Db 35455 TCGCGCTCTCCCGCGAGACAGAGCGTACTTCGCGCGCTCTCGGAGAGTCAACCG 35514
 QY 2368 -----SerSerLeuSerValProAspIlePheArgIleAlaGlyAlaGlyPheA 2385
 Db 35515 AGACCAACCGCCCGGTACCGCTGCGGACGTACGAAAC---GACGGACCGCATCGGTGC 35571
 QY 2385 rGValGluVal-SerSerAlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAla----- 2402
 Db 35572 GGGCCGAGGTGAGCTCGACGCGCGCTGCGCGCGCGCTGCGGACCTC-GCCCGCGAC 35630
 QY 2403 -----ValPheHisIleCysCysSerGlnGlyAlaGlyThrLeuVal 2415
 Db 35631 CCGGCGGTACCGCGCGACGCGTCTTCATCTGAGCTGCGCGCGCTGCGCGCGGTG 35690
 QY 2416 AsnPheProThrAspHisIleuArgGlySerAspLeuThrAsn----- 2431
 Db 35691 GCCGA-CCGGAGAGACGTCTCTTCCGACCGCTCTCTGACGAGATGGCTCCGCGCC 35749
 QY 2432 -----ArgProLeuGlnArg-----LeuGlnAsn 2439
 Db 35750 CCGCGCGGTGCGCGCTCTTCATGAAACCTGCGCGGTGCGGTACGCGTTCGCGAAC 35809
 QY 2440 ArgArg-IleAlaIle---GluValArgGlnArgLeuArgSerLeuLeuProSerTyrrme 2458
 Db 35810 CCGCGCGAGGCTCTGGACAGGTGCGCGACCGCTCGCGAGCTGATGGCGCAC----- 35864
 QY 2458 tIleProSerAsnIleValValLeuAspIleMetProLeuAsnAlaAsnGlyValAs 2478
 Db 35865 -----GAGCACCGCGCCCTC----- 35879
 QY 2478 pArgGlyGluLeuSerArgAlaValValProGlyGlnGlnIleAlaProLe 2498
 Db 35880 -----GCGCTGCGCGACGAGCGCGCTGCC-----GCCGGAGCGCGCT 35923
 QY 2498 uProThrPheProIleSerGluValGluValIleLeuGlyGluAlaThrGluValPh 2518
 Db 35924 GTTCACG-----TCGTT-GTTCACATACCGCTATGCGCGCGCGCGCGCACGC 35973
 QY 2518 eGlyMetIleValAspIleThrAspHisPhePheAsnLeuGly-----Gly 2533
 Db 35974 CGGACGATCCGCTGCGCGCGGTGCGCGCTGCTCCGCTGGAGAACGACACATACCGCG 36033
 QY 2533 yHisSerLeuLeuAlaThrIleSerLeuIleSerArgIleAspGlnArgLeuValArgIle 2553
 Db 36034 TCAC-----CGTGTGATCGACGAGACGACGCGGAT 36066
 QY 2553 e-ThrValIleAspValPheAspHisProValPheAlaAsp----- 2566
 Db 36067 TCGCGGTGACGTCGACGTCGTCGCGCGCGCGCGCGCGCGGTCTCCGCTGCTCC 36126
 QY 2567 -----LeuAlaSerValIleArgGln----- 2573
 Db 36127 GCACGACCTGACCCCGCTGCGCGCGCTCGACGACCTCCGAGACCTCCGAGATGCGGTGCGC 36186
 QY 2574 -----GlyLeuGlyLeuGlnGlnProValS 2582
 Db 36187 AGCTGGCGCGCGCGGTCTCCGCGCGCGCGCGCGCGCGGTCTCGTGTGCGGTCC 36246
 QY 2582 eArgPheGlnGlyGlnAspArgSerAlaHisMetAlaProArgTrpGlnThrGluAlaI 2602
 Db 36247 CGGCGCGCGAG-----CGGGGACCGCGCGCGGTCTCGGCGACCGCGCTACGAGAGC 36303

QY 2602 LeuLeuCysAspGluPheAlaValValLeuGlyPhe---GlnValGlyIleThrAspAsn 2621
 Db 36304 TATCTGCCAGCGGTACGCCACAGGTCTGAGGTGACGGTGGCGCGGACGACACT 36363
 QY 2621 hePheAspLeuGlyGlyHisSerLeuMetAlaThrIleValAlaValArgIleGlyHisA 2641
 Db 36364 TCTTTCGCGCGCGCGCACTCGCTCTCGCACGCGCGGTGTCAGCGCGGATCGCTCGC 36423
 QY 2641 rGLeuAspThrThrValSerValIleAspValPheAspHisProValLeuPheGlnLeu 2661
 Db 36424 CGCTGGCGGTGAGGTTCACCATCGCGCGCTCTTCAGAGCTCACCGCGGACGCGTGG 36483
 QY 2661 lAlaIleAlaLeuAspAsnLeuValGlnSerIleThrAsnGlnIleValGlyIleArgGlu 2681
 Db 36484 CCGCGCGGTG-----ACCGCGCTCGGACCGCGGCGG----- 36518
 QY 2681 eAlaGluTrpSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAla 2701
 Db 36519 -----GTCCGACCGCGCGCG-----AGACACGCGCGGAGCGGATTCGCTGT 36561
 QY 2701 eGluIleIleProGlnLeu-----GluLeuGlnGluIleIleGlnAspIle 2717
 Db 36562 CTTTCGCGACGCGCGCTGTGCTCTGCGCGAGCTGAG----- 36602
 QY 2717 yProSerThrGlnMetGlnValAlaPheLeuPheAspHisThrAlaArgProArg 2737
 Db 36603 -----GCGACGAGCGCGCACCTACGACGACGCGCG----- 36635
 QY 2737 rObPheValProPheTyrlleAspPheProSerThrSerGluProAspAlaAlaGlyLeu 2757
 Db 36636 -----CTCGCGCTCTCGCGCGGTCTGACCGCGCGCGCTCA 36672
 QY 2757 lLeuValAcysGluSerLeuValAsnHisIleuAspIlePheArgThrValPheAlaGlu 2777
 Db 36673 CCGCGCGGTGACGACGATATGCGCGCGGACGAGGCTGCGGACGATGCTCGCGCG 36732
 QY 2777 lAspGlyGluLeuTyrlleGlnValValLeuSerCysIleuAspLeu-----ProIleGln 2795
 Db 36733 AGGACGCGCGCGGTACGACGTGTTCTCGCGCGGAGGAGCGCGCGGTGAGA 36792
 QY 2795 allleGlu---ThrGluAspAsnIleAsnThrAlaThrAsnGluPhe-----L 2810
 Db 36793 TCGTTCGAGTCTGCTCCGCGGACCTGCGCGCGCGCTGCGACGAGTGGCGGTACCGCT 36852
 QY 2810 eAspGluPheAlaValGluProValArgLeuGlyHisProLeuIleArgPheThrIle 2830
 Db 36853 TCGACCTCGCGCGGATACGATCGGTGCGCG-----CGGTGATCGGTGCGCGCG 36906
 QY 2830 lLeuGlnThrIleSerMetArgValIleMetArgIleSerHisAlaLeuTyrrAspGly 2850
 Db 36907 CGGACGACGTC-----CTGCTCTGTGATTCACCATGCGACGACGAGGAT 36954
 QY 2850 euserLeuGlnHisValValArgIleValIleuHisMetLeuTyrrAsnGlyArg-----SerL 2868
 Db 36955 GTTCGATGCGCGCTGCGCGGACCTCGCGCGCTCGACGAGCGCGGTGCGCGCG 37014
 QY 2868 euleuPro-----ProHisGlnPheSerArgTyrrMetGlnTyrrThr----- 2881
 Db 37015 GGGCACCGCTGAGGACCGCTCGCTCGATGACGAGCTACGAGCTGCGGTGAGGAGG 37074
 QY 2882 -----AlaAspGly-----ArgGluSerGlyHisGlyPheTyrrA 2893
 Db 37075 AGTTGCTGGCGCGCGGTGACCGGAGAGCTGCGCGGAGCGCGAGCTGCTACTGCG 37134
 QY 2893 rAspValIleGlnAsnThrProMetThrIle-----LeuSerAspAsp 2908
 Db 37135 GCGACACCTGCGCGGAGATCGCGGAGATCCGCTTCGCGCGGACCGGTTCGCGCGC 37194
 QY 2908 hValValAsp-----GlyAsnAspAlaThrCysIleValAlaLeuHisLeuSerTyrrIle 2926
 Db 37195 CGGTGCTCGACCGCGCGGAGGTGCGG-----A 37227
 QY 2926 alAsnIleProSerGlnValIleuArgGlySerSerAsn-----IleIleThrGlnAlaI 2944

| | | | |
|---|-------|---|-----------------|
| Db | 37228 | TCGCCATCCCGGACCTGACGCGCGCGCTGGCCAGCTGGCGCTGCGGACGGGACCA | 37287 |
| Qy | 2944 | hrvalphe-----AsnAlaAlaCysAlaLeuValLeuSerArgIuSerApsSerL | 2961 |
| Db | 37288 | CCGCTTCATGAGTCTGTGAGAGCGCGGCTTCGCGGGCGGCTGTGAGACCGCGGCTGGGCGCGCA | 37347 |
| Qy | 2961 | yvaarvalValPheGlyAArgIleValaSerGlyAArgInGlyLeuPProvalGluTyGlnA | 2981 |
| Db | 37348 | CCGAGCTCCCGCATCGGACCGCGCTCCGCGCGCGCACCGACGAGCGGCTCGAC-----G | 37401 |
| Qy | 2981 | spIleValGlyProCysGlyThrAsnAlaValProValaArgAlaHisIleGluSerSer---A | 3000 |
| Db | 37402 | AGCTGGTCGGCTTCTTGTCACACATGCTTGCTGCTGCGCACCGACGCTGCGGCGACCCG | 37461 |
| Qy | 3000 | spTyAsnGlnLeuLeuHisIleAspIleGlnAspGlnTyLeuLeuSerLeuProHisGluT | 3020 |
| Db | 37462 | GGTTCGGAGCGCTCTGTCGCGCGGGTGGCGAGACCGGCGCTCGCGGGGTAGCGCCATCAG | 37521 |
| Qy | 3020 | hrIleGlyPheSerApsLeuLyAArgAncYsThrApsTyPrProGluAlaIleThrApsP | 3040 |
| Db | 37522 | ACGTTCCCTTCGACCGACGCTGCTCGAGGAG----- | 37550 |
| Qy | 3040 | heserCysCysIleThrCysIleAsnIleGluTyHisIleProGluSerGlnPheGluGlnG | 3060 |
| Db | 37551 | -----CTGGTACCGACGCGTTCCTGCGCGCGCAT----- | 37580 |
| Qy | 3060 | lnArgValGluMetGlyValLeuThrArgPheValAsnIleGluMetAerGluProLeuT | 3080 |
| Db | 37581 | ----- | 37587 |
| Qy | 3080 | yrAapLeuAlaIle-----AlaGlyLeuValGluProAerGlyAlaGlyLeuL | 3096 |
| Db | 37588 | TCCAGGTCGCGCTGACCGTCGAGAACCGCGCGCGCGCGCGCGCGCGCTGCGCGGCTCG | 37647 |
| Qy | 3096 | ysValIleThrValIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle | 3113 |
| Db | 37648 | AAGTC-----GGCACCGAGCGCATCGAGCAC | 37673 |
| RESULT 11 | | | |
| US-10-156-761-1/c | | | |
| ; Sequence 1, Application US/10156761 | | | |
| ; Publication No. US20030119018A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: OMIURA, SATOSHI | | | |
| ; APPLICANT: IKEDA, HARUO | | | |
| ; APPLICANT: ISHIKAWA, JUN | | | |
| ; APPLICANT: HORIKAWA, HIROSHI | | | |
| ; APPLICANT: SHIBA, TADAYOSHI | | | |
| ; APPLICANT: SAKAKI, YOSHIYUKI | | | |
| ; APPLICANT: HATTORI, MASAHIRA | | | |
| ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES | | | |
| ; FILE REFERENCE: 249-262 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/156, 761 | | | |
| ; CURRENT FILING DATE: 2002-05-29 | | | |
| ; PRIOR APPLICATION NUMBER: JP 2001-204089 | | | |
| ; PRIOR FILING DATE: 2001-05-30 | | | |
| ; PRIOR APPLICATION NUMBER: JP 2001-272697 | | | |
| ; PRIOR FILING DATE: 2001-08-02 | | | |
| ; NUMBER OF SEQ ID NOS: 15109 | | | |
| ; SEQ ID NO 1 | | | |
| ; LENGTH: 9025608 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Streptomyces avermitilis | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: misc_feature | | | |
| ; LOCATION: (4187715) | | | |
| ; OTHER INFORMATION: a, t, c, g, other or unknown | | | |
| US-10-156-761-1 | | | |
| Alignment Scores: | | | |
| Pred. No.: | | 1,11e-138 | Length: 9025608 |
| Score: | | 1804.50 | Matches: 842 |

| Percent Similarity: | 35.12% | Conservative: | 516 |
|--|---|---------------|------|
| Best Local Similarity: | 21.77% | Mismatches: | 1242 |
| Query Match: | 11.19% | Indels: | 1269 |
| DB: | 15 | Gaps: | 137 |
| US-09-482-788-2 (1.3129) x US-10-156-761-1 (1.9025608) | | | |
| QY 7 | ValAlaArgValArgGlnAblPLeuProProThrProAlaSerPheCySerHisIGLYAAspSer | 26 | |
| DB 4514414 | GTGAGACGACGGGCCCCAGATCGCCCGCTCCCGGACCC-----GGGACCTC | 4514367 | |
| QY 27 | ProLeuAnserSerGTYrGLGlnLeuPheHisLeuYrGLYLeuAAspSerArgIle | 46 | |
| DB 4514366 | CCCCCTCTCTCCGCTCAGCGCCGCGCTCTGTTCTTGACCGAGATGCACCCCGGAGCCCC | 4514307 | |
| QY 47 | GLuAlaIleLeuYrPProGTYrProPheGlnLeuAAspMetIleAAspCyAAsnAlaLeuAAsp | 66 | |
| DB 4514306 | GAGTGGGTCCGCCCG-----CTCTTCCTGGCGTCCGGAGTCTCCCTGACCGCGGAC | 4514292 | |
| QY 67 | LygGlnSerAlaIleGLYHisAlaValYrAAspValProThrAAspIleAAspIleSerArg | 86 | |
| DB 4514291 | -----CTCTTCCTGGCGTCCGGAGTCTCCCTGACCGCGGAC | 4514253 | |
| QY 87 | PheAlaLeuAlaIATrPlyrGLuIleValAAsnGlnThrProAlaLeuAAspAlaPhe | 106 | |
| DB 4514252 | GTGGCGCGGCGCTGACAGCGCTGCCCGCGGACGACGCGCGTCCGACC--CGCTAC | 4514196 | |
| QY 107 | ThrSerAAspSerGTYrThrSerGlnValIleLeuYrAAspSerPheValPheSerTrp | 126 | |
| DB 4514195 | GTGCACACGAGCGCGGACCGCGCCGACATATC----- | 4514163 | |
| QY 127 | MetCyATrpSerSerSerSerPro-----AAspGlu | 137 | |
| DB 4514162 | -----GACGCGCGGCGGCGGACCGTGCAGCTGCGGTCGACGAC | 4514121 | |
| QY 138 | ValValAAspArgAluAlaAlaIle-----Ala | 146 | |
| DB 4514120 | ACCGCGCGGACGCGGCGGCGCGCTTTCGGCGCACAGTTCAGCGGCGCTTCGACCTC | 4514061 | |
| QY 147 | AlaSerGlyProAAspCyAAsnArgPheValLeuGlnAAspMetGlnThrYrAAspCys | 166 | |
| DB 4514060 | GCCGCGGCGCGCTGTGGCC-----CGCGTCTGGCGCGGCGGCGGACGACAT | 4514007 | |
| QY 167 | GlnLeuValYrThrPheSerHisAlaLeuValAAsp-----ValThrPheGlnGln | 183 | |
| DB 4514006 | GTCTCTCTTCGACGATGCATCATCATCATCGTGCAGCGCTGTGTCAGCGGTATCTTGAA | 4513947 | |
| QY 184 | ArgValLeuSerArgValPheAlaAlaIATrYrHisIGLYAAspTrpGlu | 203 | |
| DB 4513946 | CGGAGCTGCGGACGTGTGCGCGCGACCGGCGCGCGCGCGGACCTGCGGAA | 4513887 | |
| QY 204 | ThrPro-----GlnSerSerAAspAlaIATrAAspThrAAsp | 214 | |
| DB 4513886 | CTGCGCTTCACGATACGGGACCTACGGCTCTGGAGAGGCTGCCCGCTCACCGACCGCTC | 4513827 | |
| QY 215 | SerGlnSerValSerValAAspMetSerCyGlnAAspAAsnAlaValSerAlaThrHis | 234 | |
| DB 4513826 | GTCGAGGCGC-----GAGCTGACCCAC | 4513806 | |
| QY 235 | PheTrpGlnThrHisLeuAAsnAAspLeuAAsnAlaSerValPheProHisLeuSerAAspHis | 254 | |
| DB 4513805 | ---TGGCGCGCGCGCTCGACGAGCATCGCCCGCTGACCTGCC-----GCCGACAC | 4513755 | |
| QY 255 | LeuMetValProAAspProThrThrThrAlaGlnHisArgIleThrPhePro----- | 271 | |
| DB 4513754 | -----CCCGCGCGCGCGGTCCGATGCCGCGCGCGCGGTCTGACCGCTCCGCTC | 4513704 | |
| QY 272 | -----LeuSerGlnHisAlaLeuSerAAsnSerAla----- | 281 | |
| DB 4513703 | GCCCCCGAACCTCGCGCTCAACTGACCGAGTGGCGGACGACCGACCGGCGACCCGCTTC | 4513644 | |
| QY 282 | ---IleCyAAspThrAlaLeuSerTrileuLeuSerArgTrpThrHisAAspGluAla | 300 | |

QY 946 a-----HisIleuAspH1AspAlaThrIleAlaIleAsnIleLysLe 961
Db 4511658 CGCGCGCCCGCTGCCCGACCTGCGCCCACTGCGCCGACGC----- 4511616
QY 961 uGUGInValLeuProArgHisSerIleProSerPheTyrIleGlyMetLeuGluLeuP 981
Db 4511615 -----CTGCCGAGTACATGATCCCGGACCACTTCCACCGCGCTCCGACACGATCC 4511566
QY 981 oATGThrAlaThrGlyIleAlaAspArgArgLeuArgIleMetGlyLysAspIleLe 1001
Db 4511565 GGTCAACGCCAAGCGCAAGGTCCGACCGGAGCCCTCCCGCGCGGAGCGACCGCGCA 4511506
QY 1001 uAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAl 1021
Db 4511505 CGACGAGAGC-----CATGTGCGACCGAC-----CG 4511479
QY 1021 aAspThrAlaAlaLysLeuHisSerIleTyrValGlnSerLeuGlyIleAspProAlaTh 1041
Db 4511478 CCGCGTCGAGAGAGCGCTCCCGGATCTGACCGGAACGTGCTGGC----- 4511433
QY 1041 rValAsnValGlyAla-----ThrPheGluLeuGlyIleAsnSerIleThrAlaI 1059
Db 4511432 -GTCCAGCGCGGACACACGACAACTTCTCCACATGCGCGCAATTCCATCTCGCGAT 4511374
QY 1059 eLysMetVal--AsnMetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTy 1078
Db 4511373 CCGCGTATCTCCCACTCCAGCGAGTTGAGATGACCTTCCGCGTCCGACGCGCTT 4511314
QY 1078 rGlnHisProThrLeuAlaGlyIleSerAlaValValLysGly----- 1092
Db 4511313 CGAGGACCGACAGCGGTCCCGTATCGCGGACCGCTGCA--GAGCGGTCACCGCCACA 4511255
QY 1092 ----- 1092
Db 4511254 TCGCGCGCTCTCCGACGCGGACCTCTCGACGAGCGGCGCGACCGACACACACC 4511195
QY 1092 ----- 1092
Db 4511194 TCACGAAACAACCGACCGTGAAGAGACGACGAGTATGACACCGGGAAATGAGAAACC 4511135
QY 1093 -----ApprLeuSerTyrThrLeu----- 1099
Db 4511134 CGTCTCTCGGACATGATGCCGACGCGCTCCGCGCAATGCTGCGCGCGCTCTCGC 4511075
QY 1100 -----IleProLysSerThrHisGluGlyPr 1108
Db 4511074 GGGCGCGGACGCGGCGGACCGCGCGCGGACATCCCGCGCGGACCGGAGCGGCC 4511015
QY 1108 oValGluGlnSerTyrSerGlnGlyArgLeuTyrPheLeuAspGlnLeuAspValGlySe 1128
Db 4511014 GCTGCCGCTGTCTGACGCGGACGAGATGTGTTCTCAGCGCGCTGAGCGCGGACG 4510955
QY 1128 rLeuTyrTyrLeuIleProTyrAlaValArgMetArgGlyProValAsnValAspAlaLe 1148
Db 4510954 CCGCGAATACCTGTGCTCCGCTGCTGCGGCTCGCGGCGCTCCGACACGAGGCCCT 4510895
QY 1148 uATGArgAlaLeuAlaIleLeuGlnArgHisGlnThrLeuArgThrThrPheGluAs 1168
Db 4510894 CGACAAGCGCTGGACACACAGTGTGAGCGGACGAGATCTCGGACCGCGCTACGCGCT 4510835
QY 1168 rGlnAspGlyValGlyAlaGlnIleValHisGluLysLeuSerGluLysValI 1188
Db 4510834 GACGCGGACGAGCGCTCCAGATCATCATGAC-----GCGCGCGCGCCCTGCGCT 4510784
QY 1188 eAspLeuLysGlyY--SerAspLeuAspProPheGluValLeu--AsnGlnGluGlnTh 1206
Db 4510783 GGAACCGTCCGAGCGCGGAGACGAGCGGCTCGCGCGCTGTCAGAGCGGACCTGGC 4510724
QY 1206 rThrProPheAsnLeuSerSerGlnAlaGlyTyrArgAlaThrLeuAspLeuGlyG 1226
Db 4510723 CCGCGCGTTCGACCTCGCGCGGACGCTGCGGCGCGCTGATCCGCGCTCGCGA 4510664
QY 1226 uAspAspHisIleLeuThrIleValMetHisIleIleSerAspGlyTyrSerIleAs 1246

Db 4510663 CGACGAGCAGTCTCTGCGGTGTCTTCCACACATCGCTGCGAGCGCTGCTCACCGG 4510604
QY 1246 rValLeuArgArgAspLeuAsnGlnLeuTyrSerAlaIleLeuLysAspSerLysAspPr 1266
Db 4510603 CGTCTTCGACACAGAACTACGCCCTGTACAGGGC----- 4510567
QY 1266 oLeuSerAlaLeuThrProLeuProIleGlnTyrSerAspPheAlaLysTyrGlnLysAs 1286
Db 4510566 ----TCGCGCGCGCGCGCTGACCGGTACGTCAGCGGACCTACCGCGCTGCGAGCGCGC 4510511
QY 1286 rGlnPheIleGluGln-----GluLysGlnLeuAsnTyrThrLysGlnLeuLysAs 1304
Db 4510510 CGAGCTGACCGGAGAGTCTGTCAACGTCACTTCGACACTGGAAGGCGGCTGCGCGA 4510451
QY 1304 pSerSerProAlaLysIleProThrAspPheAlaAspProAlaLeuLysSerGlyAspAl 1324
Db 4510450 CTTGCGCGCGCTGAACTGCCACGACCGGCGCGCGCGCGCTGCGCGACGCGCGCG 4510391
QY 1324 aGlyCyValHisValThrIleAspGlyLeuTyrGlnSerLeuArgHisPheCyAs 1344
Db 4510390 TTCGCGCGCTGCTGACAGTGCAGCGCGCGCGCGGACCGCGCTGCGAGCTGGCGC 4510331
QY 1344 nGlnHisAsnThrThrSerPheValValLeuLeuAlaIlePheArgAlaIleHisTyrAr 1364
Db 4510330 CGCGCAGACGACCGCGCTGATGCTTCTTCGCGCGCTTACAGAGCTGCTGGCGCG 4510271
QY 1364 gLeuThrAlaValAlaGluAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProG 1384
Db 4510270 CCACACCGCGCGCGCGGACATGCCCGTCCGACCGAGTCTCGCGCGCGCGCGCGCG 4510211
QY 1384 uLeuGluAspHisIleGlyCyAsPheValAsnThrGlnCyMetArgIleAsnIleAspHis 1404
Db 4510210 GCTGCAACGCTCATGCGGTACGCGGACATCAACCTGTGATCGCGCGGACCTTCCGG 4510151
QY 1404 sHisAspThrPheGlyThrLeuIleAsnGlnValLysValaThrThrAlaIlePheG 1424
Db 4510150 CGACCGCGCTTACCGGACCTGTGCGCGCGACGAGGCGGACCGCTTGGACCGCTTACGA 4510091
QY 1424 uAsnGluAspIleProPheGluArgValValSerAlaLeuGlnProGlySerArgAspLe 1444
Db 4510090 CCACACGAGCTGCGCTTCCGCGGACAGGTCTGTGACAGCGCTCTGCGCGC---GAGCGGACCT 4510034
QY 1444 uSerSerThrProLeuAlaGlnLeuIlePheAlaValHisSerGlnLysAspLeuGlyAr 1464
Db 4510033 CTCGCGGACCGCGCTGTCAGAGTCTGTCAGAGTACGAGTACGAGCGGACGCGCAGC---TCGCG 4509977
QY 1464 gPheLysPheGlnGlyLeuGluSerValProValProSerLysAla---TyrThrArgPr 1483
Db 4509976 GTTCGCGTTCGCGGCGTCTGAGGTGCGCGCTTGCAGGCGCGGCGCGGCGGCTGCCAAGTT 4509917
QY 1483 eAspMetGluPheHisLeuPheGlnGluThrAsp---SerLeuLysGlySerValAspPr 1502
Db 4509916 CGACCTGACCTCCAGTACGTAGGAGGCGGAGCGGCTGTTGGGCGGACCTGAGGTA 4509857
QY 1502 eAlaAspGlyLeuPheLysMetGluThrValGluAsnValAlaArgValPhePheGluI 1522
Db 4509856 CGCCACCTCGCTGTGACCGCGGCGGACGTCGAG-----CGGTCCGCGCGGACATCT 4509806
QY 1522 eLeuArgAsnGlyLeuGlnSerSerArgThrProValSerIleLeuProLeuThrAspG 1542
Db 4509805 GCTGCGCTGCTGTCAGGAGTCCCGGACGCGCGGCGGCGCGCTGCGCGTACAGAT 4509746
QY 1542 yIleValThrLeuGluLysLeuAspValLeuAsnValLysHisValaAspTyrProArgG 1562
Db 4509745 CTTGCGGAGAGGAGAGAGGCGCTCTGCTCGCGCGCGCGCGGAGCGCTGAGCGCTGAC 4509686
QY 1562 uSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspSerLeuAlaVa 1582
Db 4509685 GCGCGCGTTCACAGATGTTTCAGAGGACGATGCGGCGGACCGCGCGGCGCTCGCGGT 4509626
QY 1582 lValaAspSerSerCyArgLeuThrTyrThrGluAspArgGlnSerAspIleLeuAl 1602

Db 4509625 CTCCTTCGAGGGAGCGATCTGACGTACCGGAGCTGAACGCCGCCGCAACCGGATCGC 4509566
QY 1602 AGITrPleuArgArgSerMetProIaGIuThrLeuValAlaValPheAlaProAr 1622
Db 4509565 CACGCCCTGATCGGAGGGGGGCGGCCGAGAGCGCTGCGGGCTGAGCGG 4509506
QY 1622 gSerCySGIuThrIleValAlaPhePheGlyValLeuValAsnLeuAlaTyrLeuPr 1642
Db 4509505 CGGCATCGAAGTATCCCGGCTCGGCATCTCAAGTCGGGTCGCGATCTGCC 4509446
QY 1642 oLeuAspValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyPr 1662
Db 4509445 GCTGGACCGCGGACCGGCGGATCGGTCATGTCGCGGAGCCGACAGGCGCC 4509386
QY 1662 oThrIleValLeuIleGlyHisAspThrAlaProProAspIleGluValThrAsnValG 1682
Db 4509385 GGTGGTGGTGTG-----ACACCGCGGAGACCGCGCATGTTCACGCGGA 4509341
QY 1682 uPheValArgIleArgAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleG 1702
Db 4509340 GCTGCTGCTCTC-----GACACGAGCGCGCGGACCTGGCGCG 4509302
QY 1702 uHisAspSerThrLysPro-----SerAlaThrSerLeuAlaTyrValLeuTyr 1718
Db 4509301 GCGGCGGACCTCGGACCGCGGCTGCGCGGACCGCGAGAACCTGATCTACACGATCTA 4509242
QY 1718 rThrSerGlySerThrGlyArgProGlyGlyValMetIleGluHisArgValIleLeu 1738
Db 4509241 CACCTCGGCTCGAGCGGCGCGGAGGCGGTCGCTCAACCCACCAACGTCGTAAG 4509182
QY 1738 gThrValThrSerGlyCysIleProAsnTyrProSerGluThrArgMetAlaHisMetAl 1758
Db 4509181 CTCCTCGAGCGCGG-----AACGAGCATCTACGC 4509152
QY 1758 a-----ThrIleAlaPheAspGlyAlaSerTyr 1767
Db 4509151 CTTCACCGACACCGACGCTGCGCCCTCTTCCACAGCTACGCTTCACGCTCGCTCG 4509092
QY 1767 rGluIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCysValAspTyrMetThr 1787
Db 4509091 GAGGATGTGGGTGCTCTGTCGACGCGCGCGCTGATGTCGTCTCCCTACGACGTCA 4509032
QY 1787 rLeuAspAlaArgAlaLeuLysAspValPhePheArgGlyHisValAsnAlaIleSerH 1807
Db 4509031 CGCCTCGCGGAGAGTCTCTCACTGCTGTCGCGGACGCGTCAACCTGCTCAACCA 4508972
QY 1807 sValThrSerSerSerGlnAspValProLeuArgValProArgIleuSerArgThrIle 1827
Db 4508971 GACGCCCTCGGCTCGCTGCTGTCGCGGAGCGCGAAGCTGCTGCGCGCGGT 4508912
QY 1827 uMetPhePhePheLeuValValThrAspSerThrAlaProAspAlaLeuAspAlaGln 1847
Db 4508911 GGTCTTCGCGGAGAGAGTGAAGATCTCGAAGCTGCGCCCTGGCGGACCGGTTCG 4508852
QY 1847 yLeuTyrGlnGlyValGlnCysTyrAsnGlyTyrGlyProThrGlnLysGlyValMetSe 1867
Db 4508851 GCTC---GACCGGATCGCGTCTGTCACATGATGAGGATACCGAGCACCGTCCACAC 4508795
QY 1867 rThrIleTyrProIleAspSerThrGlnSerPheIleAsn-----GlyValProI 1884
Db 4508794 CACTACACACCGGCTG-----ACCGAGCGGAGCTGACCGCGCGGCGGCAACGCGGT 4508741
QY 1884 eGlyArgAlaLeuAsnAspSerGlyAlaTyrValValAspProGlnGlnIleuValG 1904
Db 4508740 CGGCATCGCGTGCACCTGCGGAGTGTACTCTGACGCGGACCGACGACGCGGTCC 4508681
QY 1904 yIleGlyValMetGlyCyluLeuValValThrGlyAspGlyLeuAlaArgGlyTyrSerAs 1924
Db 4508680 GGTGCGGTGCGCGGTGAGTTCACGTCGCGCGCGCGCGGTGACAGCGGCTCACTCA 4508621
QY 1924 pLys---AlaLeuAspGlnAsnArgPheValHisIleThrValAsnAspGlnThrVal 1943
Db 4508620 CCGGCGGAGCTGACGCGCGAGGCTTGTCTCCGAGCCCGTACGCGTCCGCGGCGGTCCG 4508561

QY 1943 sAlaTyrArgThrGlyAspArgValArgTyrArgIleGlyAspGlyLeuIleGluPheP 1963
Db 4508560 TCTCTACAGAGCGGAGACTCGCGCG---CGGCTGCCGAGCGGACGCTGAGATTCT 4508504
QY 1963 eGlyArgMetAspThrGlnPheLysIleArgGlyAsnArgIleGluSerAlaGluIleG 1983
Db 4508503 GGGCGGATTCGACAGCAGGTCAGATCCCGGCTTCGCGATGAGCTGGCGAGATCGA 4508444
QY 1983 uAlaAlaLeuLeuAspSerSerValArgAspAlaAlaValIleuGlnIleAsn-- 2002
Db 4508443 GACCGGCTGGCGCGCATCCGAGGTCGTGAGCGCTGCTGTCTGTCGCGAGGACAC 4508384
QY 2003 -----GluAspGlnAla----- 2006
Db 4508383 CCGCGGACAGACGCGCTGCTGCTGCTCAACAGACCGCGCGCGGACCGCGCGCC 4508324
QY 2007 -----ProGluIleLeu-----GlyP 2012
Db 4508323 CGCGACCTGCTGCTCCACTGCGCGCGCGCTGCGCGGATCATGATGCTCCGCGCGCT 4508264
QY 2012 eValValAlaAsp-----HisAspHisSerGluAsnAspLys----- 2024
Db 4508263 GGTGCGCTTCGACGCGCTGCTGCTGCTGACCAACAGCGCAAGCTGACAGCGCGCTGCC 4508204
QY 2025 -----GlyGlnSerAlaAsnGlnValGluGlyTyrGlnAspHisPheGluSerGly 2042
Db 4508203 CGCGCGCGCGCAGAGCGC----- 4508185
QY 2042 tTyrSerAspIleGlyCyluLeuAspProSerThrIleGlySerAsp-----PheLysG 2060
Db 4508184 -CTCGGCGCGCGCGCACAGCTGCGCGCGCGCGCGCGCGCGAGAGCGGATCCCGCGAG 4508126
QY 2060 yThrThrSerMetTyrAspArgLysArgIleSerGlnIleAspPheAspGluMetHisGluTrpLeuG 2080
Db 4508125 GTGCGCGAGCTGCTGCGCTGCTGACCGGAGTGTGAGAGAGCGCTTTCAGACTCGG 4508066
QY 2080 yGlu----- 2081
Db 4508065 CGGTCACTCATCGCGCGCTGACCGCTGCTGCGCGCGCTGCGCGGATCGGCTACAGACT 4508006
QY 2082 -ThrThrArgThrLeuHisAspAsnArgSerLeuGlyAsnValLeuGluIleGlyThrG 2101
Db 4508005 CGCGGTGCGGAGCTTTCAGATACGACGACGACGCGCGCGCTGCGGAACTGGTCAACCG 4507946
QY 2101 ySer----- 2102
Db 4507945 GCGCGCGGACCGAGAGACCGGACCGGACCGGACCGGCTTCTCTGCTCAACCGCGA 4507886
QY 2102 ----- 2102
Db 4507885 GAGCGCGCGCGGCTGCGGACCGGCTGCGCGGACCTTACCGCTGTCAGGTGACGT 4507826
QY 2103 -GlyMetIleLeu-----PheAsnLeuAspSe 2111
Db 4507825 CGGATGATGTGAGATGTCTCAACGACGAGGACCGGACCGGATCAACAGACCTTC 4507766
QY 2111 r-----ArgLeuGlnSerTyrValGlyLeuGluProSerArgSerAlaAlaPhe 2128
Db 4507765 GTTCGATATCGGACGAGGAGGCGCTTCTGCTGACGAGCGCTGCGCGCGCGCGG 4507706
QY 2128 eVal-----AsnLysAlaThrGlnSerIleProSerLeuAlaGly----- 2141
Db 4507705 GGTGCGCGCGCGGACGAGGCGCTGCGGACCTCGCTGACCTTCAACCGGCTACCTCCG 4507646
QY 2142 -----LysAlaLysValGlnValGly----- 2148
Db 4507645 CTGCAACTGTGTCACACACGCGGAGATGCGGTGAGTCCGCGACCTGACTCTCT 4507586
QY 2149 -----ThrAlaThrAspIleGlyGlnVal 2156
Db 4507585 CACCGAGAGAACTCTTCTCTCTGCGGAGTTCACGCGGCAAGAGCGCTCCGAGCT 4507526

QY 2156 laapApleu---HisProaspLeuVal1ValLeuAsnSerVal1le-----G1 2171
:|||||
Db 4507525 GTTCGACCTGCGCGACCCCGCCCTGCTGCGCTGCGCACACACATGCGCGCGCGACGCGCAG 4507466
QY 2171 nryrPheProSerSerGluThrLeuVal1Val1Leu1AspThrLeu1Leu1HisLeuProAs 2191
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Db 4507465 CTGTGATGATCAACACACCGAGTCCACGCGATCTTGCACGCGTGGAGCCACATCTCCT 4507406
QY 2191 nvalGlnArg1LeuPhe-----PheG1YAspVal1ArgSerGln1Leu1ThrAsnGln1His-- 2208
:|||||
Db 4507405 GGTGATGAGAGTCTCTGAGAGATACGCGCGCTGCGGAGCGCGGACAGCGCTCCGAGGC 4507346
QY 2209 -----PheLeu1Ala1Arg-----Ala1Leu1Ser1 2217
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Db 4507345 CCCCCTGCGCGCGCTCCGCTTCCGCGCATTCGTCGCGCGCGAGCTGGACGTGCTGACATC 4507286
QY 2217 rLeuG1YLeuAsn1AlaThr1YsAspAspVal1ArgGln1YMer1AlaGluLeu----- 2234
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Db 4507285 CGCGGGAGCCCGCGCTTACTGGCAGTGGTGTGACGCGCTACGCGGCTCACCGTGC 4507226
QY 2234 ----- 2234
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QY 2235 -GluAspMetGluGlnGluLeuLeuVal1----- 2243
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Db 4507165 CCACGACCTGAGAGACCGGCTGCGCGCTGCGCACGAGCGCGCGCTTCCCTCAAGAG 4507106
QY 2244 -----GluProAlaPhePh 2248
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QY 2248 eThrSerLeu-----LysAspArgPheProG1YLe 2258
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QY 2258 uValGlnHisVal1GluLeuPro----- 2266
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QY 2266 ----- 2266
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QY 2267 -----LysAs 2269
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QY 2268 nMetGluAlaValAsnGlnLeuSerAla1YrArg1YrAla1Val1HisVal1Arg1 2288
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QY 2288 YSerLeu-----GlyAspGlnLeuVal1-----LeuProVa 2298
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Db 4506637 CGTCTGAGAGCGATGCGCGCGGACCCGAGGGCGACGCGCGAGCGTCTGTTCTGCGCGG 4506578
QY 2298 1-----GluYsAsp-----AspTrp----- 2303
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Db 4506577 GGGGAGCGGAGCGGACGCTCTGAGTGAACGACACGCGCTTACAGGCGGAGACCGC 4506518
QY 2303 ----- 2303
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QY 2304 -----1LeaspPheGln1AlaasnGlnLeu----- 2311
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Db 4506457 TCACGAGAGCGGACGCTCTGTAACCGCGAATCTGACGTGCGCGCACCACTGTTGGCGCA 4506398
QY 2312 -AsnGlnYSerLeuG1Y----- 2317
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QY 2318 -AspLeuLeu-----LysSerSerAspAla----- 2325
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QY 2326 -----Ala1Leu1Ala1Ser1Ys1Leu1ProPh 2335
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Db 4506277 GACCCCTCTACCCGCGCGACCGCGCTACCGGACATGCGGAGCTGTCCGCGCCCGT 4506218
QY 2335 eGlu1Leu1Ala1PheGln1Arg1Val1Ala1SerLeu----- 2348
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QY 2349 -AsnSerAsn1LeaspGlu----- 2354
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QY 2355 -----TrpGlnLeuSer1 2359
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QY 2359 r1LeArgSerSerAlaGln1YAspSer-----SerLeuSe 2371
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QY 2371 rVal1ProAsp1LeuPheArg----- 2377
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QY 2377 ----- 2377
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Db 4505917 CGTGCATGCGCGACCTGGCGGACGACCTGTGCGATCGGCGCGGTACACTTCATCA 4505858
QY 2377 ----- 2377
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QY 2378 -----1Lea1Gln1YAla-----GlyPh 2384
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Db 4505797 CTTGCGCGCGGTCTGTGTGTGGCGGCGAGGCTTCAACCGCGCGACCTTGAAGCGCTG 4505738
QY 2384 eArgValGlnValSerSer1AlaArg1InrPserGlnAsnG1YAlaLeuAspAlaValPh 2404
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Db 4505737 GCGGCGCTGCGCGCGGACCGCGCTGATCAACGAGTACGCGCGCACGAGGCA----- 4505683
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Db 4505682 -----TCCGTGGCAACGACGCTTCAACGAGTGCCTCCGCGGACCCGAGACCGA 4505636
QY 2422 ----- 2422
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QY 2422 ----- 2422
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QY 2422 ----- 2422
:|||||
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QY 2423 -----LeuArg1Ys1Asp1Leu1Thr1Asn1ArgPro----- 2433
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Db 4505455 CAGAGCGCGCGCGCGGTACCGCACCGGCGACCTGTACGCGCAACCGCGGAGGAA 4505396
QY 2434 -----LeuGlnArg1LeuGlnAsn-----ArgArg1Lea1Ala1Gln1-- 2445
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CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242, 578
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: SeqIntln version 3.1
SEQ ID NO 33665
LENGTH: 10296
Type: DNA
ORGANISM: Pseudomonas syringae
US-10-282-122A-33665

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QY 1212 -----SerSerGluAlaGly-----TyrArgAla 1219
 Db 3499 CAGGCCAATGCCGAGACAACACTGTTTCTCTGCAAAAAAGGCCATTGTTTCGGCC 3558
 QY 1220 ThleuLeuArgLeuGluValAspAspHisIleLeuThrIleValMetHisIleIle 1239
 Db 3559 TCCTGTTAAGACTGGCGAGCAACATATCTGTGTGGACCCGACCAATATGTC 3618
 QY 1240 SerAspGlyTyrSerIleAspValIleArgAspLeuSerGlnLeuTyrSerAlaIle 1259
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 QY 1260 LeuLysAspSerLysAspProLeuSerAlaLeuThrProLeuProIleGlnTyrSerAsp 1279
 Db 3679 GCACAGGCGCAACCTCGCCCTGGCA-----CCTCTGATATTACAGTACGGTGAC 3729
 QY 1280 PheAlaLysTyrProGlnLysAsp-----GlnPheIleGluGlnLysGlnLeuAspTyr 1297
 Db 3730 TATGCTGCTGGGACCGCGAGTGGCAGGCGCCCATCAAGTTCCGCGTGAACCGATTAC 3789
 QY 1298 TyrLysLysGlnLysLysAspSer---SerProAlaLysIleProThrAspPheAlaArg 1316
 Db 3790 TGGTCTCGCATCTGGGCCAGGCCCGACCACTGTGAACCTGCTACCGACCGCGCGC 3849
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 Db 4030 ATGCGCAACCGCACACCAAGCCGAGATCGAGCGCTGATCGGCTTGTTCATCAATACCTT 4089
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 Db 4210 TTGGCCATC---CCGCTGATGATGATGCTCGCTGCTTGTCCAGGTGCTGTGCTCTG 4266
 QY 1457 HisSerGlnLys-----AspLeuGlyArgPheLysPhe 1467
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 QY 1468 GlnGlyLeuGlnSerValProValProSerLysAlaTyrThrArgPheAspMetGluPhe 1487
 Db 4321 ---GCGCTTAGTGCACACA-----GCCAAGTTGATCTACCTCG 4359
 QY 1488 HisLeuPheGlnGluThrAspSerLeuLysGlySerValAsnPheAlaAspGluLeuPhe 1507
 Db 4360 GAACCTGACGCGCTCATCCGAGGGTTATCAGATGGCGGGAATCAACAGGACCTTTT 4419
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Db 4531 AAACAAACATCTCTCCAGCAATGAACCGCACTCAGAGGTTTAT---CGCCATTGGCG 4587
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 QY 1645 ValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyProThrIle 1664
 Db 4828 CCGAGCTATCGAACCGAGCGCTGCGCTTATGCGCCAGAGATGCCGTCGCACTGATC 4887
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 Db 4942 TGCATG-----GACCAATGCGCGGATGCTGGCATGAGCATGCTCAAT 4986
 QY 1705 SerThrLysPro---SerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThr 1723
 Db 4987 CCGGCGAGACCGCAAACTGCTTGAACCTGTGATGCTTACATCACTGACCTGGGCTCCAC 5046
 QY 1724 GlyArgProLysGlyValMetIleGluHisArgValIleIleArgThrValIleThrSerGly 1743
 Db 5047 GGGCTGCCCAAGCGCGCGGCTGACTCAGCAAAATGCTGACCAACTCGGCAATGGCAA 5106
 QY 1744 CysIleProAsnTyrProSerGluThrArgMetAla-----HisMet 1757
 Db 5107 CTC-----ACTGAATGCGCTGAGCGGAGCGGACCAATACGCTGCATTC 5151
 QY 1758 AlaThrIleAlaPheAspGlyAlaSerTyrGluIleTyrSerAlaLeuLeuPheGlyArg 1777
 Db 5152 TCGCATTAGCTTTCATGATGATGTTTCGAGAAATTTCTTCCACTGGGCAAGCGGCGC 5211
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 QY 1798 PheArgGluHisValAsn-----AlaAlaSerHisValIleThrSer 1810
 Db 5272 CAGCGACAGAACATTCGCCGCTTTCATTCCTTGTCTGCTCGCAAGCATTCGTGAC 5331
 QY 1811 SerSerGlnAspVal-----Pro 1816
 Db 5332 GCTGCCGAGATGATGATTAACCTGCGCTGAGAACTGCTGCGCGGAGACAA 5391
 QY 1817 LeuArgValProArgArgLeuSerArgThrLeuMetCphePheLeuValIleThrAsp 1836
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 QY 1837 SerThrAlaProAspAlaLeuAspAlaGlnGlyLeuTyrGlnGlyValGlnCysTyrAsn 1856
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 QY 1857 GlyTyrGlyProThrGluAsnGlyValMetSerThrIleTyrProIleAspSerThrGlu 1876
 Db 5455 CAGTAGGACCGAGAGGATCA----- 5475
 QY 1877 SerPheIleAsnGlyVal-----Pro 1883

[illegible]

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|----|------|---|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| QY | 2239 | GIU | GIU | LEU | LEU | Val | GIU | Pro | Ala | Phe | He | He | Thr | Ser | Leu | Ys | Asp | Arg | Phe | Pro | Gly | Leu | 2258 | |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | |
| QY | 2259 | Val | GIU | His | Val | GIU | Ile | Leu | Pro | Ys | Asn | Met | GIU | Ala | Val | Asn | GIU | Leu | Ser | Ala | Trp | 2278 | | |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | | |
| QY | 2279 | Arg | Trp | Ala | Ala | Val | His | Val | Arg | Gly | Ser | Leu | Gly | Asp | GIU | Leu | Val | Leu | Pro | Val | 2298 | | | |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | | | |
| QY | 2299 | GIU | Ys | Asp | Asp | Trp | Ile | Asp | Phe | GIU | Ala | Asn | GIU | Leu | Asn | GIU | Ys | Ser | Leu | Gly | Ys | Asp | 2318 | |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | | |
| QY | 2319 | Leu | Leu | Ys | Ser | Ser | Asp | Arg | Ala | Ala | Ile | Met | Arg | Ala | Val | Ser | Ys | Ile | Pro | Phe | GIU | Ile | Thr | 2338 |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | | |
| QY | 2339 | Ala | Phe | GIU | Asp | GIU | Val | Val | Ala | Ser | Leu | Asn | Ser | Asn | Ile | Asp | GIU | Trp | GIU | Leu | Ser | 2358 | | |
| Db | 5931 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5931 | | | |
| QY | 2359 | Thr | Ile | Asp | Ser | Ser | Ala | GIU | Gly | Ys | Asp | Ser | Ser | Leu | Ser | Val | Pro | Asp | Ile | Phe | Arg | Ile | 2378 | |
| Db | 5932 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5932 | | | |
| QY | 2379 | Ala | Gly | GIU | Ala | Gly | Phe | Arg | Val | GIU | Val | Ser | Ser | Ala | Arg | GIU | Trp | Ser | GIU | Asn | Gly | 2398 | | |
| Db | 5958 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5958 | | | |
| QY | 2399 | Ala | Leu | Asp | Arg | Ala | Phe | His | Ile | Cys | Cys | Ser | Gln | Gly | Arg | Thr | Leu | Val | Asn | Phe | Pro | 2418 | | |
| Db | 5958 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5958 | | | |
| QY | 2419 | Thr | Asp | Arg | His | Leu | Arg | Gly | Ser | Asp | Leu | Leu | Thr | Asn | Arg | Pro | Leu | GIU | Asn | Gly | Leu | Gln | 2438 | |
| Db | 5958 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 5958 | | | |
| QY | 2439 | Asn | Arg | Ala | Gly | Ile | Ala | Ile | Gly | Val | Arg | GIU | Arg | Leu | Arg | Ser | Leu | Leu | Pro | Ser | Trp | Met | 2458 | |
| Db | 5959 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 6003 | | | |
| QY | 2459 | Ile | Pro | Ser | Asn | Ile | Val | Val | Leu | Asp | Ys | Met | Pro | Leu | Asn | Ala | Asn | Gly | Ys | Val | Asp | 2478 | | |
| Db | 6004 | GTGGCGACACACCTTCATCTCTGCGACACCTGGCCCTGCACCCCAAGTGGCAAAAGTCGAC | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 6063 | | | |
| QY | 2479 | Arg | Gly | GIU | Leu | Ser | Arg | Arg | Ala | Leu | Val | Val | Pro | Ys | Gln | Gln | Trp | Ala | Ala | Pro | Leu | 2498 | | |
| Db | 6064 | AAACGC | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 6065 | | | |
| QY | 2499 | Pro | Thr | Phe | Pro | Ile | Ser | GIU | Val | GIU | Val | Ile | Leu | Cys | GIU | Ala | Thr | GIU | Val | Phe | 2518 | | | |
| Db | 6069 | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | ---- | 6065 | | | |
| QY | 2519 | Gly | Met | Ys | Val | Asp | Ile | Thr | | | | | | | | | | | | | | | | |

QY 2599 ThrGlnAlaIleuCyAargGluPheAlaIleValLeuGlyPhe---GlnValGlyIle 2617
 DB 6130 GCTGAAGACAACTCGCTGCATCTGGCGAGTGTCTGATCTGTGCAGTGTGATTC 6189
 QY 2618 ThrAspAsnIlePheArgLeuGlyGlyHisSerLeuMetAlaThrValPheAlaIleValArg 2637
 DB 6190 ACCGATACCTCTTGCAGACTGTGGGACCTTTGTGCTGCACCTACAGTGTGTTCCGCT 6249
 QY 2638 IleGlyHisArgLeuAspThrThrValSerValIleAspValPheAsnIleProValIle 2657
 DB 6250 ATTGCAAAACAGCGATGTGCATATGCGCTGCACCTGTGTAAGCGCCAGCATC 6309
 QY 2658 PheGlnIleu-----AlaIleAlaLeuAspAsnIleValGln 2669
 DB 6310 GAACAAATGTGCTCCGCTGAGCACAAGCCGCGTACCTCTGACGATGATCGCC 6369
 QY 2670 SerLeuThrAsnGlnIleValGlyIleArgLeuMetAlaGluIlePheProPheGlnIle 2689
 DB 6370 ACCAAGCCGCGC-----TCCGGCATGAAAGTGTCTGTCTATGCGCAAGACGCTGTG 6420
 QY 2690 LeuPheThrGlnIlePheProGluIlePheMetAlaSerGlnIleIlePheProGlnIle 2708
 DB 6421 TTCTTCTGATGCTGTGCATGCTGCATGCTGCATGCTGCATGCTGCATGCTGCAT 6480
 QY 2709 LeuGlnIleIleIleGlnAspIleIleIleProSerThrGlnMetGlnValAlaPheLeuPhe 2728
 DB 6481 CTG----- 6483
 QY 2729 AspHisThrThrAlaArgProArgProPheValIleProPheIleIleAsnIlePheProSerThr 2748
 DB 6483 ----- 6483
 QY 2749 SerGluProAspAlaAlaGlyLeuIleValIleValIleCys---GlnSerLeuValAsnHisLeu 2767
 DB 6484 AAGGCGCGCTGAAGAAAGCGGCTGTGCAGCAATGCTGCAGCGATGCTGCAGCGTGCAC 6543
 QY 2768 AspIlePheArgThrValPheAla---GlnAlaSerGlyLeuIleValIleValIle 2785
 DB 6544 GAACCCCTGCGCAGCATTCGCTGCGTGCAGGAGACCGCGCTGTGCAGCGCTGTGCAT 6603
 QY 2786 -----LeuSerCysLeuAspLeuProIleGlnValIleGlnIleThrGln 2799
 DB 6604 CCCCCGAGCTCGATACGCTGATCTCTGATTTGCGC-----CATACCGCT 6651
 QY 2800 AspAsnIleAsnThrAlaThrAsnGluPheLeuAspGlu-----PheAlaIle 2815
 DB 6652 CAGCGCGTGTGCGTGTGTAAGAAAGCATGACGATGCTGCAGCTGCTGCTGCTGCTGCTG 6711
 QY 2816 GluProValArgLeuGlyHisProLeuIleArgPheThrIleIleIleGlnIleIleIle 2835
 DB 6712 GAAGACC-----GGTCCCTGCTGCTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 6759
 QY 2836 MetArgValIleMet---ArgIleSerHisAlaLeuIleArgIleIleIleIleIleIle 2854
 DB 6760 CACCAATGTCTGCTGTTTACCGTGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6819
 QY 2855 ValValArgIleValIleMetIleIleIleIleIleIleIleIleIleIleIleIleIle 2869
 DB 6820 CTTACCGCGAGATCATGCGGCTGTACAGCGTTTGCAGACAGCGAGATCATCGCTTG 6879
 QY 2870 ProProHisGlnPheSerArgIleIleIleIleIleIleIleIleIleIleIleIleIle 2886
 DB 6880 CCGCTCTGGAATC---CAGTACAGCGATACCTCTTGCAGCGCTGCTGCTGCTGCTGCTGCTG 6936
 QY 2887 -----SerGlyHisGlyPheThrArgAspValIleGlnAsnIleProMet 2901
 DB 6937 CCAAGCGTTTGTGAGCGAGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6996
 QY 2902 ThrIle---LeuSerAspAsp-----ThrValAlaAspValIleAsp 2914
 DB 6997 CGGCTGAGGTGCGAGGACGACCGCGCTGCGCGATGACGATGACGATGACGATGACGATG 7056
 QY 2915 AlaThrCysValAlaLeuHis-----LeuSerIleValAlaAsnIlePro 2929

DB 7057 GTTACC-----CATACATGCGCCCAACCTGTCCAGAGATCGATACGTTG 7104
 QY 2930 SerGlnValLeuArgIleSerSerAsnIleIleIleThrGlnAlaThrValPheAlaIleVal 2949
 DB 7105 AGCCAAAGCTTG---GGAGTGACACCGCTTATGACCTGCTGCACCTGCTGCTGCTGCTGCTG 7152
 QY 2950 CysAlaLeuValLeuSerArgIleIleIleIleIleIleIleIleIleIleIleIleIle 2969
 DB 7153 ---AGTCTGCTGTGAGCCCGGACAGCGGCGACGCGATGATGCTGCGGACGCGCCATC 7209
 QY 2970 SerGlyArgGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 2989
 DB 7210 GCCAAGCGGACCGGACCGAGGTCGAA-----CCCTGTATGAGCTGTGCTGCTGCTGCTG 7263
 QY 2990 ValProValArgAlaHisIleIleIleIleIleIleIleIleIleIleIleIleIle 3008
 DB 7264 CTGGACGTGCGCACACCGATGAAAGGACACCGCATGCTGCGCATTTGCGCAATTTGCAACAGTGC 7323
 QY 3009 GlnAspGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 3024
 DB 7324 AGGAACACACACCTCGCGCTGTATGCCCAACAGACCTGCGTTCGAAAGATGCTGAA 7383
 QY 3025 -----AspLeuValArgAspCysThrAspTrpProGlnAlaIleThrAsnIlePheSer 3042
 DB 7384 GCGCTGATACGCGCTCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7431
 QY 3043 CysIleThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 3060
 DB 7432 ATGTTGTGCTACAGAACAGCG 7491
 QY 7492 ATCTTCGATCTCGGAGCACCGACG-----GCCAATTC 7524
 DB 3081 AspLeuAlaIleAlaGlyIleValIleIleIleIleIleIleIleIleIleIleIleIle 3100
 QY 7525 GACTTGAAGCTG-----GAGCTGAGCGCCGACGCTGCGAGGCTGATGATGATGATGATGATG 7578
 QY 3101 AlaIleThrGlnIlePheGlyArgIleValIleIleIleIleIleIleIleIleIleIle 3114
 DB 7579 TACAACCTGCACTGTTTCGACGCGCAGCATGATGAAAGCTG 7620
 DB
 RESULT 13
 US-10-282-122A-33846
 : Sequence 33846, Application US/10282122A
 : Publication No. US20040029129A1
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Liangsu
 : APPLICANT: Zamudio, Carlos
 : APPLICANT: Malone, Cheryl
 : APPLICANT: Haselbeck, Robert
 : APPLICANT: Ohlsen, Karl
 : APPLICANT: Zyskind, Judith
 : APPLICANT: Wall, Daniel
 : APPLICANT: Trawick, John
 : APPLICANT: Carr, Grant
 : APPLICANT: Yamamoto, Robert
 : APPLICANT: Forsyth, R.
 : TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 : FILE REFERENCE: EITRA.034A
 : CURRENT APPLICATION NUMBER: US/10/282,122A
 : CURRENT FILING DATE: 2003-02-20
 : PRIOR APPLICATION NUMBER: 60/191,078
 : PRIOR FILING DATE: 2000-03-21
 : PRIOR APPLICATION NUMBER: 60/206,848
 : PRIOR FILING DATE: 2000-05-23
 : PRIOR APPLICATION NUMBER: 60/207,727
 : PRIOR FILING DATE: 2000-05-26
 : PRIOR APPLICATION NUMBER: 60/230,335
 : PRIOR FILING DATE: 2000-09-06
 : PRIOR APPLICATION NUMBER: 60/230,347


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/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 33846
/ LENGTH: 6288
/ TYPE: DNA
/ ORGANISM: Pseudomonas syringae
/ US-10-282-122A-33846

Alignment Scores:
Pred. No.: 5,57e-139 Length: 6288
Score: 1752.00 Matches: 591
Percent Similarity: 44.30% Conservative: 338
Best Local Similarity: 28.18% Mismatches: 849
Query Match: 10.86% Indels: 321
DB: 16 Gaps: 65

US-09-482-788-2 (1-3129) x US-10-282-122A-33846 (1-6288)
QY 39 TyrGlyLeuaspserArgIleGluAlaIleLysPro-----CysThrProPhe 55
DB 161 TAGGGCTGGCTGTTCC---ATGAGGCGATATAGCAGGAGGGCTGCTGCATCTG 217
QY 56 GluLeuaspMetIleaspCysasnAlaLeuaspLysGlnSerAlaIleGlyHisAlaVal 75
DB 218 TCGATATCA-----GACTCGCATCTGTCGATTTTTCAGACTACG 256
QY 76 TyrAspValProThrAspIleaspIleSerArgPheAlaLeuAlaTyrLysGluIleVal 95
DB 257 TTGACAGTGTGCGAGCGAG-----CGCTGGAATACCTTCAAC 292
QY 96 AsnGlnThrProAlaLeuArgAla-----PheAlaPheThrSerAspSer 110
DB 293 AATCATTTTCCGACGCTTCAATCCCTTGAAGGCACTTTGGGAGTGCAGCTCGTAC 352
QY 111 GlyLysThrSerGlnValIleLeu-----LysAspSerPheValPheSerTrpMet-- 127
DB 353 GGTGCAATGCATCCCATCATTTACTGTGCTGGGCGGTCGCATCATTTGTGCATGCGCG 412
QY 128 -----CysTrpSerSer 131
DB 413 CAGGGGTACGCTGTTCTGCGCATGAGTGAGAAAGCTCAATATTGTGGCGGCA 472
QY 132 SerSerProAspGlu-----ValAlaArgAspGluAlaAla 144
DB 473 TCGACCAAGCTC-GAGGAGGCCCTTCTCAAGACACTTCTGATCAAGACAAAGCCTAT 531
QY 145 AlaAlaAlaSerGlyProArgCysAsnArgPheValIleuLeuGluAspMetGlnThrLys 164
DB 532 CTGAGTTCGTGCGG-CCTGAGCGCGCAGGCGCTTTTGGCGGCAACGCTATACACA--- 587
QY 165 LysCysGlnLeuValTyrThrPheSerHisAlaLeuValAspValThrPheGlnGlnArg 184
DB 587 ----- 587
QY 185 ValLeuSerArgValPheAlaAlaTyrLysHisGluLysAspThrHisArgProGluThr 204
DB 587 ----- 587
QY 205 ProGluSerSerAspAlaThrAspThrAspSerGlnSerValSerValSerMetSer 224
DB 588 -----ACTGCGCGCACCTCTGCTGCAGTGCAGTCCGCGCATCA 623

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QY 225 CysGlu-AspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnAspLeu-- 243
DB 624 TGGCGTGGTTCATATGCAAGCGGCTATATTCGTCGACGATTAAGGTACCTGTT 683
QY 244 -AsnAlaSerValPheProHisLeuSerAspHisLeuMetValProAsnProThrThr 263
DB 684 CAATGCCCTGTGCT-----GCCGTTC 704
QY 263 rAlaGlnHisArgIleThrPheProLeuSerGlnLysAlaLeuSerAsnSerAlaIleCys 283
DB 705 CACCGAGCAT-----GACCTTCTCTCTGTCGGATATT 737
QY 283 sArgThrAlaLeuSerIleLeuLeuSerArgTyrThrHisSerAspGluAlaLeuPheG 303
DB 738 CTTCGCCCGCTGAGCGGCTATTTTACCGTGTGGATGCTGAAAGAGTCATCATCGG 797
QY 303 yAlaValThrGluHisLeuProPheAspLysHisTyrLeuAla----- 318
DB 798 C-----ATGCCCTGCATTAACCGCAGCAGCGCTGTGAGAAAGAC 839
QY 319 -AspGlyThrTyrGlnThrValAlaProLeuArgValHisCysGlnSerLeuAlaGAl 338
DB 840 GATCGGTATGTTTCTTCCGTTATTCGATGCGGCGATCGGTCGACCCCATGCTGCT 899
QY 338 aserAspValMetAspAlaIleSerSerTyrAspAspArg----- 351
DB 900 GCTCGAATTATGAGCATATGCGCCGCGCAATTCGACGCTGTACCCCATAGCATTT 959
QY 352 -----LeuGlyHisLeuAlaProPheGlyLeuAr 361
DB 960 TCCAAATCGGAACTGAATGCGCGCTCAATATTGGGATTTCCAGCGCAAGCATCTT 1019
QY 361 gAspIleArgAsnThrGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeu 381
DB 1020 CGATATCAGCCTTTCATTCGAAATTTGACGG-----GACTTT- 1059
QY 381 uValThrAspGlySerHisValAsnAsnGlyIleAsnGlyPheLeuGlnIleThrG 401
DB 1060 -ATCTTTGGCGGCTCCCTCGG-----CAGCGCATCAGAT 1094
QY 401 uSerSerHisPheMetProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlu 421
DB 1095 GTACAGCGGCTTC-----GATCAGACGCCACT 1121
QY 421 rSerGlyAlaLeuLeuValAlaTyrTyrAspHisAsnValIle----- 435
DB 1122 CTCAATCGCTATCTGCGATTACTTCAAGATGACATTTGTGACTTTAACTTCAA 1181
QY 436 -----AspSerLeuGlnThrThrArgLeuLeuGlnGlnPheGlyHis 449
DB 1182 TTGACCTGCTTTGGCCAGACGAAATTGAA-----CGAATTCGGAGCCGATTAAGCT 1235
QY 449 sLeuIleLysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeu 469
DB 1236 GCTTCCTGAAG---TTGGTTCCGCTATAGTCAACGCAATTAAGCAGCTGGCGTAT 1292
QY 469 tThrGluTyrAspArgAlaGluIle---GluSerTrpAsnSer-----GlnProLeuG 486
DB 1293 GGGCGAAACCGACGCGCGGAGGCTCTGCGAGTTCAAGCAACATGAGGCAATGCA 1352
QY 486 uValGlnAspThrLeuLeuHisHisGluMetLeuLysAlaValSerHisSerProThrLys 506
DB 1353 G---CAGGATCTATTGTGTCATCACTTTTTCGAACGCAAGCGCAGCAGCTCAAGC 1409
QY 506 sThrAlaIleGlnAlaTyrAspArgLysAspTrpThrTyrSerGlnLeuAspAsnValSer 526
DB 1410 GCTTGCACTGTGTGGCGGCGACGAGTGTGACCTTACGCGGACCTTAACGACGACAG 1469
QY 526 rArgLeuAlaValHisIleLysSerLeuGlyLeuArgAlaGlnGlnAlaIleIleProVa 546
DB 1470 CCAAGTGGCTCATGTCTTGTCTGTCATGCGGCAATTTGTTGCCAGACGCG---GTGGGAT 1526

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3519 TGTGCTGCTGTGGACCATGCACCATCGTATCGAGTGGCTGGTTCGATGGGACATTTTGAC 3578
QY 1249 gATgAspLeuAenGlnLeuTyrSerAlaAlaLeuYAspSerLysAspProLeuSerAl 1269
DB 3579 GCGCGAGTTGGAGCGCTTACCGAGCGGTTCCGAAGATGAGGACGCCG----- 3630
QY 1269 aLeuThrProLeuProIleGlnTyrSerAspPheAlaLysTrpGlnLysAspGlnPheIle 1289
DB 3631 -TTGCCGCGCTTGTATTGATACGACGCGACTACGCGATGTGGCAACGAAGTTGGTTGAG 3689
QY 1289 egluIn-----GluYsgLnuLeuAnTyrTrpLysLysGlnLeuLysAspSerPr 1307
DB 3690 CGCGGAGATTCACACAGCAAGACACTTACTGCGACAGCGCTCTGCTCAT---GCGCC 3746
QY 1307 oAla-----LysIleProThrAspPheAlaArgProAlaLeuLeuSerLysAspAlaG 1325
DB 3747 GGCATTGCTGATGTGCGCGCTACCGTACGCTCGCGCAACAGGACTATACGGGTGC 3806
QY 1325 yCyvAlHisValThrIleAspGlyLeuTyrGlnSerLeuArgAlaPheCyvAsnG 1345
DB 3807 GTCCGATAGCTGTGCTGTGATGCGACGCTGACGAATGACTCAAGACGTGAGTGGCG 3866
QY 1345 uHisAnThrThrSerPheValValLeuLeuAlaAlaPheArgAlaAlaHisTrpArgLe 1365
DB 3867 GCACGGCACACACTTTTCATGACACTACGCGCGCTGGCAACGGTATTGAGTGGCTTT 3926
QY 1365 uThrAlaValAlaAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGlu 1385
DB 3927 GTACGGGACAGATGAGGTGGTAAATCGGTGCGCGTGGCGAACCGGATGACGGGAGT 3986
QY 1385 uGluAspIleIleGlyCyvAspValAsnThrGlnCyvMetArgIleAsnIleAspHisH 1405
DB 3987 CGAGGGCTGATGCGTTTTCGCAACACCTGCGCTGCGGTGATGTGCAGACGA 4046
QY 1405 sAspThrPheGlyThrLeuIleAsnGlnValLysAlaThrThrAlaAlaPheGluAs 1425
DB 4047 CCGGACGGTGCAGGCACTTCTGAGTCAAGCTCAAGGCTGCACGCTGCGCGGTATGAACA 4106
QY 1425 nGluAspIleProPheGlnArgValAlaSerAlaLeuGlnProGlySerArgAspLeuSe 1445
DB 4107 CCGAGATCTGCTGTCGAGAGGAGTGTGAGTGTCTCAACCG---GTGGCGACGTTGTC 4163
QY 1445 rSerThrProLeuAlaGlnLeuIlePheAlaValHisSerGlnLysAspLeuGlyArgPh 1465
DB 4164 CCATACCCGCTTTCAGAGCGCATGCTGTGTGGCAGAACATG---CCGACGGCGGAAT 4220
QY 1465 eLysPheGlnGlyLeuGlnSerValProValProSerLysAla---TyrThrArgPheAs 1484
DB 4221 CCGGATTCAGACGGGCTGGAGCTGACGCTGATTCGATTCGTAAGCGCACCAAGTACGA 4280
QY 1484 pMetGluPheHisLeuPheGlnGlnLysThrAspSerLeuLysGlySerValAsnPheAlaAs 1504
DB 4281 TGTGTGCTGCACTTGGCGGAGGTAGAGGCGCGATGTGCGTTCGCTGGAATATGGAC 4340
QY 1504 pGluLeuPheLysMetGlnThrValGluAsnValAlaArgValPhePheGlnLysLeuAr 1524
DB 4341 GCGGCTTTCGACAGACATACGCGCGCAAGCTAGTGGCTATTCGAAACGGGTGCTGCG 4400
QY 1524 gAsnGlyLeuGlnSerSerArgThrProValSerIleLeuProLeuThrAspGlyLysLe 1544
DB 4401 TCGAATGTGTGAGAACGAGCGCGCAGGTAGTCGAGCGCATCAAGCTTTGGGCGCAACGA 4460
QY 1544 lThrLeuGlnLysLeuAspValLeuAsnValLysHisValAspTyrProArgLysSerSe 1564
DB 4461 ACGCCGCAAGTCTGTTCGAGTTCAACGCAACACACAGCGCTTGGCAAGGATTTAT 4520
QY 1564 rLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspSerLeuAlaValAlas 1584
DB 4521 GCTTCATACGCTTTTGAACAGACAGCGCACGACGACCGCGCTTGGCGCTGATG 4580
QY 1584 pSerSerCyvArgLeuThrTyrThrGlnLeuAspArgGlnSerAspIleLeuAlaGlyLys 1604
DB 4581 CGCGGACGAACGAGTGAATACCGCGATCTCAACAAACGAGTATCAGGTTGCTCATGT 4640

QY 1604 pLeuArgArgSerMetProAlaGlnThrLeuValAlaValPheAlaProArgSerCy 1624
DB 4641 CTTCGCTGACCTGGGCACTTGTTCGACAGACCGCGTGGCATCTGTGTGAACCATGT 4700
QY 1624 sGluThrIleValAlaPhePheGlyValLeuLysAlaAsnLeuAlaTyrLeuProLeuAs 1644
DB 4701 GGAATGTGTGTGGCTTGTGGGATCTGAAGGTGGCGGTGCATATATGCGCGTGA 4760
QY 1644 pValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyProThrIle 1664
DB 4761 CCTGGGTATCCCTGGAGCGGTGTTCATATCTGGAGAC---AGCCGCGCGTGGC 4817
QY 1664 eValLeuIleGlyHisAspThrAlaProProAspIleGluValThrAsnValGluPheVa 1684
DB 4818 GTGTCTGTACACCCGCAACCCG-----GACTGTGGGTGGCGGTGGTGC 4865
QY 1684 lArgIleArgAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGluHisAs 1704
DB 4866 GTGGCGATGCGGTGCTGTGATCTGCMAAGCGCAACTGGGCGGCTGAAGCTGACATGA 4925
QY 1704 pSerThrLysProSerAlaThr-----SerLeuAlaTyrValLeuTyrThrSerGlySe 1722
DB 4926 TCCGCTGTTCGACAGGCTCACGCGCACACCTGGCTTATGTATCTATACCTCGGATTC 4985
QY 1722 rThrGlyArgProLeuGlyValMetIleGluHisArgValIleIle---ArgThrValTh 1741
DB 4986 GACCGGCAACCCAAAGGCGCTGATGATGACATTTGGCCATTTGAAACCGCTGTATG 5045
QY 1741 rSerGlyCyvIleProAsnTyrProSerGluThrArgMetAlaHisMetAlaThrIleAl 1761
DB 5046 GCGGAGGACCACTATGCGGTGAGTGCAGAAACCGCTTCTGCGAAGACACCGTTGCG 5105
QY 1761 aPheAspGlyAlaSerTyrGluIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCy 1781
DB 5106 GTTTGACGTGTGCGTCTGGGAGTTTTCCTCTTGTGCTGCGCGGTGCAATTTGGTAT 5165
QY 1781 sValAspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGluH 1801
DB 5166 CGCACGTCGGGACGCGCATAGACACCCGAGTATCTGGCGGAGTTATCCGAGGCTGGCG 5225
QY 1801 sValAsnAlaAlaSerHisValThrSerSerSerGlnAspValProLeuArgValProAr 1821
DB 5226 AGTGAAGATTTGCATTTGTATTCCTTCATGTCAGAGCTTCCTCATGACAGTTGGCCC 5285
QY 1821 gArgLeuSerArgThrLeuMetPhePheIleLeuValValThrAspSerThrAlaProAs 1841
DB 5286 GCTGCGCATGTAGCAATTTGGCGAGGTGTC-----TGTAGCGCGAGGCGTTGCCCTA 5339
QY 1841 pAlaLeuAspAla-----GlnGlyLeuTyrGlnGlyValIleGlnCyvArgAsnGlyTyrG 1859
DB 5340 TAGTTTGCAAAAGCACTTCAGACACCGCTTGGCGCATGTGCATTTGATTAACCTGTATGG 5399
QY 1859 yProThrGluAsnGlyValMetSerThrIleTyrPro---IleAspSerThrGluSerPh 1878
DB 5400 CCTTACTGAAGCGCGCTGTCAACGCTACCTACCTGCACTGGGTGCGGACCTGCATACGGG 5459
QY 1878 eIleAsnGlyValProIleGlyArgAlaLeuAsnAsnSerGlyAlaTyrValValAspPr 1898
DB 5460 GATC-----GTGCGGATTTGGCGGCGCGCTGCGCAATACCGGCTGTATCTGTGGACC 5513
QY 1898 oGluGlnGlnLeuValGlyIleGlyValMetGlyGlnLeuValValThrGlnAspGlyLe 1918
DB 5514 GCATATGCAACCGGTCCCGGTGGCTGCGCGGAGATTTATCATCGCGGTATATACAGCT 5573
QY 1918 uAlaArgGlyTyrSerAspLys---AlaLeuAspGluAsnArgPheValHisIleThrVa 1937
DB 5574 CGCTCGCGCTATTTGAATGTGATGCGTGAACGCGGACGATTCGTGAAGACCGTTT 5633
QY 1937 l---AsnAspGlnThrValLysAlaTyrArgThrGlyAspArgValArgTyrArgIleG 1956
DB 5634 CAGTAAACGCCACGACGCGCGGATGTATAGAGAGCGGATCTGGGCGTGG---CTGGC 5690

QY 1956 yAepGlyLeuIleGluPheGlyArgMetAspThrGlnPheIleArgGlyAsnAr 1976
DB 5691 AGACGGTAATATATGAGATATCGGACCAAGACGATCAGTCAATCCGTCGGTCCG 5750
QY 1976 gIleGlySerAlaGluIleGluAlaIleuLeuArgAspSerSerValArgSerAlaI 1996
DB 5751 TATTCGACTGGCGACACTTAAAGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCT 5810
QY 1996 aValIleuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2012
DB 5811 GGTGGTGGCCACAGAGACACGCGGCTGAGAAACGCTGATCCCTTAT 5859
RESULT 14
US-10-369-493-42604 ; Sequence 42604, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42604
; LENGTH: 9399
; TYPE: DNA
; ORGANISM: Arabidopsis FCCT120
US-10-369-493-42604
Alignment Scores:
Pred. No.: 1.68e-138 Length: 9399
Score: 1749.50 Matches: 628
Percent Similarity: 43.85% Conservative: 427
Best Local Similarity: 26.10% Mismatches: 894
Query Match: 10.85% Indels: 460
DB: 15 Gaps: 91
US-09-482-788-2 (1-3129) x US-10-369-493-42604 (1-9399)
QY 61 AspGlyAsnAlaLeuAspGlyGlnSerAlaIleGlyHisAlaValIleArgValProThr 80
DB 2942 GATTGGCTTT-CTAGATTAATTAACAGCA--GGATTATCAGTTATTAACGTAACCTGCG 2997
QY 81 -----AspIleAspIleSerArgPheAlaLeuAlaIleArgValIle 94
DB 2998 GCTTAAAGTTAGCGGTAATCTGATGTCACCGCTAGACAAAGTATTAACATCAT 3057
QY 95 ValAsnGlnThrProAlaLeuArg--AlaPheAlaPheThrSerArgSerGly--Lys 112
DB 3058 TTGTGGGTATGATGATTTACGACACAGTTTGTCTTAATTAATGATGAACCTGTAACG 3117
QY 113 ThrSerGlnValIleLeuLysAspSerPhe--ValPheSerThrMetCysTrpSerSer 131
DB 3118 AATATTGCTTTAAAGCTAAATTAATCTACTATTAATGATTTGCGGGAATTAACCA 3177
QY 132 SerSerSerProArgGluValAlaArgAsp-----GluAlaAlaAlaAla 146
DB 3178 GAAATCAAGAAATACAGATCATACAGCAAGCTAAATTAATCTACAGACAGCAACGTTTCA 3237
QY 147 AlSerGlyProArgCysAsnArgPheValIleuLeuGluAspMetGlnThrLysLysCys 166
DB 3238 CTTAACAGAACCGCTTATTATTCGTGCGCTACTACAA--CTGAGTGAATCTGATTT 3294
QY 167 GluLeuValIleThrThrPheSerHisAlaIleuValAspValIleThrPheGlnGlnArgValLeu 186
DB 3295 GATTTGATTTTGTCTATGACACCATGATTAACAGATTAC--TGGTCAATTTTGTGTTTG 3351

QY 187 SerArg--ValPheAlaAlaIleArgHisGluLysAspThrHisArgProGluThrPro 205
DB 3352 GTGCGGAATTAATTCATCTTATCA-- 3378
QY 206 GluSerSerAspAlaThrAspThrAspSerGlnSerValSerValAlaSerMetSerCys 225
DB 3379 -----GGTCAACCTTACCAAAATTAACCAATTCATTT 3411
QY 226 GluAspAsnAlaVal-----SerAlaThr 233
DB 3412 GCAGATTTTGCACCTTGCAACAAATAGCTGCAAGTACAGTACAAATTCATTA 3471
QY 234 HisPheTrpGlnThrHisLeuAsnAspLeuAsnAlaSerValIleProHisLeuSerAsp 253
DB 3472 TTAATGCGCAAGAACATTAATAAAT--TATCCCGCT----- 3507
QY 254 HisLeuMetValProAsnPro-----ThrThrAlaGluHisArg 267
DB 3508 GAATTAATCTTACCAAGATTAATCCAGTACGTAATCAAACTTTAAAGTGCAAG 3567
QY 268 IleThrPheProLeuSerGln-----LysAlaLeuSer----- 278
DB 3568 CTATTTTCTTATCTTATCAACAGATTAATTCGACATTTGACAAATTCAGTAT 3627
QY 279 AsnSerAlaIle-----CysArgThrAlaLeuSerIleLeuLeuSerArgTrpThr 295
DB 3628 AATGCTACGCTGTTACGACTCTTTTAACAGCATTAATTAATTAATTAATTCCTACAGT 3687
QY 296 HisSerAspGluAlaLeuPheGlyAla--ValThrGluIleSerLeuProPheAspLys 314
DB 3688 GACAGATGATTAATTAATGTTGTTCTACAGTACTACGCGGACGCGCAAAATTCCT 3747
QY 315 HisTrpLeuAlaAspGlyThrTrpGlnThrValAlaProLeuArgValHisCysGlnSer 334
DB 3748 AACCTCATTT-----GGTCTATTGTTAATATCTCATATTGCGACCAATTAATCTGCT 3801
QY 335 -----AsnLeuArgAlaSerAspValIleAspAlaIleSer 346
DB 3802 AAACCCAGTTTATTCGAACTCTTAAACCAAGTAAAGAAACAGTTTACGCGGCTATCT 3861
QY 347 SerTrpAspAspArgLeuGlnHisLeuAlaProPhe-----GlyLeuArg 361
DB 3862 CACCAAGAT-----TTACCTTTGAGATTTAGTACAAACCTGCA 3903
QY 362 AspIleArgAsnThrGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeu 381
DB 3904 CCAAGACGAATTTTAAGTCAAAATCCCTTA-----TTCCAGTAAATGTTGTT 3951
QY 382 ValIleThrAspGlySerHisValAsnAsnGlyIleAsnGlyPheLeuGlnIleThrGlu 401
DB 3952 CTCATTAACACACCGAATAAAGACAAATTAATCTGATTAATAAATTTGAACCTTGA 4011
QY 402 SerSerHisPheMetProCysAsnAsnArgAlaIleLeuLeuHisCysGlnMetGluSer 421
DB 4012 ACCGAATTAATCAATCTCGCTTGAATGATGATGATGATGATGATGATGATGATGAT 4062
QY 422 SerGlyAlaLeuLeuValAlaTrp--TrpAspHisAsnValIleAspSerLeuGlnThr 440
DB 4063 CCAACCGTTTAAAGCGGAATCTTGGAATTCAGTACAGATTAATTTGACAAAGTACTAT 4122
QY 441 ThrArgLeuLeuGlnGlnPheGlnHisLeuIle--LysCysLeuGlnSerProLeuAsp 459
DB 4123 GAAAGATTAATGCACTTTTCAAAATTTTATTAATTAATTAATTTGATTAATCC----- 4176
QY 460 LeuSerSerMetAlaGluValAsnLeuMetThrGluTrpAspArgAlaGluIleGluSer 479
DB 4177 AAACAACTTAATGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 4236
QY 480 TrpAsnSerGlnProLeuGlnValGlnAspThrLeuIleHisIleGluMetLeuValAla 499
DB 4237 TGGAACTATCAATTTATCAAGATTAATCCAGAAATTAACAGTTTATTAATTAATTAATCA 4296

Db 6310 ATACCAAGTATGATTTACAGGGA-----TTACCGGAATTTGAACAACAGCAGCGTGG 6363
 QY 1205 Gln-----ThrThrProPheAenLeuSerSerGluAlaGly--- 1216
 Db 6364 CAGAGTGTGGCGGCACTCAGCGCCAGCAGCTTTGATTTG-----GCTGGTTTG 6414
 QY 1217 ---TTPATGAlaThrLeuLeuArgLeuGlyGluAAspPhePhePheLeuThrLeuValMet 1235
 Db 6415 TTGTGGCGGCGGTGGTGAATAATGGGGGAGGAGATCAGATATTATTGTTGACTTTTG 6474
 QY 1236 HisHisIleIleIleSerAspGlyTyrPheSerIleAspValLeuArgAspLeuAsnGlnLeu 1255
 Db 6475 CATCATATTATTGCTGATGCTGTGGTGGGCTGTGTGGTGGGAAATTTCTCGGCA 6534
 QY 1256 TySer-----AlaAlaLeuLysAspSerLysAspProLeuSerAla 1269
 Db 6535 TTGCGCGAGCGTCCCGAGGGAAGCCCAAGACCGCAGAGAGAGAG----- 6582
 QY 1270 LeuThrProLeuProIleGlnTyrSerAspPheAlaLysTyrGlnLysAspGlnPheIle 1289
 Db 6583 -----AGGATTTCAGTATGTGATTTTCTTTTGGCAGAGAGAGTGGTGGCG 6630
 QY 1290 GluGln-----GluLysGlnLeuAsnTyrTyrLysGlnLeuLysAspSerPro 1307
 Db 6631 GGGAGGGTTTAAAGGAACAATTGGAGATTGGCGCGACAGTTG---GAGTTCGCGCG 6687
 QY 1308 Ala-----LysIleProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGly 1325
 Db 6688 GTGATGTGGAAATTACGACTGATTAACCCGCTCGGCTGACAGCTTTT-TCGGGGGGC 6746
 QY 1326 CysValHisValThrIleAspGly-GluLeuTyrGlnSerLeuArgAlaPheCysAsnGln 1345
 Db 6747 TGTATATGGGTTGGTGTGTGGCGGAATTGACTCAGCGGTTTGCAGAGGTTGAGTCCGCG 6806
 QY 1345 HisAsnThrThrSerPheValValLeuLeuAlaAlaPheArgAlaHisTyrArgLe 1365
 Db 6807 TTATACAGACCTTATTATTAAGACTTTGTGGCTGTGGAGTGGCTGTTAATTCGTA 6866
 QY 1365 uThrAlaValAlaAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLe 1385
 Db 6867 CAGTGTGATGATGATATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 6926
 QY 1385 uGluAspIleIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHisIle 1405
 Db 6927 GGAAGGGTTATGT 6986
 QY 1405 AspThrPheGlyThrIleuLeuAsnGlnValLysAlaThrThrAlaAlaPheGluAs 1425
 Db 6987 TCCTAGTTTGTGATTTATTTGTCAGGGTTCGGGCAACTGCTTGGGTCGTTAGCTCA 7046
 QY 1425 nGluAspIleProPheGluArgValValSerAlaLeuGlnProGlySerArgAspLeuSe 1445
 Db 7047 TCAGATTTTACCTTTTGAACAATTGTAAGTGTGCTCAACA-----GTGCGATGCGCTCAG 7103
 QY 1445 rSerThrProLeuAlaGlnLeuIlePheAlaValHisSer-----GlnLysAs 1461
 Db 7104 TCATTCGCCCTTTTCAAGATGATGCTGTGTCAAAATTTTACCTTTCGACAGAGTTGGA 7163
 QY 1461 pLeuGlyArgPheLysPheGlnGlyLeuGlnLysSerValProValProSerLysAlaTyrTh 1481
 Db 7164 TATGGGGGCGCATAGAAATGCAAGTAATTGAGCG-----GATAGTGTATACAC 7211
 QY 1481 rArgPheAspMetGluPheHisLeuPheGlnGluThrAspSerLeuLysSerValAs 1501
 Db 7212 AAAATTTGACTGACTGCTTGTGCGAGCAAACTGCTCAAGGCTTAAGCTTAAGCTTGA 7271
 QY 1501 nPheAlaAspGluLeuPheLysMetGluThrValGluAsnValValArgValPhePheGln 1521
 Db 7272 ATATTAATGATGATTTATTCAGCCACACATATGACGCTTACCTGG-ACATTTAGAAA 7330
 QY 1521 uIleLeuArgAsnGlyLeuGlnSerSerArgThrPro-ValSerIleLeuProLeuThr 1541
 Db 7331 CATTAATTACAGCAGTATGTTCTCAATCCGAAACGATATTAAAGAAATTACCGTTA--- 7386

QY 1541 spGlyIleValThrLeuGlu-----LysLeuAspValLeuAsnValLysHisValAspT 1559
 Db 7387 -----TTAACCACTGTTGAACAGACAGCACTCCACAAATGAAACGCACTCAAGCCAGT 7441
 QY 1559 rProArgGlnSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspS 1579
 Db 7442 ATCTTCAGCGAG---TGTTTACATGATTTATTAAGCAGGATGAGCAAAACCCGGGAAA 7498
 QY 1579 rLeuAlaValAlaAspSerSerCysArgLeuThrTyrThrGluLeuAspArgGlnSerA 1599
 Db 7499 AGATAGCAATGATTTGGGGTGAAGAAACAGCTTAATTCAGAAATTAAACCAACCA 7558
 QY 1599 spIleLeuAlaGlyTyrPheArgArgSerMetProAlaGluThrLeuValAlaValP 1619
 Db 7559 ATCAATTAGCTGTGATCTGCAAAAGTTAGTGTCAGCCAGAAACCGCGTGGGAAATT 7618
 QY 1619 heaLarProArgSerCysGluThrIleValAlaPhePheGlyValLeuLysAlaAsnLeuA 1639
 Db 7619 GCGTTGACCGTCCCTAGATATGATTAATCGGCTTATGCTTACCAAGCTGACGCTG 7678
 QY 1639 lATyrLeuProLeuAspValArgSerProSerAlaArgValGlnAspIleLeuSerGlyL 1659
 Db 7679 CTTAAGTTCCTTACAGCCCACTTATCCGAAGCCAGATTAAGCATTTATTATGAAGT- 7737
 QY 1659 uSerGlyProThrIleValLeuIleGlyHisAsp-----ThrAlaProProAspIleG 1677
 Db 7738 --TCCCAATGACAGGTGTACTACCCAGCAAAACAAATTAACTCCCAACTCC 7795
 QY 1677 LuValThrAsnValGluPheValArgIleArgAspAlaLeuAsnAspSerAsnAlaAspG 1697
 Db 7796 AAATC----- 7800
 QY 1697 rPheGluValIleGlnHisAspSerThrLysPro----- 1708
 Db 7801 -----CCCATATTCCCTTACAGACCCCAATCCCACTCCCAATCCCACTCCCACTCC 7855
 QY 1709 ---SerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyArgProL 1727
 Db 7856 CCAAGTCCCAACCAACCTAGCTTACATCATCTACCTCCGACATACAGGCACTTCCCA 7915
 QY 1727 yGlyValMetIleGlnHisArg-----ValI 1736
 Db 7916 AAGAGTCCGCACTTACTCATCAAAAGTCCGGTAAAGCTAGTATGGCGCGGAATTTT 7975
 QY 1736 lLeuArgThrValThrSerGlyCysIleProAsnTyrProSerGluThrArgMetAlaH 1756
 Db 7976 ACACAGAGCAGAAATTAAACAGGTGTTTACCTCC----- 8010
 QY 1756 lAsnAlaThrIleAlaPheAspGlyValAspTyrGluIleTyrSerAlaLeuLeuPheG 1776
 Db 8011 -----ACTTCATTTGTTTGACTTCAATATTGAAATCTTCCCTCAAGTTGGG 8065
 QY 1776 lYargThrLeuValCysValAspTyrMetThrThrLeuAspAlaAspAlaLeuLysAspV 1796
 Db 8066 GAGGTGCGTCACTCCGCTGATTAATGCCCTTACAACTA----- 8103
 QY 1796 aPhePheArgGlnHisValAsnAlaAsnHisValThrSerSerGlnAspValP 1816
 Db 8104 -----CCAGAAATTACAGACCGCCACAAAGTACTTTTAATCAAT----- 8142
 QY 1816 rLeuAspValProArgArgLeuSerArgThrLeuMetPhePheLeuValValThrA 1836
 Db 8143 -----ACAGTCCCTCAGCGCGCAGAGAACTGTAAGTTAAATGATATGGCCGCAACAG 8197
 QY 1836 spSerThrAla-----ProAspAlaLeuAspAlaGlnGlyLeuT 1849
 Db 8198 TACAGACAGTAACTTAGCCGCGCAACCTTACCGAAATGGTGG--GTAGACGAATCTT 8254
 QY 1849 rGlnGlnGly-----ValGlnCysTyrAsnGlyTyrGlyTyrProThrGluAsnGlyValM 1866
 Db 8255 ATCAACATTCACAAATTGAGCGGCTATTAATCTTTTACGGGCTTCCAGAAATACCACT 8314

QY 1866 eSeRThr-----lIeTyRProIleAspSerThrgIuSerPheIleasnGlyValProI 1884
 DB 8315 ACCTTACCACATGCGGAGTCTCTCACTCTATTACGAAATGTTCTTT-----CCGACAA 8362
 QY 1884 lEgIyRgAlaLeuAsnSerGlyAlaTyRValValAspProGluGlnLeuValG 1904
 DB 8363 TCGGTCAACCCATCGCCACATCAAGTTATATCTTAGACCAAAACCTCAACCCGCTTC 8422
 QY 1904 lYlIeGlyValMetGlyGlnLeuValValThrgIAspGlyLeuAlaArgGlyTyR 1922
 DB 8423 CCTTGGCATACCCGGGAAATTTACTCTAGTGGCGAGGTTAGCAAGAGTTACTGGA 8482
 QY 1923 --SerAspIysAlaLeuAspGlyAsnArgPheValHisIleThrValAspGln---- 1940
 DB 8483 AGCGTCCAAATTCAGCGAGAGAGGTTTATAACGTCAACGTCAACAGTCAACAGT 8542
 QY 1941 --ThrValIysAla--TyRArgThrgIAspArgValArgTyRArgIleGlyAspGlyL 1959
 DB 8543 CAACAGTCAACACTCTCTACAAAACAGCGATCGCGCTCTTAT---CTTCCAGATGTA 8599
 QY 1959 eulIeGluPhePheGlyArgMetAspThrgIuPheIysIleArgGlyAsnArgIleGluS 1979
 DB 8600 ATATTAAATATCTGGGCGGTTTCACCATCATGAAATTCGCTGTTTCGCAATTAAT 8659
 QY 1979 eRAlaGluIleGluAlaLeuLeuArgAspSerValArgAspAlaAlaValValL 1999
 DB 8660 TGGGGGAAATTCAGCGTCTTCTTATCATCAACATCCAGAGTTACCGCGCCATTG 8719
 QY 1999 eugIuGlnAsnGluAspGlnAlaProGluIleuGlyPheValValAlaAspHisAspH 2019
 DB 8720 TTGCGATATGATCGCCAGAACATAGCCGCTAGAGCTTATGTTGCCAAATCTCACA 8779
 QY 2019 lAspSerGluAsnAspIysGlyGln----- 2026
 DB 8780 TTGAAGCAGCAATTAAGCAATTTTACGCGGCAAACTCTCTTATATGCTACCGA 8839
 QY 2027 -----SerAlaAsnGlnValGluGlyTyRglnA 2036
 DB 8840 CACCGTTTGCATCTCGAAACTTACCTTACAGCTTAT-----GGTAAATAG 8890
 QY 2036 sPHisPheGluSerGlyMetTyRserAspIleGlyGluIleAspProSerThrIleGlyS 2056
 DB 8891 ACCGTTTGTCT-----TTACCAATACCTGATTAATGCCAGTCACC----- 8931
 QY 2056 eRAspPheIysGlyTyRThrSerMetTyRAspGlySerGlnIleAspPheAspGluMetH 2076
 DB 8932 -----ACCACAAACCGCACCCGCGACACCCATACCAATTAATTA 8974
 QY 2076 lEgIuTyR-----LeuGlyGluThrThrArgThrLeuHisAspAsnArgSerIeuG 2093
 DB 8975 ATATTGGACTCAGGTTTAGGGTAGAATCTATCAGCATTCATGATAC----- 9024
 QY 2093 lYAsnValIeuGluIleGlyThrcIySerGlyMetIleuPheAsnLeuAspSerArgL 2113
 DB 9024 ----- 9024
 QY 2113 euGluSerTyRValGlyLeuGluProSerArgSerAlaAlaPheValAsnIysAlaT 2133
 DB 9025 -----TTCTTAGATGGGTG 9040
 QY 2133 hrcIuSerIleProSerLeuAlaGlyLysAlaIysVal---GlnValGlyThrAlaThra 2152
 DB 9041 GTGATTCATTTTATAGCATTCAGACAGTACCAAGGAAATCAACAAAGGCTGGCT--- 9096
 QY 2152 sPrlIeGlyGlnValAspAspLeuHisAspAspLeuValValLeuAsnSerValIleGlnT 2172
 DB 9097 -----TTACGACCC-----CGCAGATGTTCCAAAT 9121
 QY 2172 yRPhrProSerSerGlyTyRLeuAlaGluIleAlaAspThrLeuIleHisIleuProAsnV 2192
 DB 9122 ATCAAAACAGTGCAGAA---CTAGCAGCCATTTGTGACACTGATACCAATTAATCTGTG 9178
 QY 2192 aGlnuArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGluHisPheLeuAla 2212

DB 9179 AGCAAAACCAATACACAGGGAGTCTCTCACTCTATTACGAAATGTTCTTT----- 9234
 QY 2212 lAaRgAlaIleHisThrLeuGlyLysAsnAlaThrIysAspAspValArgGlnIysMetA 2232
 DB 9235 -----GACCAAAATTTAG 9247
 QY 2232 lAgluIleuGluAspMetGluGluIleuLeuValGlu-----ProA 2246
 DB 9248 TAGATGCATCATTTGAAATCAAGCCATTCTTTAGAAAGTACACCAATCTTTAACCTTG 9307
 QY 2246 lApePheThrSerLeuIysAspArgPhe-----ProGlyLeuValGluHisV 2262
 DB 9308 ATTACTTACGCGAAGCATTTAGATCAACTATTAGCACACATGATGATTCGATCGCACT 9367
 QY 2262 aGlnuIleuPro 2266
 DB 9368 TCCAAACAAACCCC 9381
 RESULT 15
 US-10-329-079-46
 : Sequence 46, Application US/10329079
 : Publication No. US20030198981A1
 : GENERAL INFORMATION:
 : APPLICANT: FARMET, Chris
 : APPLICANT: ZAZOPOULOS, Emmanuel
 : TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 : FILE REFERENCE: 3002-1105
 : CURRENT APPLICATION NUMBER: US/10/329, 079
 : CURRENT FILING DATE: 2002-12-24
 : NUMBER OF SEQ ID NOS: 66
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 46
 : LENGTH: 15738
 : TYPE: DNA
 : ORGANISM: Streptomyces refuineus
 US-10-329-079-46
 Alignment Scores:
 Pred. No.: 4.06e-138 Length: 15738
 Score: 1749.00 Matches: 786
 Percent Similarity: 35.06% Conservative: 404
 Best Local Similarity: 23.16% Mismatches: 1125
 Query Match: 10.84% Indels: 1080
 DB: 15 Gaps: 112
 US-09-482-788-2 (1-3129) x US-10-329-079-46 (1-15738)
 QY 9 GllYArgGlnAspLeuProPheGlnProAlaSerPheCysSerHisGlyAspSerProLeu 28
 DB 4618 GGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4677
 QY 29 AsnSerSerTyRgIuGlnIleuPheHisIleuTyRgIyLeuAspSerSerArgIleGluAla 48
 DB 4678 -----GAGACGCTGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4716
 QY 49 lIeIysProCysThrProPheGlnIleuAspMetIleAspCysAsnAlaLeuAspIysGln 68
 DB 4717 GTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4776
 QY 69 SerAla-----lIeGlyHisAlaValTyRAspAlaProThrAspIleAspIleSer 85
 DB 4777 GCCCTGAGCTTACGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4836
 QY 86 ArgPheAlaLeuAlaTrpIysGluIleValAsnGlnThrProAlaLeuArgAlaPheAla 105
 DB 4837 GCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTC 4896
 QY 106 PheThrSerAspSerGlyTyRThrSerGlnValIleuLeuIysAspSerPheValPheSer 125
 DB 4897 CAGCAGCGGAGTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4944

QY 126 TrpMetCysTrpSerSerSerSer-----SerProAspGluValValArgAspGluAla 143
DB 4945 GACCTGCGGCGCTGCTCTGCGACCTGCGCGCTGCGAGAGCGCGCGG 5004
QY 144 AlaAla-----AlaAlaSerGlyProArgCysAsnArgPhe----- 155
DB 5005 GCGCGCGAGCGCGCGCTGACGAACTGCGCGCGCGCGAGCGACCGAGAGTTTGACCTC 5064
QY 156 -----ValLeuLeuGluAspMetGlnThrIleValCysGlnLeu 168
DB 5065 ACCGCGCGCGCGCTGCTCTCTCTCTGCGCGCGCGCGCGCGCGCGAGAGTACCGGTTTC 5124
QY 169 ValTrpThrPheSerHisAlaLeuValAsp-----ValThrPheGlnGlnArgVal 185
DB 5125 GTATATCAACACCCACACAGATGCTGAGCGCTGTCATCCCATCTCTCTGCGCGAG 5184
QY 186 Leu-SerArgValPheAlaAlaTrpValTrpValGluValAspThrHisArgProGluThrPr 205
DB 5185 CTCTCTGCGGCTTACGCGCGCGG-----CCCGCTGCGCGAGCGC 5223
QY 205 ogLuserSerAspAlaThrAspThrAspSerGlnSerValSerValValSerMetSerCys 225
DB 5224 CCGCGCGACCGCGCTACCGCGAGCTGCGCTGCGCGCGCGCGAC----- 5266
QY 225 ArgAspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnAspLeuAla 245
DB 5267 -----TCCGG-CCGCGCGCGAGCGCTGACCGCGGACCTGAGAGCGCGCGCG 5315
QY 245 aserValPhe-----ProHisLeuSerAsp-----HisLe 255
DB 5316 GCGGACCTGATGCGCGCGCGCGCGCGCGCGCGAGAGATCCCGAGTCCGCGCGCT 5375
QY 255 umetValProAsnProThrThrAlaGluHisArgIleThrPheProLeuSerGlnIly 275
DB 5376 GAACCTCCCGAGAGACTCTCGCG-----CGACTGCGAGCGCGCGCGCGCGAGCG 5426
QY 275 ValLeuSerAsnSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArgTrp 295
DB 5427 CGAGATCACTCACTCCGCTGCGAGCGCGCTGCGCGCTGCTCTCTCGCGCGAGAGAC 5486
QY 295 rHisAspArgLysAlaLeuPheGlyAlaValAlaThrGlnGlnSerLeuProPheArgVal 315
DB 5487 CCGCGCGAGCACTCACTCTCGCG--ATCACCGTCTCGCGCGCGCGCGCGAGACTCC 5543
QY 315 gTrpLeuAlaAsp-----GlyThrTrpGlnThrValAlaProLeuArgVal 330
DB 5544 CCGCGCGAGAGCACTGCTCGCATGCTGTCACAAATCCCGTGGCGCTCGCGCTCG 5603
QY 330 ----- 330
DB 5604 CCGCGCGAGACCTGCTGGAAGTGTGCGCGCGCTGAGAGAGAGAGCTGGAAGTCT 5663
QY 331 -----HisCysGlnSerAsnLeuArgAlaSerAs 340
DB 5664 GAGACACAGACACTCCCGCTGACCGCGCTGACCGCTGAGCGCGCTG-----CCCGA 5717
QY 340 pValMetAspAlaIleSerSerTrpAspAspArgLeuGlnHisLeu-----Al 356
DB 5718 ACTCTTGCACACCACTGCTGTCGAGAACTACCGCGCGAGATACACCGCGCGAGCG 5777
QY 356 aProPheGlyLeuArgAspIleArgAsnThrGlyAspAsnGlySerAlaAlaCysAsp 376
DB 5778 GCGCTTC-----CGCGCGCTGCGGACGCGCGCTACAGCGCGACACACTA 5822
QY 376 eGlnThrValLeuLeuValThrAspGlySerHisValAsnAsnGlyIleAsnGlyPheLe 396
DB 5823 CCGCGTACCTGCTG-----GGGCGAGTCCGCGCG----- 5853
QY 396 uGlnGlnIleLeuGlnSerSerHisPheMetProCysAsnAsnArgAlaLeuLeuLeuHis 416
DB 5854 -AGGAGACTACCTCGCATGACTACCGCGCG-----GACTCTTTCGCGGA 5900
QY 416 wCysGlnMetGlnSerSerGlyAlaLeuLeuValAlaTrpTrpAspHis----- 432

DB 5901 GACCTGCGCGCGCTCTCTGCGCGAGAGTGTGCGCGCGCTGACCGAGCGCGCGACCG 5960
QY 433 -----AsnValIleAspSerLeuGlnThrThrArgLeu 444
DB 5961 CCGCGCGCGCGCTCGCGACAGCTGCTGCTGACGCGAGAGAGCGCGCGCGCTGCT 6020
QY 444 uGlnGlnPheGlyHisLeuLeuIleValCysLeuGlnSerProLeuAspLeuSerMetAl 464
DB 6021 GAGAGACTGAGGCG-----GCCGCGCGCGCGCGCGAGAGCGCTCG----- 6060
QY 464 ArgValAsnLeuMetThrGluTrpAspArgAlaGluIleGlnSerTrpAsnSerGlnPr 484
DB 6061 -----CGCGCTACGTGAGCTGTTCAGAGACG-- 6090
QY 484 oLeuGluValAlaAspThrLeuLeuHisArgIleMetLeuValAlaValSerHisSerPr 504
DB 6091 -----CTCGCGCGCGACACC 6104
QY 504 oThrTrpThrAlaIleGlnAlaTrpAspGlyAspTrpThrTrpSerGlyLeuAsnAsnVa 524
DB 6105 GAGAGCGCGCGGATGCTACGTGCGCGCGCGAGCTGACTACCGAGCTGAGCGCGCA 6164
QY 524 lSerSerArgLeuAlaValHisIle-----LysSerLeuGlyLeuArgAlaGlnGlnAl 542
DB 6165 GCGGAGCGGCTGCGCGCGTGTGCGCGACCGACCGCGCGGACCGCGCGCGCGAGT 6224
QY 542 alleleProValTrpPheGlyLysSerLysTrpValIleAlaSerMetLeuAlaValle 562
DB 6225 CTACGTGCGGCTGTGCGCGCGCGCGCGCGAGAGCGCGCTGCTCTGCTCGCGCTCT 6284
QY 562 uLysSerGlyAsnAlaPheThrLeuLeuAspProAsnAspProProAlaArgThrAlaG 582
DB 6285 GAAGTGGCGCGCGCTTACGTGCGCGTGCAGAGAGAGTGCAGCGCGAGACCGCGCG 6344
QY 582 nValValThrGlnThrArg--AlaThrValAlaLeuThrSerLysLeuHisArgGlu 601
DB 6345 GTGTCTGAGAGACTGCGCGCGCGACTGTGTGCGCGCGCGCGCGAGCGCGCGCGAG 6404
QY 601 rValGlnLeuLeuValGlyArgCysValValValAspAspGlyLeuLeuGlnSer----- 649
DB 6405 CGTGCGGAGAGCGCGCGAGAGTGTCTGCGCGTGCAGCGCGCGCGCGCTCTCGCGCG 6464
QY 620 -----ValSerAlaSerAspAspPheSerSerLeuThrLysSerGlnAspLeuAlaTr 637
DB 6465 GCGCGACCGCGCGCGCGAGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCTGA 6524
QY 637 rValIlePheThrSerGlySerThrGlyAspProLysGlyIleMetIleGluHisArgAl 657
DB 6525 CGCATCTTACACTTCGCTGTCACCGCGCGCGCGCGAGGCGGTGATTCAGACACAGCGC 6584
QY 657 aPheSerSerCysAlaLeuAspPheGlyAlaSerLeuGlyIleAsnSerAspThr----- 675
DB 6585 CTGCGCGCGTACGCT-----GGCGCGACAGCGCGCGCTACCGCGCGCGCGCG 6635
QY 676 -ArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGluIleMetThr 695
DB 6636 GACCTGCTGCCACACACTGCGCTTGCAGCTGACCGTACCGTACCACTCTGACCGCC 6695
QY 695 rLeuIleAsnGlyGlyCysValCysValleProSerAspAspArgTrpMetAsnSerIlePr 715
DB 6696 GCTTCGCGCGCGCGCGCGCTG-----CGGCTGCGCGAGCTGGA 6734
QY 715 oSerPheIleAsnArgTrpAsnValAsnTrpMetMetAlaThrProSerTrpMetGlyTh 735
DB 6735 GAGTCCGCGCGACAGCGCGCGCGCGCGCGCTGTCAGAGCGAGCGCTTGCAGCTGCGCAT 6794
QY 735 rPheSerProGluAspValProGlyLeu-----AlaThrLeuValLeuValG 751
DB 6795 GCTG-----CGGAGCTGCGCGAGTCTCGCGCGAGCGCGGAGACCTGATCTCGCGCG 6848
QY 751 yGlnGlnMetSerSerSerValAsnAlaIleTrpAla-----ProLysLeuGlnLe 768

| | | | |
|----|------|--|------|
| QY | 1430 | EGLNARGVAlValSerAlaLeuGlnProGlySerThrArgPheLeuSerThrProLeuAl | 1450 |
| Db | 8835 | CGAAAGCGCTTGAGAGGCTTCAACCG--GTGGCTGCTGCTGGCGCCACCGGCTT | 8891 |
| QY | 1450 | AGLNLeuLePheAlaValnIsSerGlnLysArgPheuGlyArgPheLysPheGlnGly-- | 1469 |
| Db | 8892 | CGAGGTGCTGCTGGCTTCAACAAC-----GGCGGGGGCGCCGCGAAGGAC | 8939 |
| QY | 1470 | -----LeuGlnSerValProValProSerLysAlaIleIleArgTh | 1481 |
| Db | 8940 | CGCCGACCGGGGCTCGAGAGTCTGGTCTGGGCTCGGCGCTGTGACGGTAGACCGGGCG--GC | 8996 |
| QY | 1481 | ARGPheArgPheMetGlnPheHisLeuPheGlnGlu-----ThrArgPse | 1495 |
| Db | 8997 | CAGGTTCACCTGTCTGCTGCTGCTTTCACAGAGACCGGGCGGCGCGAGCTCGGGCGCGG | 9056 |
| QY | 1495 | rLeuLysGlySerValaAnPheAlaABPGLuLeuPheLysMetGluThrValGluAsnVa | 1515 |
| Db | 9057 | GATCGGGGGCGGATCGAGATCAGACAGCAGCACTGTGTGACAGAGACAGGCGCCACAGGAC | 9116 |
| QY | 1515 | lValArgValPhePheGlnLulleuXArgnGlyLeuGlnSerSerArgThrProValSe | 1535 |
| Db | 9117 | GGTCGGGTACTTCTCCCGGCTGCTGGGGCGGGCGGTGAGAGAGCGCCCGACACCGCTGAG | 9176 |
| QY | 1535 | rLleuLeuProLeuThrArgGlyIleValThrLeuGlnLysLeuAsnArgValLeuAsnVally | 1555 |
| Db | 9177 | CGGCTTCTCCGCTCGAGCGAGCGGAGCGGACGAGCTGCTGCTCGGCGCCACAGAC | 9236 |
| QY | 1555 | SHlEvAlaAPrYrProArgGlnSerSerLeuAlaABrValPheGlnThrGlnValSerAl | 1575 |
| Db | 9237 | CGCCCGGACCTGGCTTGAGACTCGCGCTGGCGGC--TTGAGAGCCAGGGCGCGCCG | 9293 |
| QY | 1575 | aTyrProABrSerLeuAlaValABrPseSerCyABrGLeuThrTyThrGluLeuAB | 1595 |
| Db | 9294 | GACCCCGCGGCGACGCGCTGTGTGCGCGGAGAGGGAGATGTGCTACGCGCACTCGA | 9353 |
| QY | 1595 | rArgGlnSerAPrLleuAlaGlyTyrrLeuArgArgArgMetProAlaGluThrLe | 1615 |
| Db | 9354 | CGACAGGGCGGACCGGCTGCGCGGGCTGTGTGGACGAGCGCGGAGCGAGCGAGCGAC | 9413 |
| QY | 1615 | vAlAlaValPheAlaProArgSerCyAGluThrLleValAlaPhePheGlyValLeuLy | 1635 |
| Db | 9414 | GGTCGGGCTCGGCTGCGCGGCGGCGGCGCTGTGCGGATGACGTCTGCGGCTGTGGAA | 9473 |
| QY | 1635 | aAlaAsnLeuAlaTyrrLeuProLeuABrValArgSerProSerAlaArgValGlnABrIl | 1655 |
| Db | 9474 | GCGGGGACTGCACTACGTCCCTGTGAGACCGCGCACCGAGAGAGCGGCTGGCGGACGT | 9533 |
| QY | 1655 | eLeuSerGlyLeuSer----- | 1660 |
| Db | 9534 | CCTCGCCACATGGCGCGCGGCGGATGATCCACCGCGAGCTCGCGCGGACCTCC | 9593 |
| QY | 1661 | ---GlyProThrLleValLleuLleGlyHisABrThrAlaProProABrLleGluValTh | 1679 |
| Db | 9594 | TCCGCGGCGCGCGCGCTGTGTCTGTGTGAGACACCGGCGCACCGCGGA----- | 9642 |
| QY | 1679 | rAsnValGluPheValArgLleArgABrAlaLeuABrAsnSerAsnAlaABrGlyPheG1 | 1699 |
| Db | 9643 | -----CGCTGTGGCGCGCGCGCGGACGACCGCGCGGGCGCGGCGCA | 9686 |
| QY | 1699 | vAlLleGluHisABrSerThrLysProSerAlaThrSerLeuAlaTyrrValLeuTyTh | 1719 |
| Db | 9687 | CGCTCGGGGCGCACCGGAC-----GACCTGGGGTACACATCTTACAC | 9728 |
| QY | 1719 | rSerGlySerThrGlyArgProLysGlyValMetLleGluHisArgValLleIleArgTh | 1739 |
| Db | 9729 | CTCGGAGCTTCACCGGCGCGCCCAAGGGGTATG----- | 9762 |
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[illegible]

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Db 10564 -----CGGACCGCCCGCGCGCG----- 10581
Qy 2130 nlyValaThrGluSerIleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAl 2150
Db 10582 -----CGCCCGGATCCCGCGCGCGCGCGCTG-----GTGGGG----- 10617
Qy 2150 aThrAspIleGlyGlnValAspAspLeuHisProAspLeuValValLeuAsnSerValI 2170
Db 10617 ----- 10617
Qy 2170 eGlnTyrPheProSerSerGluTyrLeuAlaGluIleAlaAspThrLeuIleHisLeuPr 2190
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Qy 2190 aAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGlnHisPheLe 2210
Db 10635 ----- 10635
Qy 2210 uAlaAlaArgAlaIleHisThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLy 2230
Db 10635 ----- 10635
Qy 2230 sMetAlaGluLeuGlnAspMetGluGluLeuLeuValGluProAlaPhePheThrSe 2250
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Qy 2290 uGlyAspGluLeuValLeuProValGlyLysAspAspTrpIleAspPheGlnAlaAsnG 2310
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 5, 2004, 19:00:24 | Search time 464 Seconds
(without alignments)
4793.223 Million cell updates/sec

Title: US-09-482-788-2

Perfect score: 16128
Sequence: 1 MEYLRVADRDQDLPPTPASF.....RVHLLBEVSKTFEGNLSSL 3129

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delcext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool_h/US09482788/runat_04112004_165914_26738/app_query.fasta_1.3271
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Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 5004.5 | 31.0 | 46899 | 1 | US-08-471-119A-1 Sequence 1, Appli |
| 2 | 1715.5 | 10.6 | 7374 | 4 | US-09-252-991A-9100 Sequence 9100, Ap |
| 3 | 1641.5 | 10.2 | 6573 | 4 | US-09-252-991A-9183 Sequence 9183, Ap |
| 4 | 1618 | 10.0 | 10023 | 4 | US-09-252-991A-6997 Sequence 6997, Ap |
| 5 | 1517 | 9.4 | 11601 | 2 | US-08-222-617A-3 Sequence 3, Appli |
| 6 | 1517 | 9.4 | 11601 | 2 | US-08-222-617A-24 Sequence 24, Appli |
| 7 | 1506.5 | 9.3 | 7527 | 4 | US-09-252-991A-71 Sequence 71, Appl |
| 8 | 1429 | 8.9 | 6968 | 4 | US-09-710-279-759 Sequence 759, App |
| 9 | 1428 | 8.9 | 29555 | 4 | US-08-956-171E-206 Sequence 206, App |
| 10 | 1428 | 8.9 | 29555 | 4 | US-08-781-986A-206 Sequence 206, App |
| 11 | 1425.5 | 8.8 | 7215 | 3 | US-09-134-001C-627 Sequence 627, App |
| 12 | 1383 | 8.6 | 1713 | 1 | US-08-471-119A-4 Sequence 4, Appli |

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| 13 | 1342.5 | 8.3 | 11444 | 2 | US-08-222-617A-26 Sequence 26, Appli |
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| 15 | 1307.5 | 8.1 | 7911 | 4 | US-09-252-991A-9182 Sequence 9182, Ap |
| 16 | 1220 | 7.6 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appli |
| 17 | 1220 | 7.6 | 4411529 | 3 | US-09-103-840A-1 Sequence 1, Appli |
| 18 | 1144.5 | 7.1 | 4411529 | 3 | US-09-103-840A-1 Sequence 1, Appli |
| 19 | 1143.5 | 7.1 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appli |
| 20 | 1141 | 7.1 | 3315 | 4 | US-09-252-991A-8892 Sequence 8892, Ap |
| 21 | 1129 | 7.0 | 77536 | 4 | US-09-410-551B-1 Sequence 1, Appli |
| 22 | 1129 | 7.0 | 77536 | 4 | US-09-940-316B-1 Sequence 1, Appli |
| 23 | 1128 | 7.0 | 4236 | 4 | US-09-252-991A-7057 Sequence 7057, Ap |
| 24 | 1061.5 | 6.6 | 6858 | 4 | US-09-252-991A-1219 Sequence 1219, Ap |
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| 26 | 913 | 5.7 | 3602 | 4 | US-09-710-279-3430 Sequence 3430, Ap |
| 27 | 855 | 5.3 | 2219 | 3 | US-08-510-646B-17 Sequence 17, Appl |
| 28 | 799.5 | 5.0 | 71989 | 3 | US-09-443-501A-2 Sequence 2, Appli |
| 29 | 798.5 | 5.0 | 68750 | 3 | US-09-335-409-1 Sequence 1, Appli |
| 30 | 798.5 | 5.0 | 68750 | 3 | US-09-568-102-1 Sequence 1, Appli |
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| 36 | 781 | 4.8 | 2744 | 4 | US-09-710-279-4069 Sequence 4069, Ap |
| 37 | 770 | 4.8 | 7586 | 4 | US-10-011-146-2 Sequence 2, Appli |
| 38 | 755.5 | 4.7 | 3456 | 4 | US-09-252-991A-7025 Sequence 7025, Ap |
| 39 | 745 | 4.6 | 3981 | 4 | US-09-328-352-760 Sequence 760, App |
| 40 | 731 | 4.5 | 2022 | 4 | US-09-252-991A-8890 Sequence 8890, Ap |
| 41 | 716 | 4.4 | 4563 | 4 | US-09-252-991A-4765 Sequence 4765, Ap |
| 42 | 684.5 | 4.2 | 2301 | 4 | US-09-710-279-419 Sequence 419, App |
| 43 | 681 | 4.2 | 2823 | 4 | US-09-252-991A-7100 Sequence 7100, Ap |
| 44 | 631.5 | 3.9 | 2634 | 4 | US-09-710-279-4189 Sequence 4189, Ap |
| 45 | 629.5 | 3.9 | 6129 | 4 | US-09-489-039A-6882 Sequence 6882, Ap |

ALIGNMENTS

RESULT 1
US-08-471-119A-1
Sequence 1, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Leteiner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergerdoffer, Kurt
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: No. 5827706art1s Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471, 119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kasenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8807
TELEFAX: 201 503 8474
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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/ LENGTH: 46899 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Tolypocladium niveum
/ STRAIN: ATCC 34921
/ US-08-471-119A-1

Alignment Scores:
Pred. No.: 0 Length: 46899
Score: 5004.50 Matches: 1237
Percent Similarity: 44.04% Conservative: 441
Best Local Similarity: 32.47% Mismatches: 857
Query Match: 31.03% Indels: 1276
DB: Gaps: 66

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QY 502 HisSerProThrLysThrAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeu 521
DB 35685 TCGATACCCAGATGATCGCTTATCGATGCTTTCACAGCTCCTTACACCGAGCTC 35744
QY 522 AspAsnValSerSerArgLeuAlaValHisLeuSerLeuGlyLeuAlaGlnGln 541
DB 35745 GACGAGAGATCTAGCCAGCTCGCCAGCTGACCGCA--CAAGTCACAGTCCCTGAG 35801
QY 542 AlaLeuLeuProValLysPheGluLysSerLysThrValLeuAlaSerMetLeuAlaVal 561
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DB 35862 ATCAAGCGAATCTCGCTATCTGCCACTTACGCTCAACGACCGCGTGGATGAG 35921
QY 582 GlnValVal-----ThrGlnThrArgAla 589
DB 35922 ACATCTCTCATCTTACACGAGAAACAGCTTATTTACTTGATCAGATACCGACGCG 35981
QY 590 ThrValAlaLeuThrSerLysLeuHisArgGluThrValGlnLysLeuValGlyArgCys 609
DB 35982 GTC-----AGCTTCACGCAACACGCT-----CGATTC 36011
QY 610 ValValValAspArgGluLeuGlnLysValSer--AlaSerAspAspPheSerSer 628
DB 36012 ACCCGATCAGCGACGCGCTCTGTCGAGAGCGGCGACCTCCCTACCGAAGACTTCCACA 36071
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DB 36834 TTCCTGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 36893
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| OY | 1116 | GlyArgLeuThrPheLeuAspGlnLeuAspValGlySerLeuThrProTyThrLeuIleProTy | 1135 |
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| OY | 1136 | AlaValArgMetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaLeu | 1155 |
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| OY | 1196 | AspProPheGluValLeuAsnGlnGlnThrThrProPheAsnLeuSerSerGluAla | 1215 |
| Db | 37782 | GAT---CTTGGCAAGCTGGAAGAGAGACACAGAGCTCTTCAATCTCTACTGAAGTC | 37838 |
| OY | 1216 | GlyThrArgAlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMet | 1235 |
| Db | 37839 | GCTTGGAGGGAGACACTCTTCAACGGCTGGAAGAACACACCACTCTCTATTCGTCATG | 37898 |
| OY | 1236 | HisHisIleIleSerAspGlyTrpSerIleAspValLeuArgArgAspLeuAsnGlnLeu | 1255 |
| Db | 37899 | CATCACTAATATTCAAGATGGCTGTCTCACTTCACTTCCAGACGAGCTTGCCCAATTC | 37958 |
| OY | 1256 | TyrsSerAlaAlaLeuIleuysAspSerLeuAspProLeuSerIleLeuThrProLeuProIle | 1275 |
| Db | 37959 | TACTCGGAGCTGTAACA---GGCAATGACCCCTTTCCAGGTCAAAACCGCTCCCATTT | 38015 |
| OY | 1276 | GlnTySerAspPheAlaIleTyTrpGlnIleAsp---GlnPheIleGluGlnIleuys | 1293 |
| Db | 38016 | CACATACCGCGCATTTTGTCTGTCTGGCAGACACAAGATAAAGCAATGGCCGTTACGAAGC | 38075 |
| OY | 1294 | GlnLeuAsnTyTrpTrpIleysGlnLeuIleAspSerSerProAlaIleProThrAsp | 1313 |
| Db | 38076 | CAACTTCAGTACTGGATAGACACACTCGCGATAGACACCGCACCGCAATCTTAATGTGAT | 38135 |
| OY | 1314 | PheAlaArgProAlaIleLeuLeuSerGlyAspAlaGlyCysValHisValThrIleAspGly | 1333 |
| Db | 38136 | TTTAAACGACCGGAGGCTTGTCTCGCGGAAAGCTGTACAGTTCCTCATCTGATCGAGAC | 38195 |
| OY | 1334 | GlnLeuTyrglnSerIleuArgAlaPheCysAsnGlnHisAsnThrThrSerPheVal | 1353 |
| Db | 38196 | GAGGTTTATGAGAGCTCTCCCTCTTCTGCGCAATCATCAGGTCAACACTTCGTCGTC | 38255 |
| OY | 1354 | LeuLeuAlaIlePheAlaGlyAlaHisIleTyArgLeuThrAlaValGluAspAlaValIle | 1373 |
| Db | 38256 | CTTGTGCTGTTCGCGCGTCGACATTAATCTGCTTAATCGGCGCAGAGATGCGACTATTC | 38315 |
| OY | 1374 | GlyThrProIleAlaAsnArgAsnArgProGluLeuGlnIleAspIleGlyCysPheVal | 1393 |
| Db | 38316 | GGTACCACTATGGCAACCGCAACCGCCCGCAACTTGAAGACTTGATCGGTTCTTTTGTTC | 38375 |
| OY | 1394 | AsnThrGlnCysMetArgIleAsnIleAspHisIleHisAspThrPheGlyThrLeuIleAsn | 1413 |

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|----|-------|---|-------|
| Db | 38376 | AATTCACAAATGCATGAGAAATCGCGCTCGAAAGAACAGATTAATTTCTTACAGTAAGTCCGA | 38433 |
| Qy | 1414 | GLNVALYSVALATHRTHRTHALALAPHEGLAASGLNLSAPLLEPROPHGLUARGVAL | 1433 |
| Db | 38436 | AGAGTGTCTCAACACGCGGAGAGGCGCTTCGAAACCAAGATGTGCATTCCGAGCCGCTT | 38495 |
| Qy | 1434 | VALSERLALAEGLINPARGLYSERARGAPLSERSETHRPROLEUALAGLNLLE | 1453 |
| Db | 38496 | GTATCTCGACCTTCGCCCGGCTCTAGAGAGCCCTCCCGAATCCCTCGTCAACTCATG | 38555 |
| Qy | 1454 | PHLELVALHISSEGLNLSAPLLEGLVARGPHLSYPHEGLINGLYLEUGLUSERVAL | 1473 |
| Db | 38556 | TTTGTGTCACCTCCACGCAAAATCTCGTAACTCGCAACTGGAGGACTTGGAAAGCCGA | 38615 |
| Qy | 1474 | PROVALPROSERLYSVALTYRTHRARGPHEASPMEGLUPHEHISLEUPHEGLINGLTHR | 1493 |
| Db | 38616 | CCAACCCCTGACACCGGAGAGACCCGCTTGATGTTGATGCCACCTCTTCGAACAAGAC | 38675 |
| Qy | 1494 | ASPSELEULYSGLYSERVALASPHEALASPGLULEUPHELSMETGLUTHRVALGLU | 1513 |
| Db | 38676 | AAAGCGCTCCGCGGAAATGTTGTCTTCGACGACAGACTGTTCCAGCTGCGCATTCACCCG | 38733 |
| Qy | 1514 | ASNVALVALARGVALPHEPHEGLULEULARGASGLYLEULINSESERARGTHRPRO | 1533 |
| Db | 38736 | AGCGTTGTGAAGCTTCCACGAGATCTCCGTCGTGCTTCACCAACCCAGATATCCGA | 38795 |
| Qy | 1534 | VALSERLEULPPOLEUTHRASPGLYLEVALTHRLEUGLULYSLEUASPVALLEAEN | 1553 |
| Db | 38796 | ATTTCACACATGCACACTTTCGATGCGCTGCGCGCGCTCAACAGCCGTAACTTACC | 38855 |
| Qy | 1554 | VALYSHISVAL-----ASPTYRPROARGLUSERSERLEUALASPVALPHEGLINTHR | 1571 |
| Db | 38856 | GTGAAGAATCGAACCTGACTTCGCCACCGAGAGCCCTCGGTGTGATGCTTCCAGACA | 38915 |
| Qy | 1572 | GLNVALSERLALATYRPROASPSELEUALALVALASPSESERCYBARGLEUTHRYR | 1591 |
| Db | 38916 | CAAGTGTGCTGAACCCAGATGCCCTGCTGTAACCGACACATCCCAAGCTTAACTAT | 38975 |
| Qy | 1592 | THRGLULEUSPARGLINSERASPLLEUALAGLYTRPLEUARGARGSERMETPRO | 1611 |
| Db | 38976 | GCGAGCTGCATCAACATCCGATCATGTGCGCGCTTGCTGCCAAACGAAGCTACCA | 39033 |
| Qy | 1612 | ALAGLUTHRLEUVALALVALPHEALPROARGSERCYSGLUTHRILEVALALAPHEP | 1631 |
| Db | 39036 | GCAGAGAGCATCGTCGTTGTTCTTGCGGCCACGATCCCTGAGACTTCGATGAGCATCAT | 39095 |
| Qy | 1632 | GLYVALLEULYSALAEULLEUALATYRLEUPROLEUASPVALARGSERPROSERLALARG | 1651 |
| Db | 39096 | GGCATCTCTCAAAAGGAACCTCGCATATCTCCATGGATTTCCAAACGTCCCGAAGCCGT | 39155 |
| Qy | 1652 | VALGLINAPLILEUSERGLYLEUSERGLYPROTHRILEVALLEULIEGLIHISAPTHR | 1671 |
| Db | 39156 | CGCCAGACAAATCTTTCGAGATTCACAGGGGAGAAAGTTCGTTTGCTTGAGCAGGAGTG | 39215 |
| Qy | 1672 | ALAPROPROAPLILEGLUVALTHRASPVALGLUPHEVALARGILEARGAPLALAEAN | 1691 |
| Db | 39216 | CCTATCTCTGACAAACAGACAGCGATGTGAGGATGCTTCAACGAGTATTCGTCGCC | 39275 |
| Qy | 1692 | ASPSEASNALASPGLYPHEGLUVALILEGLIHISAPSERTHRYSPROSERLALATHR | 1711 |
| Db | 39276 | AGCAAGACAGACAAAGTCTACTCA-----CCCGGCACTCGGCATCTGCATCA | 39332 |
| Qy | 1712 | SERLEULATYRVALLEULYRTHRSEGLYSERTHRGLYARGPHROLYSGLYALMETILE | 1731 |
| Db | 39324 | AGCCTTGTCTATGTTATCTTCACTACGCTCGACAGGTGCGCAAGGGGTGCATGTC | 39384 |
| Qy | 1732 | GLUHISARGVALILELLEARGTHRVALTHRSEGLYCYSLLEPROANTRYRPROSERGLU | 1751 |
| Db | 39384 | GAGCATCGGGGTATATTTCTTGTGTGAACAGAAAGCT--TCAGAAATACCAAAAGT | 39446 |
| Qy | 1752 | THRARGMETALHISMETALATHRILEALAPHEASPGLYALASERTYRGLULIETYSER | 1771 |

Dh 39441 CTGCGATGGACATGTTTCCAACTCGCATTCGATTCCTCGTGCGAGATATTCACC 39500
Qy 1772 ALeuLeuPheGlyArgThrLeuValCysValAspIleMetThrThrLeuAspAlaArg 1791
Dh 39501 ACCGTGTTCAATGAGAGAGCGCTTTTCTGTATCGACTACTTACTGTCTGGACAGCAA 39560
Qy 1792 ALeuLeuAspValPhePheArgGluHisValAsnAlaAspSerHisValThrSerSer 1811
Dh 39561 GCACCTTCTCGCGCTTCTCGCATCATCGCATTAAC----- 39596
Qy 1812 SerGlnAspValProLeuAspValProArgArgLeuSerArgThrLeuMetPhePhePhe 1831
Dh 39597 -----ATCACCTGCTCCACCGCGCTTCTCTCAAGCAATGCTT----- 39635
Qy 1832 LeuValValThrAspSerThrAlaProAspAlaLeuAspAla---GlnGlyLeuThrGln 1850
Dh 39636 -----GCAGACGCCCATCTGTCTGTAGAGTCCCTCGAGTCTCTGTATCAATT 39680
Qy 1851 GLy----- 1853
Dh 39681 GGAGGCGACCGCTTGATGAGTGTATGCAACCAAGGTGAAGGACTCGTCAAGGCAAG 39740
Qy 1854 CysThrAsnGlyArgArgProThrGluAsnGlyValMetSerThrIleThrProIleAsp 1873
Dh 39741 GCCTACAACTGCTAAGGATCCACCGAGAAATTCCTCATGAGCAGATCTAATCCATGAA 39800
Qy 1874 SerThrGluSerPheIleAsnGlyValProIleGlyArgAlaLeuAsn---AsnSerGly 1892
Dh 39801 CAC---GAGACTTTTGGGAGATGGCGTTCCATCGGCACATCTTAAGGCCCAATCCAG 39857
Qy 1893 AlaThrValAlaAspProGluGlnGluLeuValGlyIleGlyValMetGlyLeuVal 1912
Dh 39858 GCCTACATTATGGACCAAGATCAACAGACTCGTACACAGCGCGTGATGGAGACTTGTC 39917
Qy 1913 ValThrGluAspGlyLeuAlaArgGlyThrSerAspIleValAlaLeuAspGluAsnArgPhe 1932
Dh 39918 GTTGCTGCGCATGTCTCGACGAGGATATCCGATCCATCATCGAACAAGCGCGGCTTC 39977
Qy 1933 ValHisIleThrValAsnAspGlnThrValIleValAlaThrArgThrGlyAspArgValArg 1952
Dh 39978 ATCCACATCCAGATCGATCGAACAACAAAGTTACGSCATACCGGACCGGCGATCGAGT 40037
Qy 1953 TyrArgIleGlyAspGlyLeuIleGluPhePheGlyArgMetAspThrGlnPheIle 1972
Dh 40038 TACCGACTGAGGACTCAACCAATCGAATCTTTGGCGTTAATGACAGATCAAGATT 40097
Qy 1973 ArgGlyAsnArgIleGlySerAlaGluIleGluAlaLeuLeuAspSerSerVal 1992
Dh 40098 CGCGGTATCGCATCGACCGACGCTGAAGTGAGCGAGCTTCTCAGCGACTCATCGATC 40157
Qy 1993 ArgAspAlaAlaValValLeuGlnGlnAsnGluAspGlnAlaProGluIleLeuGlyPhe 2012
Dh 40158 AACGATCCCTGTGTGTGTGCGGCACAAACAAAG---GAGGCACTCGAAATGCTGTGTTAC 40214
Qy 2013 ValValAlaAspHisAspHisSerGluAsnAspIleGlyGlnSerAlaAsnGlnValGlu 2032
Dh 40215 ATCAGCAGCCAGGCTGACCAATCCGTC---GACAAAGAGGAAGCACACCAAAAGTGACAG 40271
Qy 2033 GlyThrGlnAspHisPheGluSerGlyMetCysSerAspIleGlyGluIleAspProSer 2052
Dh 40272 GAGTGGAGGCTCATTTCTGATCAACTGCATATGCAACATCGGGGATATGATCGCGAT 40331
Qy 2053 ThrIleGlySerAspPheGlyArgThrSerMetCysArgGlySerGlnIleAspPhe 2072
Dh 40332 GCCCTCGACAGGACTTCTTATCTGTGACATCTATGTAACGCGCTCATTTGATTCGCCGT 40391
Qy 2073 AspGluMetHisGluThrPleuGlyGluThrThrArgThrLeuHisAspAsnArgSerLeu 2092
Dh 40392 GAAGAGATGACGAGATGCTCAACGACATATGCGCTCACTCCCTCGAACCAACCAACCC 40451
Qy 2093 GlyAsnValLeuGluIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAsp----- 2110
Dh 40452 GGAATAAGTCTCGAGATCGAATCGGTACCGGTATGTGTCTCAATCTCGGCAAGGTT 40511

Qy 2111 SerArgLeuGluSerTyrValGlyLeuGluProSerArgSerAlaAlaAlaPheValAsp 2130
Dh 40512 GAGGACATCAAGAGATATGCGGCTTGAGACCTCGCGCTCCGCTCAACCGGCTGGTTAAC 40571
Qy 2131 LysAlaThrGluSerIleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAla 2150
Dh 40572 AAGGCAATCCAACTTTCCCAACCTCGGACGAGAGCGCCGAGCTTCCAGTTGAACCGCC 40631
Qy 2151 ThrAspIleGlyGlnValAspAspLeuHisProAspLeuValValLeuAsnSerValIle 2170
Dh 40632 GAGATATCAAGTCTCCATGTATGAGACTTCTCGCATCTCTGTGTATCAACTAGTCCGC 40691
Qy 2171 GlnThrPheProSerSerGlyTyrLeuAlaGluIleAlaAspThrLeuIleHisLeuPro 2190
Dh 40692 CAATACTTCCCAAGTCAAGATATCTCGTGAAGTCAAGGCGCAACCTGATTCAGTCCGC 40751
Qy 2191 AsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGluHisPheLeu 2210
Dh 40752 GCGGTAAAGGATTTTCTTCTCGGTGACATGAGAACGTATCTCAATAAGACTTCTTG 40811
Qy 2211 AlaAlaArgAlaIleHisThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLys 2230
Dh 40812 GTGGCAGACAGACTCCATACCTTAAGGCTCCAAATGATCGAAGGCCATGTTCAACAACAA 40871
Qy 2231 MetAlaGluLeuGluAspMetGluGluGluLeuValGluProAlaPhePheThrSer 2250
Dh 40872 GTGGCCAAAGCTTGAAGATGACGAGAAAGATTCTGTGTAACCTCGCTTTCACACAGC 40931
Qy 2251 LeuLysAspArgPheProGlyLeuValGluHisValGluIleLeuProLysAsnMetGlu 2270
Dh 40932 CTAGGCCACCAAGTTCCTCTGCAAAATCAAGATGTCAAAATTTGCGCAAGAGATGGCC 40991
Qy 2271 AlaValAsnGluLeuSerAlaTyrArgTyrAlaAlaValValHisValArgGlySerLeu 2290
Dh 40992 GCGACCAACCAATCACTGACTTTCACAGATATGCTGTCTATCATGTGGAGGCCACCCAG 41051
Qy 2291 -----GlyAspGlu-----LeuValLeuProValGluLysAspAsp 2302
Dh 41052 ATGCCGAATGGGAGATGAGATTAAGCAATGGGCTGTCAAGATATCAATCCGAAGGCC 41111
Qy 2303 ThrIleAspPheGlnAlaAsnGlnLeuAsnGlnLysSerLeuIleAspLeuLysSer 2322
Dh 41112 TGGGTGACTTGTCTGGCACGAGATGAGCGTCAAGGCTCTTTCGACGCTTTCAGGAC 41171
Qy 2323 SerAspAlaAla-----IleMetAlaValSerLysIleProPheGluIleThrAlaPhe 2340
Dh 41172 CGCCACGTCGCGATGACGCTGTTCCTCGCTCAGTAACTCCCATACAGCAAGACCATCATG 41231
Qy 2341 GluArgGlnValValAlaSerLeuAsnSerAsnIleAsp----- 2353
Dh 41232 GAGGCGCATGTCTCAGTCACTTGAATGATGAGACGAGACCGGCACTTCAGCGTGAACGGA 41291
Qy 2354 ---GluThrGlnLeuSerThrIleArgSerSerAlaGluIleLysPheSerSerLeuSerVal 2372
Dh 41292 ACCGCGCTCG---ATATGCGCTACGCAATCAAGGCGGAAGAAATGCCCTGCTTCTCATGTG 41348
Qy 2373 ProAspIlePheArgIleAlaGlyGluAlaGlyPheArgValGluValSerSerAlaArg 2392
Dh 41349 GCGGACTGATTAAGATTTGTTAAGGAGATCGGCTTGCAAATTGAAGCCACTGGCGTCCA 41408
Qy 2393 GlnThrSerGlnAsnGlyAlaLeuAspAlaValPheHis-----His 2406
Dh 41409 CAACACTCCAGCGCGGCGGAGCTCGATGCTGTTTCCACGATTCGAACCAACCAAGCAC 41468
Qy 2407 CysCysSerGlnGlyArgThrLeuValAsnPheProThrAspHisHisLeuArgGlySer 2426
Dh 41469 -----TCAGATCATGTCAATGTTCAAGGTTCCTCCGATCAACAAGGCGGCTTCCG 41519
Qy 2427 AspLeuLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluVal 2446
Dh 41520 AGCAGTCTCAAGATGCCCGGCTTACACTGCTTCAAGAGCCGCGGACTGAGGCAAGGTC 41579

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|----|-------|--|-------|
| Qy | 2447 | ArgGluArgLeuArgSerLeuLeuProSerTyrMetLeIeProSerAsnIleValIleu | 2466 |
| Db | 41580 | CGCAGGCGGCTGCACATCACTGCTTCCACCGTACATGATTCGCTCGAATCGTTGGCTC | 41639 |
| Qy | 2467 | AspLysMetProLeuAsnIleAsnGlyLysValAspArgLysGluLeuSerArgArgAla | 2486 |
| Db | 41440 | GATCAGATGCTCTTCACGCTCCACCGGACGGAAGGTGATGCGAAGAAGCTTGCTGCACAAAGCC | 41699 |
| Qy | 2487 | LysValValProLysGlnIntrAlaAlaProLeuProThrPheProIleSerGluVal | 2506 |
| Db | 41100 | CGGCTCATCCCAAGATGGCGGCAAGCAGCTTGGAATTTGTGGCGGCACGCAAGAAATC | 41755 |
| Qy | 2507 | GluValIleLeuCyGylGluGluAlaThrGluValPheGlyMetLysValAspIleThrAsp | 2526 |
| Db | 41760 | GAAGTCCCTCCCTCGCGAAGAAATTTACCGAATCTCTAGCGCTCAAGGTGGCATCACAGAC | 41819 |
| Qy | 2527 | HisPhePheAsnLeuGlyLysIleSerLeuLeuAlaThrLysLeuIleSerArgIleAsp | 2546 |
| Db | 41820 | AACCTCTTCAGATTGGCGGCGCATTCGCTGCGCCGAACTGAAAGGACGATCTTAAGT | 41877 |
| Qy | 2547 | GlnArgLeuLysValArgIleThrValLysAspValPheAspHisProValPheAlaAsp | 2566 |
| Db | 41880 | CGCAGACTGGACCGCGGTATCACTGTAGAGAGAGTCTTTGACACGACAGATCTTGCTGAT | 41933 |
| Qy | 2567 | LeuAlaSerValIleArgGlnGly----- | 2574 |
| Db | 41940 | CTTGCTCTCTTATCTTCAAGGCTCGCTCGTGCACAGTCTATGCCGTTTACCTTAC | 41999 |
| Qy | 2574 | ----- | 2574 |
| Db | 42000 | GAAAGACCCGTGAGCAGACTCTTTGCCAAGGGCGCTGTGGTTCTCGACCAATTCAAC | 42055 |
| Qy | 2574 | ----- | 2574 |
| Db | 42060 | ATCGATGCCCTTGTGTACTTATTTCATTTGSCACTCCGCATGGCGGGCGGCTGCAAGTT | 42113 |
| Qy | 2574 | ----- | 2574 |
| Db | 42120 | GACGCCCTCGCTGCTGCCCTGTGTGGCACTTGAAGCGCTCATGATATCTGCGCACAAGC | 42179 |
| Qy | 2574 | ----- | 2574 |
| Db | 42180 | TTTGAGGAACGAGACGAGAGTCCGATCCAAAGTGTGCAACCCCTCGCACACCAAGAT | 42233 |
| Qy | 2574 | ----- | 2574 |
| Db | 42240 | ATCCGATCATCGACGTGTCAAGGATCGGAGACGACGACCCCTAATCTCGAGCCATTGGCAG | 42299 |
| Qy | 2574 | ----- | 2574 |
| Db | 42300 | AAAGAACGACGACTCTTTTCGACTTTGCTTCAAGAGCTGTGAGGGTAGACATTGCTG | 42355 |
| Qy | 2574 | ----- | 2574 |
| Db | 42360 | AAGCTTGAAAAGATGACCAATCTCTCTATTGTGTATGACCAACATCATCTCTGACGGG | 42411 |
| Qy | 2574 | ----- | 2574 |
| Db | 42420 | TGGTCTACTGAAGTCTTGCAAAAGGAACTGGGTCAATTCTAATTGGGACGAGAAATCCGGG | 42477 |
| Qy | 2574 | ----- | 2574 |
| Db | 42480 | AAAGCCCCCTTATCGCAGGTGGCCCCGCTTCTATTCATGATGCGCATTTTGTGCTTTGG | 42533 |
| Qy | 2574 | ----- | 2574 |
| Db | 42540 | CAGAGACAAAGAGAACAGTGTGCTGAGAGTCAAAGGACGCTCGACTACTGGAAGAAACAG | 42599 |
| Qy | 2574 | ----- | 2574 |
| Db | 42600 | CTTGCGGACAGTACGCCGGCTGAGCTTGTGCTACTTACACAGGCGGAAAGTACTGTCT | 42655 |
| Qy | 2574 | ----- | 2574 |

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|----|-------|---|-------|
| Db | 42660 | GGAGAGCAGGACGCGGTCTTTCGTGATCAAGATTCCGTTTACAAGAGCCCTCGTCTCC | 42719 |
| QY | 2574 | ----- | 2574 |
| Db | 42720 | TTCTGCCGGTCTCGCAAGTAACCACTTTACGATTTACTGGCAGCGTTTCGCGCGCT | 42779 |
| QY | 2574 | ----- | 2574 |
| Db | 42780 | CACATCGAATGACCGGGTCAGACGACGAACATAATTGGACCGCAATTGCCAATCGCAAC | 42839 |
| QY | 2574 | ----- | 2574 |
| Db | 42840 | AGGCTTAGCTTGAAAACTTGATCGGCTGCTTGTGATTAACCAAGTCATGGGTACT | 42899 |
| QY | 2574 | ----- | 2574 |
| Db | 42900 | ATGGCGCAGATGAGAGCTTTGAATCACTGTACAAAGGTACGGTCTACACCGCGACA | 42959 |
| QY | 2574 | ----- | 2574 |
| Db | 42960 | GCTTTCGAGATCAAGACGTTCCGTTTGAACGAATCGTTTCCACCTCAGTCCGGGTC | 43019 |
| QY | 2574 | ----- | 2574 |
| Db | 43020 | AGGATACGTCGCCAAACCCCTATGACGCTTCTTTGGGTTCAATTCACAAGGC | 43079 |
| QY | 2574 | ----- | 2574 |
| Db | 43080 | CTGGGCAAGATCCAGCTCGACGGGTGTGTGATGAGCGGTTCTGTCAACGTTTGACT | 43139 |
| QY | 2574 | ----- | 2574 |
| Db | 43140 | CGTTTCGATCTCGAATTTCCAGCCTTCCAAAGAGCGGACCGGCTCAATGAAATGTATG | 43199 |
| QY | 2574 | ----- | 2574 |
| Db | 43200 | TTTGCCACGGAAGCTGTTCCAGCCCGGAGACCAATCCAAAGTTTCGTTCCGTTTCGAAGAG | 43259 |
| QY | 2575 | -----LeuGIleuGIInProValSer----- | 2582 |
| Db | 43260 | GTTCTACAGCGTGGCTCTGAGACAGCGGCAAGTCCATCGCAACATGCGCGTGGCGAA | 43319 |
| QY | 2582 | ----- | 2582 |
| Db | 43320 | GGCATTCGCTCAGCTCCGAGATGCGCGCGCTGCAGATGCCAAAGTGTATTAACCTCGC | 43379 |
| QY | 2582 | ----- | 2582 |
| Db | 43380 | AACGCGTCCCTCGTGAATGTTCTTCAGACAGCAGGCTATGAGCCAGCCGTCACACTGTGCC | 43439 |
| QY | 2582 | ----- | 2582 |
| Db | 43440 | GTCACACTGACCACTCCAAAGCTGACGTATGCCAGCTGATGACTTCCGATCAAGCT | 43499 |
| QY | 2582 | ----- | 2582 |
| Db | 43500 | GCTTCCTATCTGCGTCGAGCAACATCCCGGCGAGACAATGTGTGCCGTTCTGCACCG | 43559 |
| QY | 2582 | ----- | 2582 |
| Db | 43560 | CGCTCTGTGAGACCAATCATCGCGTCTTAGCTAATTCAAAGCAAACTTGGCTACATG | 43619 |
| QY | 2582 | ----- | 2582 |
| Db | 43620 | CCTTCGACGTCAACAGCCATCTGCTCGATGGAAAGCATCATATCTCCGTCACAGGG | 43679 |
| QY | 2582 | ----- | 2582 |
| Db | 43680 | CGTAGGCTCATCTTGTTGGTCGGGCGTCCGCGCATGTGATATCAACGTACCAACGCA | 43739 |
| QY | 2582 | ----- | 2582 |

Db 43740 AAGACGATGCTGATCAGCAGCAGGTTACGGGACTGATGCTATTTGCACTCCCGAACT 43799
QY 2582 ----- 2582
Db 43800 CTGGTGTCCGACCCAGTGTCTACAACTCTGGCATATGTCACTTTCAGGTTCAAG 43859
QY 2582 ----- 2582
Db 43860 GGCAAGCCAAAGGGTGTATGTGTGAGCACCCTGCTATCAGCGCTTGTGAAGACAGT 43919
QY 2582 ----- 2582
Db 43920 AACGTGTGACTCATGCAACGACGACGAGTGGCCACGTCACGAATATCGCAATTC 43979
QY 2582 ----- 2582
Db 43980 GACGTTTCACTGTTCCGAGATGTGGCAACGCTCTCAACGGCGGAACCTTAGTCTGCATT 44039
QY 2582 ----- 2582
Db 44040 GACTACCTGACCTTCTTTGACAGCACCATGCTCCGGAGACGTTTGAGCGTAGCAGGTT 44099
QY 2582 ----- 2582
Db 44100 CGCGCAGCCATCTTCCCGCAGACCTCTCGACAGTGTGTGCAATGATCCGATGCG 44159
QY 2582 ----- 2582
Db 44160 ATCGGCGATTTAGAGCTGTTTACGTTGCGGTGATGCTTCCACTCCCGCAGCGCCGC 44219
QY 2582 ----- 2582
Db 44220 GCAACCCAGGCACTGCGCGGCTCGTGTGTACAACCGTATGCCCCAAGTAGAAGCA 44279
QY 2582 ----- 2582
Db 44280 ATCCTTAGCAGATATATTAACATCGATAGACAGATCCGATGTGAACGGTGTCTTATC 44339
QY 2582 ----- 2582
Db 44340 GGTAGCGCTGTCAACATTTCAAGGGCTATGTCTATGTAGTAGGAAACAGCAGCTTCTCCT 44399
QY 2582 ----- 2582
Db 44400 CCCGCTGTGATGGAGAGCTGTTGTTACAGAGAGGGTGTAGCTCCGCGCTATACCGAC 44459
QY 2583 ----- 2587
Db 44460 GCAAGTCTGATACGACCGCTTCTGTACCGTCAAGATCGATGGCCAGCGCCAGAGGCG 44519
QY 2587 ----- 2587
Db 44520 TACCGCAGCGGTGACCGGGTGCATATCGAACAAAGGATTCAGATAGAGTTCTTGGC 44579
QY 2587 ----- 2587
Db 44580 CGCGTGGACAGCAGCCAAAGATTCCGGGCCACCGTGTGAATCGGCGAGTGCAGAT 44639
QY 2587 ----- 2587
Db 44640 GCTCTGCTACGAGAAATTACATCAGAGATGGCGCTGTCTGACTCCGACCAATGAAGAG 44699
QY 2587 ----- 2587
Db 44700 GAGGACCCGCAACTGTGCTTGTGTGACTACTAGTATACGAATATCGCTGGGTTCCAGC 44759
QY 2587 ----- 2587
Db 44760 AACGAGAGAGATCCGTACGCCACACAGCAGAGCGATATGCCAAGCACTCCGG 44819
QY 2587 ----- 2587
Db 44820 TCGCTTCTGCATATCTACATGTGTCGCTCCGGGTCACAATATCTCAGGCAATGCTCTC 44879

QY 2588 -----AspArgSer----- 2590
Db 44880 AACGCCACGGCAAGGTGACCGAAAAAGACCTGCTGGCGGCCAGATGATCTCCGACA 44939
QY 2591 -----AlaHisMetCysProArgThrGluThrGluAlaIleLeuGly 2604
Db 44940 GCAAGCAGCTCGGGCCCCCGTCATGTGGCTCCGCAACAGACAGCTGAGGAGCAATTTGC 44999
QY 2605 AspGluPheAlaLeuValLeuGlyPheGluValGlyIleThrAspAsnPhePheAspLeu 2624
Db 45000 GACGAGTTTCAGACATATCTACTCGAGTCAAGTGGATTCACAGAACATCTTTCGAACCTA 45059
QY 2625 GlyGlyHisSerLeuMetAlaThrIleValAlaValArgIleGlyHisArgLeuAspThr 2644
Db 45060 GCGCGGCACTCACTCCGCGCCACCAACCTGCTGCTCAGCCGCGGATGGGCTT 45119
QY 2645 ThrValSerValIleAspValPheAspPheProValLeuPheGluLeuAlaIleAlaLeu 2664
Db 45120 CGCATATCCGTCAAGATCTGTTGACGATCTGTTCTCTCTCGCCGCGCAAGCTG 45179
QY 2665 AspAsnLeuVal-----GlnSerIleThrAsnGluIleValGly 2678
Db 45180 GAACACAGCAGGGGTTCTCGGAGAAAGATGAAGCTCGACAGTGGTATGTC----- 45233
QY 2679 ArgGluMetAlaGluIleSerProPheGlnLeuLeuPheThrGluAspProGluGluPhe 2698
Db 45234 -----CCTTCAACTCTCTCCCGGAAATGTCGAGAGATC 45272
QY 2699 MetAlaSerGluIleAspProGlnLeuGluLeu-----GlnGluIleIleGlnAspIleTyr 2717
Db 45273 ATCCAGCGCATGTTGATCTCAGATTGAGAACCGTCAACAGCACACCTTGACATGTAT 45332
QY 2718 ProSerThrGlnMetGlnValAlaPheLeuPheAspHisThrThrAlaArgProArgPro 2737
Db 45333 CCAGCCAGCAGACGAGATCTTCTCTCAGACAAAGCAGCGGCCACCCAGCCAGC 45392
QY 2738 PheValProPheThrIleAspPheProSerThrSerGluProAspAlaAlaGlyLeuIle 2757
Db 45393 CCGCAGCTGTTCTCTGAGCTCCCGAGACCGC-----GACTGCCGCTCTGCA 45446
QY 2758 LysAlaCysGluSerLeuValAsnHisLeuAspIlePheArgThrValPheAlaGluAla 2777
Db 45447 AGCGCTCGCGCCCTCGTCCAGCACTTGACATATTCGAACCGGTGTCTGTCAAGA 45506
QY 2778 SerGlyLeuLeuTyrGlnValIleLeuSerCysLeuAspLeuProIleGlnValIleGlu 2797
Db 45507 GCGGCGCGCTTCAACAGTGTCTTCTGCTCATCTGATCTGATCTGCGAGTCACTGAG 45566
QY 2798 ThrGluAspAsnIleAsnThrAlaThrAsnGluPheLeuAspGluPheAlaLeuGluPro 2817
Db 45567 ACCGAGCAAGATGATGATGAGTGTGCTCTCGCGCTGCATGAACAGACAGCAGAGCCC 45626
QY 2818 ValArgLeuGlyHisProLeuIleArgPheThrIleIleLeuGlnThr-----LysSerMet 2836
Db 45627 CTACGCTGGAGCTGAGTGGATGCGGATCGCATCTTCAAGAGACCGGAGCCCAAGATG 45686
QY 2837 ArgValIleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGlnHisValIle 2856
Db 45687 CGACTTGTCTCCGAAGTCTCATCTCTTACGACGCGCTTGAGTGTGAACACATGTC 45746
QY 2857 ArgIleLeuHisMetLeuTyrAsnGlyArgSerLeuLeuProHisGlnPheSerArg 2876
Db 45747 AACGCTTACATGCTGTACAGATGAACACCTTCCGACAGACCAAGTTTGGCTC 45806
QY 2877 TyrMetGlnTyrThrAlaAspGlyArgGluSerGlyHisIleGlyPheThrPalaAspValIle 2896
Db 45807 TACATGATCAACATGCTGATCCGACGAGGAGGCTTACAAATTTCCGCGCATCTATTCTT 45866
QY 2897 GlnAsnThrProMetThrIleLeuSerAspAspThr-----ValValAspGlyAsnAspAla 2915
Db 45867 CAGGCTCTTCATATGATATCTCTGAAGCGCTCTGTGCGGCCCTTCGA-GGCCATGAGGCC 45925

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QY 2916 Thrcyslysalaleu-HisLeuSerLysIleValAsnIleProSerGlnValLeuArgI 2935
D 45926 GTCTGCCGATACATGGCAGACGTCAAGTCCATGAGATCCCTCTCGGCGACCAAG-- 45983
QY 2935 ySerSerAsnIleIleThrGlnAlaThrValPheAsnAlaIaCysAlaLeuValLeu 2955
D 45984 -----AACGGCAATTACGACAGGCGACCTCTTCACCGCGCCCTCTCTCTCTCGC 46036
QY 2955 rArgGluSerAspSerLysArgValValPheGlyArgIleValSerGlyThrGlnGlyLe 2975
D 46037 CAAGCATACCAAGTCCAGACAGTCTGCTTCGCGCGCGCTGATCTGAGACGACGATCT 46096
QY 2975 uProValGluThrGlnAspIleValGlyProCysThrAsnAlaValProValArgAlaH 2995
D 46097 CTCCTAAATCGCAACACATCGTGACCTTGATCAAGAGTGTGCGCGCTTCG 46156
QY 2995 sIle---GluSerSerAspTyrAsnGlnLeuLeuHisAspIleGlnAspGlnTyrLeu 3014
D 46157 GATCGACGAGGCGGACACATGGGTGCTGCTCGCGCATTCACAGACGATACACAG 46216
QY 3014 uSerLeuProHisGluThrIleGlyPheSerAspLeuLysArgAsnCysThrAspTrp 3034
D 46217 CACCTTCGCGACGACGCTTGCGCTTCGCAAGAGTAAAGAGAACTGCACGCGCTGAC 46276
QY 3034 ogIuaIaIeThrAsnPheSerCysCysIleThrTyrHisAsnPheGluTyrHisProG 3054
D 46277 TGATGGACCAAGAGATTTCAAGTTCGCTGCTGCTTCACAGACCTCAACCTGCATCTGA 46336
QY 3054 uSerGlnPheGluGlnGlnArgValGluMet----- 3064
D 46337 GCGCGAGATTGAAGGCGACAGATTCGCTGAGGAGTTCGACAGCAAGATCAAGCAG 46396
QY 3064 ----- 3064
D 46397 CAGGCCAATGTGTCATGCCCAATGGCAGACGACGACGACGACGACGACGACGAC 46456
QY 3064 ----- 3064
D 46457 TGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 46516
QY 3065 -----GlyValLeuThrLysPheValAsnIleGluMet-----AspG 3077
D 46517 TGGTAGCAACGGGTCTCATATGGCGCGATAGCAACGTTGTTCAAGCCCTGCGCATCAGC 46576
QY 3077 uProLeuTyrAspLeuAlaIleAlaGlyValGluProAspGlyAlaGlyLeuLysVal 3097
D 46577 TCTGTTCACGATCTGACATGTTGGGATTCGCGACCCGACGCGCAGC--GTCAGAT 46633
QY 3097 lThrValIleAlaLysThrGlnLeuPheGlyArgValArgValGluHisLeuLeuGln 3117
D 46634 TGGCATTTGGTCCAGCCGCGACGATCTTCGAGAGAGAGTGTGGGACGACATGCTCATGA 46693
QY 3117 uValSerLysThrPheGluGlyLeuAsn 3126
D 46694 ACTTGGAGACCATGCTCGCTTGAGC 46721

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/ LENGTH: 7374
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9100

Alignment Scores:
Pred. No.: 6,02e-170 Length: 7374
Score: 1715.50 Matches: 586
Percent Similarity: 44.67% Conservative: 327
Best Local Similarity: 28.67% Mismatches: 754
Query Match: 10.64% Indels: 377
DB: 4 Gaps: 75

US-09-482-788-2 (1-3129) x US-09-252-991A-9100 (1-7374)

QY 430 TyrAspHisAsnValIleAspSerLeuGlnThrThrGluLeuGlnPheGlyHis 449
D 1348 TACGCCACCGATCTGTTGACGCTCCACCGTGAAAGCGCGGCGCATTTGGCGCAAC 1407
QY 450 LeuIleLys---CysLeuGlnSerProLeuAspLysSerMetAlaGluValAsnLeu 468
D 1408 CTGTGGCGGCGCATCTGCGCAACCA-----CGACAGCGCTCGCGAGTTCGCGCTG 1461
QY 469 MetThrGluTyrAspArgAlaGlu---IleGluSerTrpAsnSerGlnProLeuGlu--- 486
D 1462 CTGATGCGCGGAGCGCGCGGACGCTCCGAAATGGAACCGCGCGACGCGAGTGC 1521
QY 487 ---ValGlnAspThrLeuIleHisIleGluMetLeuValValSerHisLeuProThr 505
D 1522 GCGGTGAGGAGGACCTTTG---CAGCAGCGTTTCGAGGAGGAGCGCGCGCAACGCGCAG 1578
QY 506 LysThrAlaIleGlnAlaTrpAspGlyAspTrpThrTyrSerGluLeuAspAsnValSer 525
D 1579 GCGGTGCGCTGATCTTCGACGAAACAGGTTGAGTACGCGCACTGAATGCCGAGCC 1638
QY 526 SerArgLeuAlaValHisIleLysSerLeuGlyLeuArgAlaGlnAlaIleIlePro 545
D 1639 AATGCGCTGCGGACCTGATCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1689
QY 546 Val-----TyrPheGluLysSerLysTrpValIleAlaSerMetLeuAlaValLeuLys 563
D 1690 GTGCGGCTGCGCGTGGACGCTTCGTCGACATGCTGTCGCGCTTCGCGGATCTCAAG 1749
QY 564 SerGlyAsnAlaPheThrLeuIleAspProAsnAspProAlaArgTrpAlaGlnVal 583
D 1750 GCCGCGCGCGCTTACCTGCGCTTGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCATATC 1809
QY 584 ValThrGlnThrArgAlaThrValAlaLeuThrSerLysLeuHisArgGluThrValGln 603
D 1810 CTGACGACAGTGGGAGTACGCTTCGCTGACCGAGGCGCATGCTCGAGCACCTGCGC 1869
QY 604 LysLeuValGly---ArgCysValValValAspAspGluLeuGlnSerValSerAla 622
D 1870 CCGGAGCGCGGCTGAGAGTGTGCGCATGACGACGACGACGACGACGACGACGACGAC 1929
QY 623 SerAspAspPheSerSerLeuThrLysSerGlnAspLeuAlaTrpValIlePheThrSer 642
D 1930 AGCGATCGCTCCGACGCTATCG--GCGACACACTGACCTCACTGATATATACCTCG 1986
QY 643 GlySerThrGlyAspProLysGlyIleMetIleGluHis-----ArgAlaPhe 658
D 1987 GCGTCGACCGCGCAAGCGCAAGGACATGCTACCAACCGCAAGCGCGCTGCGCTGTC 2046
QY 659 SerSerCysAlaLeuLysPheGlyAlaSerLeuGlyIleAsnSerAspThrArgAlaLeu 678
D 2047 AGCGCCACCGAGCGCTGCTGCGCTTCGAC-----GAGCGGACGCTGTGACATTC 2097
QY 679 GlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGlnIleMetThrThrIleAsn 698
D 2098 ---TTCATTCCTACGCTTCGATTTCTCGCTGAGAAATCTTCGCGCGCGCTGCTAT 2154
QY 699 GlyGlyCysValCysIle-----ProSerAspAspArg 710

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Dh 2155 GCGGGGTCCTGGTATCGTCCGCAATGGGTGACCGCTTCGCGGAAGACTTCTACCGT 2214
Qy 711 MetAsnSerIleProSerPheIleAsnArgTyrAsnValAsnTrpMetMetAlaThrPro 730
Dh 2215 CTG-----CTGTGCGCGGAGCGGTGAACGGTCTCAACCAACGACCGG 2256
Qy 731 Ser-----TyrMetGlyThrPheSerProGluAspVal-----Pro 742
Dh 2257 TCGGCGCTTCAAGCAACTGATGCGCGTGTCCGCCGCAATGGGAGCGACGACGCGG 2316
Qy 743 GlyLeuAlaThrLeuValLeuValGlyGluGlnMetSerSerSerValAlaMetAlaIleTrp 762
Dh 2317 GCGGTGCGCTACGATCTTGTGTGTGAGCGCTGTGATCTGCAGACCGCTGGCGCGTGG 2376
Qy 763 AlaProIleu-----GlnLeuLeuAsnGlyTyrGlyGlnSerGlnSer 777
Dh 2377 TTCACAGGCTTTGGCGATTCGCGACCGCCAGCTGTGAACAATGACGGCATCACCAGAAC 2436
Qy 778 SerSerIleCybPheAlaSerAsnMetSerThrGluPro----- 790
Dh 2437 ACG-----GTACACGTAACTACCGCTCCGCTGAGCGAAGCGGACCTGGAA 2481
Qy 791 -----AsnAsnMetGlyArgAlaValGlyAlaHisSerTrpValIleAspPro 806
Dh 2482 GGTGGCTGTGCTGACGTCCGATCGCGGAGCAATCCCGGACCTGTCTGTGATCATCTTGAC 2541
Qy 807 AsnAspIleAsnArgLeuValProIleGlyAlaValGlyLeuValIleGluSerPro 826
Dh 2542 CGTGACCTGAACCGG---GTGCGCGCGGCGCGGTGGGCGAGCTGTACATCGTCCGCGCC 2598
Qy 827 GlyIleAlaArgAspTyrIleValProProProProGluIleAspPhePheThrAsp 846
Dh 2599 GGTCTGCGCGCGCTGACTGAGCGGCGCGGCTTGAGTGCGACCGCTTC----- 2649
Qy 847 IleProSerTrpTyrProAlaAsnThrPheProAspArgIleVal-----LysLeuTyrArg 864
Dh 2650 GTGCGG-----AACCCTGTCCTCCCGCGGTGCGCGGCGGACGCGCTTACCGT 2694
Qy 865 ThrGlyAsnProLeuAlaArgTyrAlaSerAspArgIleValCysLeuGlyArgIleAsp 884
Dh 2695 ACCGGGACACTGGGACGGTTCAGCGGATGCGCAATTCAGATCATCGGCGGTATGAC 2754
Qy 885 SerGlnValIleValIleArgGlyGlnArgValGluLeuGlyAlaIleGluThrHisLeuArg 904
Dh 2755 CACGAGGTGAAGTTCGCGGCTTCGATCGAACCTGGGTGAGATCGAAGCGCGCTGCC 2814
Qy 905 GlnGlnMetProAspAspLeuThrIleValGluAlaThrLysArgSer---GlnSer 923
Dh 2815 -----GGTCTGGCGCGGAGTACGCGATCGGTGCTGGGCCATGACGCG 2859
Qy 924 AlaAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyrPheGlyAsnArgPro 943
Dh 2860 GTGCGCGGACGCAACTGTGTGGATACGTGTGGCGGACTG-----GCG 2904
Qy 944 SerAspAlaHisIleLeuAspHisAspAlaThrLysAlaIleAsnIleLysLeuGln 963
Dh 2905 GAGGATCCGACGCTCTG-----CGGAGATCGCTCGCGGAGTCCCTGAACGCG 2952
Qy 964 ValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGluLeuProArgThr 983
Dh 2953 CACCTGCGGAGCTAATGATGCGCGGACCTGATGCTGTGAGCGGAGTCCGCTGACG 3012
Qy 984 AlaThrGlyLysIleAspArgArgArgLeuArgIleMetGlyLysAspIleLeuAspLys 1003
Dh 3013 GTCAATGGCAAGCTGCAACCGGACGCGTTC-----CCG 3045
Qy 1004 GlnThrGlnGlyAlaIleValGlnGlnAla---ProAlaProIleProValPheAlaAsp 1022
Dh 3046 CAACCGGATGCGACTTGTGCGACAGCGCTTATCGAGCGCC-----GTTAGCGAG 3096
Qy 1023 ThrAlaAlaLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrVal 1042
Dh 3097 CTGGAGCAGCGCATCGCATCTGGCGGAGATCTCTGGAGTGGAA-----CGGAGTT 3150

Qy 1043 AsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLysMetVal 1062
Dh 3151 GCGCTGAGCACAACCTTCTTGAACCTGGCGGCTATCTGTGCTGCTACCCGGTCAATT 3210
Qy 1063 AsnMetAlaArg---SerValGlyMetAspLeuLysValSerAsnIleTyrGlnHisPro 1081
Dh 3211 TCTGGGTTGCGCAGGAGCGACGAGTGTGACGCAAGCTGTGAAGCGTTGTTGAGCGCGG 3270
Qy 1082 ThrLeuAlaGlyIleSerAlaValAlaValGlyAspProLeuSerTyrThrLeuIlePro 1101
Dh 3271 GTTCTGGAACGTTCCGCCAGGATTTGGAACGACAGCGGATCGGTCTGACAGATPCCG 3330
Qy 1102 LysSerThrHisGluGlyProValGluGlnSerTyrSerGlnGlyArgLeuTrpPheLeu 1121
Dh 3331 CTGCGCATCGGCGACGACCGTTGGACCTGCTTCCGCTCAGAGAGCGTCAAGTTCCTC 3390
Qy 1122 AspGlnLeuAspValGlySerLeuTrpTyrLeuIleProTyrAlaValaLysMetArgGly 1141
Dh 3391 TGGCACTGAGCGCGGAACCGCGGCTTACCATATTCGAGTCCGTTGCGCTACCGCGGG 3450
Qy 1142 ProValAsnValAspAlaLeuArgArgAlaLeuAlaLeuGluGlnArgHisGluThr 1161
Dh 3451 CGGCTGACCTGATGCTTGTGCAACGACGCTTGACAGCCTGTGCGCGGATGAAC 3510
Qy 1162 LeuArgThrThrPhe-----GluAspGlnAspGlyVal 1172
Dh 3511 TTGCGTACCGCTTCCGCTGAGAGGAGCGGCTTGTGACACGAGATGAACCTGCGGTT 3570
Qy 1173 GlyValGlnIleValHisGlyLysLeuSerGlnGluMetLysValIleAspLeuCysGly 1192
Dh 3571 AGCGTTTCCATCAGCGGGAACGTTGCTGAAAGGCGCTGATC----- 3615
Qy 1193 SerAspLeuAspProPheGluValLeuAsnGlnGluGlnThrTrpProPheAsnLeuSer 1212
Dh 3616 -----GAACGATPACAGGCCATCGTTTGACAGCATTCGACCTGGAA 3657
Qy 1213 SerGluAlaGlyTrpArgAlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThr 1232
Dh 3658 CGGCGCGCGCTGCGCGGAGTGAACCTGTGCAACTGGCCGCAACGACATGATCTGTG 3717
Qy 1233 IleValMetHisHisIleIleSerAspArgIleTrpSerIleAspValLeuAspArgAspLeu 1252
Dh 3718 CTGCTCAGACCAACATCGTGTCCGAGGTGTGTCATGAGGTGATGATGATGAGAACTG 3777
Qy 1253 AsnGlnLeuTyrSerAlaAlaLeuLysAspSerLysAspProLeuSerAlaLeuThrPro 1272
Dh 3778 GTCCAGCTCAT---GCCGCTTATGCCAAGGCTGCACCTGGTG-----TTGCCAGCC 3828
Qy 1273 LeuProIleGlnTyrSerAspPheAlaLysTrpGlnLysAsp-----GlnPheIleGlu 1290
Dh 3829 CTGCGCATTCAGTACGCGGACTAGCGCTGTGACAGCGACGTGATGAGAGCGGAGAA 3888
Qy 1291 GlnGluLysGlnLeuAsnTyrTrpLysLysGlnLeuLysAspSerSerProAla---Lys 1309
Dh 3889 AAGAGGCGCAGTGGGCTGACCGGCTGTGGCGCGGACGACGCGGTCTGGAG 3948
Qy 1310 IleProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGlyCysValHisVal 1329
Dh 3949 TTGCGCTTCATCGCGCGCTCCGCGCGGACAGACCATGTGGCGCGGACTGGGTTTC 4008
Qy 1330 ThrIleAspGlyLeuLysTyrGlnSerLeuAspAlaPheCysAsnGluHisAsnThrThr 1349
Dh 4009 GAGCTACCAAGGAACTGTCGAGGCGCTGAGAGCTTGGCCGACGCTGAAGCGCGCAGT 4068
Qy 1350 SerPheValValLeuLeuAlaIleAlaPheArgAlaAlaHisIleTyrArgLeuThrAlaValGlu 1369
Dh 4069 AGTTTCATGCTGTGCTGCGCTGCTGTCAGACCGCTGTTGATGCTTACACGCGGACGG 4128
Qy 1370 AspAlaValIleGlyThrProIleAlaAsnArgAspArgProGluGlnGluAspIleIle 1389
Dh 4129 GATATCGGTCTCGGTGCGGATCGCATTCGCAACCGCGCTGAGACCGGCGGTGATC 4188


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Db 6217 CAGCGCTGGCCGCAACCGGATGCGAGCTTGCAGACAGCCGATACGCGCCGAGTAC 6276
Qy 2057 AspPheIysGly-----TrrPheSerMetTyrAspGlySerGlnIleAsp 2071
Db 6277 GAGCTGAGACGAGCGCATCGCAGCATCTGGCGGAGATCTCCGGAGTGGCAACGGGTGGC 6336
Qy 2072 PheAspGluMetHisGluTrpLeuGlyGluThrThrArgThrLeuHisAspAsnArgSer 2091
Db 6337 CTGGACACGAC----- 6345
Qy 2092 LeuGlyAsnValLeuGluIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAspSer 2111
Db 6346 -----AAGTCTTTCGAACTGGGCG--GGTCACTCATCTGTGGCTGATGCTCAAGAG 6396
Qy 2112 ArgLeuGluSerTyrValGlyLeuGluProSerArgSerAlaAlaPheValAsnIys 2131
Db 6397 CGGATCGCGCAT-----ACCTGCCAG 6417
Qy 2132 AlaThrGluSerIleProSerLeuAlaGlyValAlaValGlnValGlyThrAlaThr 2151
Db 6418 GCTACGCTGACATCAGCCCACTGATACCCATCCGCGCGGAAACAGCGCGCATGC 6477
Qy 2152 AspIleGlyGlnValAspAsnLeuHisProAspLeuValValLeuAsnSer----- 2168
Db 6478 ATCGAGGGGAGCGCGCTGAG-----TCGTTGCTGTGGCGCTCAACGCTGAGCGCGAA 6531
Qy 2169 -----ValIleGlnTyrPheProSerSerGlyTyrLeuAlaGlnIleAlaAspThr 2185
Db 6532 GGTTCGCGCGCTTTCATCTTCATCCAGT----- 6561
Qy 2186 LeuIleHisLeuProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThr 2205
Db 6562 -----TTCCGCTCTGTGCTGACACTGTTCACAAAGCC 6588
Qy 2206 -----AsnGlnHis-----PheLeuAlaAlaArgAlaIleHis 2216
Db 6589 CTCGCCATGCGCGCTGCGGAGCTGATCCGCTCAAGGAGTGTCTGCTCCGCTGCTGCTG 6648
Qy 2217 ThrLeuGlyIysAsnAlaThrIys-----AspAspValArgGlnIysMetAlaGluLeuGlu 2235
Db 6649 GCGGCTGTGCGGAGGTCGCGGAGTGGACATGATGTTGCGGAAATACCGCGAG----- 6702
Qy 2236 AspMetGluGluLeuLeuValGluProAlaPhePheThrSerLeuIysAspArgPhe 2255
Db 6702 ----- 6702
Qy 2256 ProGlyLeuValGlnHisValGlnIleLeuProIysAsnMetGluAlaValAsnGluLeu 2275
Db 6703 -----CAATGCTGCGAGAGCAACCCCGAAGGGGTTTCAACCTG 6741
Qy 2276 SerAlaTyrArgTyrAlaAlaValAlaHisValArgIysSerLeuGlyAspGluLeuVal 2295
Db 6742 GCGGAGAGG-----TCGCTCGCGCGCAACCTGGCG 6771
Qy 2296 LeuProValGluIysAsp-----AspTrpIle 2304
Db 6772 ATGAGATCTCCGCGCCCGCTGAGACAGCGTGGCGGAGGTGCTTTCGTCGCGCTGGATC 6831
Qy 2305 AspPheGlnAla 2308
Db 6832 GATGCGCGCGCA 6843

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RESULT 3
US-09-252-991A-9183
; Sequence 9183, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9183
; LENGTH: 6573
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; OTHER INFORMATION: (5574)
; US-09-252-991A-9183

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Alignment Scores:

| Pred. No. | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|-----------|---------|---------------------|------------------------|--------------|---------|----------|---------------|-------------|---------|-------|
| 3 | 466-162 | 1641.50 | 38.96% | 10.18% | 6573 | 571 | 317 | 758 | 633 | 59 |

US-09-482-788-2 (1-3129) x US-09-252-991A-9183 (1-6573)

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Qy 430 TyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeuGlnGlnPheGlyHis 449
Db 1339 TATGCCAGGATGCTGTCGAGGCTCGACCGCTGAGCGCTGCTGCGACACTGGCAAGAT 1398
Qy 450 LeuIleIysCysLeuGlnSerProLeuAspLeuSerMetAlaGluValAsnLeuMet 469
Db 1399 CTCCTGCGCGCATCTGTCGCGCAACCGGCG--CGCGCGTCCCGCGAGTTGCCGTGTG 1455
Qy 470 ThrGluTyrAspArg-----AlaGluIleGluSerTrpAsnSer 482
Db 1456 CTGAGCAGAGAGCGCATTCCTGCTGCGGCGCTGCGGCGGCAAGAACCGGCAAGGCTGG 1515
Qy 483 GlnProLeuGluValGlnAspThrLeuIleHisGluMetLeuIysValAlaSerHis 502
Db 1516 TTGCGCGCGCTGATCGATGATCAGATCAGAGACAGGCGCGCTGCGT----- 1563
Qy 503 SerProThrIysThrAlaIleGlnAlaTrpAspGlyAspTrpThrTyrSerGluLeuAsp 522
Db 1564 ---CGCGAGCGGAGACGACGCGCTGAGGCGGAGCGGCTGAGCTTACCGCGAGCTTAC 1620
Qy 523 AsnValSerSerArgLeuAlaValAlaHisIleIysSerLeuGlyLeuArgAlaGlnAla 542
Db 1621 GCCCGGCCAATGCTCTGCTCACTGCTGATAGCGGTGGCTC---GGTCCGATGTG 1677
Qy 543 IleIleProValTyrPheGluIysSerIysTrpValIleAlaSerMetLeuAlaValLeu 562
Db 1678 CTGGTGGAATCCCGCTGAGCGCTGCGTGAATGATGATGATGATGATGATGATGATGATG 1737
Qy 563 LysSerGlyAsnAlaPheThrLeuIleAspProAsnAspProProAlaAlaGlnAlaGln 582
Db 1738 AAGCGCGTGTGCTATGTCGCGTGAACCGACCTATCCGAGAGACCGTTGGCTGAC 1797
Qy 583 ValValThrGlnThrArgAlaThrValAlaLeuThrSerIys----- 596
Db 1798 ATGCTGAGAGACAGCGCGCTGCGCTGCTGACCGAGAGCATTTGCTGCGCGGCTG 1857
Qy 597 ---LeuHisArgGluThrValGlnIysLeuValGlyArgCysValAlaValAspAspGlu 615
Db 1858 CTTTGACAGAA-----GGGCTGAGAGTGTCTCATACGACCGC 1896
Qy 616 LeuLeuGlnSerValSerAlaSer---AspAspPheSerSerLeuThrIysSerGlnAsp 634
Db 1897 CTGAAACGAGACGATGCTGCTACGAGATGCTCGGTGTGAACCTGCGCGCGAGAAC 1956
Qy 635 LeuAlaTyrValIlePheThrSerGlySerThrGlyAspProIysGlyIleMetIleGlu 654
Db 1957 CTGCGCTATGATCTACACTCGGCTCCAGCGGAAACCCAGGCGGCTGGCATGAC 2016

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QY 655 HlsARGAla-----PheSerSerCyAlaLeuYsPheGlyAlaSerLeuGlyIle 671
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 Db 2017 CAtGCCGCGCTTGCGGAGTTCTCGCGATGCCAGGTGATTATTCGCG-----CTC 2067
 QY 672 AsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCySLeuLeuGlu 691
 |||||
 Db 2068 ACCCGGAGGATGGATATTCAGATTGCCACCTGAGCTTCAGCGCTTCGTCAGACAG 2127
 QY 692 IleMetThrThrIleuAsnGlyGlyCySValCySValIleProSerAspAsp-----Asp 709
 |||||
 Db 2128 CTCTATTCGGCGCTGACCCCTGGTGGCTGGCTGGCTGGCTGGCTGGCGACCTTCGGGAT 2187
 QY 710 ArgMetAsnSerIleProSerPheIleAsnArgTyArgAsnValAsnTrpMetMetAlaThr 729
 |||||
 Db 2188 ACCGGAGAGTGTATGGCAGATAGTCAGACAG-----GGCGTACCCCTGGCGACCTGCC 2244
 QY 730 ProSerTyMetGlyThrPhe-----SerProGluAspValProGly 743
 |||||
 Db 2245 ACCGCGTACTGGAACTGTCTCTGCTGCATGCTGCTGCGACGACGACGCGCTTCCTACGGT 2304
 QY 744 ---LeuAlaThrIleuValAlaGlyGluGlnMetSerSerSerValAsnAlaIleTrp 762
 |||||
 Db 2305 GCCCTGGCGAGATCCACATCGGTGGGAGAACCTGCACTGGAGGGCGCGAAGCTTGG 2364
 QY 763 AlaPro-----LysLeuGlnLeuLeuAsnGlyTyArgGlnSerGluSerSer 778
 |||||
 Db 2365 CGGCAAGCCGCGATGGCGCCGGTGGAGTTGCTCAATCCATATGACCGACGACGACGACG 2424
 QY 779 SerIleCyPheAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAla----- 796
 |||||
 Db 2425 GTGGTGTCCAGCGCTTCGATTGTCGCGCAGAACCCCGGGGGGCAATGCGCAGTCT 2484
 QY 797 -----ValGlyAlaHisSerTrpValIleAspProAsnAspIleAsnArg 811
 |||||
 Db 2485 ATGCGCCAGCGCTACCCGCGCTGACCGTGTGGTGAATGAACAT-----CTCGGC 2538
 QY 812 LeuValProIleGlyAlaValAlaGlyLeuValIleGluSer---ProGlyIleAlaArg 830
 |||||
 Db 2539 CTACTGCGCTGAGGCGGTGAGCGATTCATATATTCGACCGCTGCGCGGCTGGCCGT 2598
 QY 831 AspTrpIleValProProProGluLysSerProPheThrAspIleProSerTrp 850
 |||||
 Db 2599 GCGCTACACAGATCGCGCGCTTGACCGCGCGCTTCCTGCGCGAC-----CCCTTCGCG 2655
 QY 851 TyrProAlaAsnThrPheProAspGlyAlaLysLeuTyArgThrArgIleAspLeuAlaArg 870
 |||||
 Db 2656 GAACCG-----GGCTCAAGGCTTACCGGACCGGCGACCTGGCCGCG 2697
 QY 871 TyrAlaSerAspGlySerIleValCySLeuGlyTyArgIleAspSerGlnValLysIleArg 890
 |||||
 Db 2698 CGACGCGGTACCGCGGTGATCGATCATGGGGGTGCCGACCATCGATCGATGAAGATCCG 2757
 QY 891 GlyGlnArgValGluLeuGlyAlaIleGlyThrHisLeuArgGlnGlnMetProAspAsp 910
 |||||
 Db 2758 GCGCTCGCGATCGAGTGGGGAGGTGAGAACCGCGCTCATG-----GAC 2802
 QY 911 LeuThrIleValAlaGluAlaThrLysArgSerGlnSerAlaAsnSerThrSerLeuIle 930
 |||||
 Db 2803 TTGAGAGGAATGACCGAACGCG-----GCGCGCTTCGCGCTGACGCGTCAACTGTGT 2853
 QY 931 AlaPheLeuIleGlySerSerTyRheGlyAsnArgProSerAspAlaHisIleLeuAsp 950
 |||||
 Db 2854 GCGTACTGGTGGCTGAGGG-----GGC 2877
 QY 951 HisAspAlaThrLys-----AlaIleAsnIleLysLeuGlnGlnVal 964
 |||||
 Db 2878 GAGAGACGAGACTCGCCAGCGCGCTTGGCGAGCGTATCCGACAGCGGTACGGCGCTCG 2937
 QY 965 LeuProArgHisSerIleProSerPheTyRileCyMetLeuGlnLeuProArgThrAla 984
 |||||
 Db 2938 CTACCGGACTACATGCGCTCGCACTGTCTTCCTCGACGCGCGCGCTGACGCTCA 2997
 QY 985 ThrGlyLysIleAspArgArgLeuArgIleMetGlyLysAspIleLeuAspLysGln 1004

Db 2998 AATGGCAAGCTGAGCCGCTCG-----GGCTGCCGACCGCG 3033
 QY 1005 ThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAspThrAla 1024
 |||||
 Db 3034 GATGCCGCGCTTGAATGACACGACACCATGGCGCGCGCGCGCTGGAGAAAGACCTG 3093
 QY 1025 AlaLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAsnVal 1044
 |||||
 Db 3094 GCC-----GCGATATGGGCGAGTTGCTGGCGCTGCA-----CGGGTTC 3132
 QY 1045 GlyAlaThr-----PhePheGluLeuGlyGlyAsnSerIleThrAlaIleLysMetVal 1062
 |||||
 Db 3133 GCGCTTACCGCAACTTCCTTCGAATTGGCGGACACTCGCTGCGGACGCGCGCTGCTG 3192
 QY 1063 AsnMetAlaArg---SerValGlyMetAspLeuLysValSerAsnIleTyRglnHisPro 1081
 |||||
 Db 3193 TCGCGATTGCGCAGATTCGTGATGATGATGATGATGATGATGATGATGATGATGATG 3252
 QY 1082 ThrIleuAlaGlyIleSerAlaValAlaValLysGlyAspProLeuSerTyRThrLeuIlePro 1101
 |||||
 Db 3253 GTCTGCGAGGATTCGTGCGAGAGCTGCGGAGAAACCGCGGAGTTCGCGCATATG 3312
 QY 1102 LysSerThrHisGluGlyProValGlnGlnSerTySerGlnGlyArgLeuTrpPheLeu 1121
 |||||
 Db 3313 CCGGTACCGCGAGCAGCGCGCTGCGCTGCTATGACAGAGCGCAGTGGTCTC 3372
 QY 1122 AspGlnLeuAspValAlaGlySerLeuTrpTyRleuIleProTyRAlaValArgMetArgGly 1141
 |||||
 Db 3373 TGGCAATTTGACCGGAGACCGCGCGCTTACATTCGCCCGCGCTGCGCTTGGCGGC 3432
 QY 1142 ProValAsnValAspAlaLeuArgArgAlaLeuAlaIleuGlnGlnArgHisGlyThr 1161
 |||||
 Db 3433 GCGCTGATGTCTGCGCGCTACAGCGCATGTTGAGAGCGCTTCGACAGCGCTACGATCG 3492
 QY 1162 LeuArgThrThrPheGluAspGlnAspGlyValGlyValGlnIleValHisGlyLysLeu 1181
 |||||
 Db 3493 TTGGGTACCGCGCTTCGCGCAGAAAGCGCTGATCGATCGATGAGGTGATGCGCATGGG 3552
 QY 1182 SerGluGlnMetLysValIleAspLeuCyArgly---SerAspLeuAspProPheGluVal 1200
 |||||
 Db 3553 CAGTTGACAGGTTTCCCGGCATAGCTGCGCATGTCGATGATGATGATGATGATGATGATG 3612
 QY 1201 LeuAsnGlnGluGlnThrThrProPheAsnLysSerSerGlnAlaGlyTrpArgAlaThr 1220
 |||||
 Db 3613 GTCGAACGAGATGGCAGAGCCCTTGACTTACAGCGGATGCGCTGCTGCGATGATGATG 3672
 QY 1221 LeuLeuArgLeuGlyIleAspAspHisIleLeuThrIleValMetHisIleIleSer 1240
 |||||
 Db 3673 CTGTTGAAATGGGTCCGAATGACATGCTGTGATGATGATGATGATGATGATGATGATG 3732
 QY 1241 AspGlyTrpSerIleAspValIleuArgArgAspLeuAsnGlnLeuTyRSerAlaIleLeu 1260
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 Db 3733 GACGTTGTGTGATGACGTTGATGTGTGAAAGATGTGTCCAGCTTACGCGCGCTAC-- 3789
 QY 1261 LysAspSerTyAspProLeuSerAlaLeuThrProLeuProIleGlnTyRSerAspPhe 1280
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 Db 3790 -----AGCAAGGGGCGCGAAGCGCGCTGCGCGCTGCGCGATACGATTCGCGACTAT 3843
 QY 1281 AlaLysTrpGlnLysAsp-----GlnPheIleGlnGlnGlnGlnLeuAsnTyRTrp 1298
 |||||
 Db 3844 GCGGTGCGGAGCGCGAATGAGATGAGAGCGCGGAGAGGAGGAGCGCGCATGCTACCTG 3903
 QY 1299 LysLeuGlnLeuLysAspSerSerProAla---LysIleProThrAspPheAlaArgPro 1317
 |||||
 Db 3904 ATCGCGCTGCGGTGGCGAAGCGCGCTGCTGAGCTGAGCTGCGCTTGCATGCTGCCGCTCT 3963
 QY 1318 AlaLeuLeuSerGlyAspAlaGlyCySValHisIleValThrIleAspGlyGlnLeuTyRgln 1337
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 Db 3964 GCGGAGCAGAGCTTTCGCGCGCGCGCGCTGAGTTCGATCTGCGCGCGAGCGGCGGACG 4023
 QY 1338 SerLeuArgAlaPheCySAsnGlnHisAsnThrThrSerPheValValLeuLeuAlaAla 1357
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QY 2034 TRGlnAspHisPheGluSerGlyMetYrSerAspIleGlyGluIleAspProSerThr 2053
 DB 6007 -----CCGGGTGGC 6015
 QY 2054 ILeGlySerAspPheGlyGlyTrpThrSerMetYrAspGlySerGluIleAspPheAsp 2073
 DB 6016 GTGGGCGCAGCATGTGGCTTAC----- 6039
 QY 2074 GluMetHisGluTrpLeuGlyGluThrThrArgThrLeuHisAspAsnArgSerLeuGly 2093
 DB 6039 ----- 6039
 QY 2094 AsnValLeuGluIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAspSerArgLeu 2113
 DB 6039 ----- 6039
 QY 2114 GluSerYrValGlyLeuGluProSerArgSerAlaAlaIlePheValAsnLysAlaThr 2133
 DB 6039 ----- 6039
 QY 2134 GluSerIleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIle 2153
 DB 6039 ----- 6039
 QY 2154 GlyGlnValAspAspLeuHisProAspLeuValValLeuAsnSerValIleGlnTrpPhe 2173
 DB 6040 -----GTGGTGGCGCCAGCGC 6054
 QY 2174 ProSerSerGluTrpLeuAlaGluIleAlaAspThrLeuIleHisLeuProAsnValGln 2193
 DB 6055 CCGGCGC-----GTGGCGGATTCG-----CCGGAAGCCGACG 6084
 QY 2194 ArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGluHisPheLeuAlaAlaArg 2213
 DB 6085 -----GCGGAGTCCGCGCGCAG----- 6102
 QY 2214 AlaIleHisThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLysMetAlaGlu 2233
 DB 6102 ----- 6102
 QY 2234 LeuGluAspMetGluGluLeuLeuValGluProAlaPhePheThrSerLeuLysAsp 2253
 DB 6102 ----- 6102
 QY 2254 ArgPheProGlyLeuValGluHisValGluIleLeuProLysAsnMetGluAlaValAsn 2273
 DB 6102 ----- 6102
 QY 2274 GluLeuSerAlaTrpArgTrpAlaAlaValAlaHisValArgGlySerLeuGlyAspGlu 2293
 DB 6102 ----- 6102
 QY 2294 LeuValLeuProValGluLysAspAspTrpIleAspPheGlnAlaAsnGlnLeuAsnGln 2313
 DB 6102 ----- 6102
 QY 2314 LysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValSerLysIle 2333
 DB 6102 ----- 6102
 QY 2334 ProPheGluIleThrAlaPheGluArgGlnValValAlaSerLeuAsnSerAsnIleAsp 2353
 DB 6102 ----- 6102
 QY 2354 GluTrpGluLeuSerThrIleArgSerSerAlaGluGlyAspSerSerLeuSerValPro 2373
 DB 6102 ----- 6102
 QY 2374 AspIlePheArgIleAlaGlyGluAlaGlyPheArgValGluValSerSerAlaArgGln 2393
 DB 6102 ----- 6102
 QY 2394 TrpSerGlnAsnGlyAlaLeuAspAlaValPheHisHisCysCysSerGlnGlyArgThr 2413

DB 6102 ----- 6102
 QY 2414 LeuValAsnPheProThrAspHisHisLeuArgGlySerAspLeuLeuThrAsnArgPro 2433
 DB 6102 ----- 6102
 QY 2434 LeuGlnArgLeuGlnAsnArgIleAlaIleGluValArgGluArgLeuArgSerLeu 2453
 DB 6103 -----TTGAAGACGGCGCTGCCGACGCC 6126
 QY 2454 LeuProSerYrMetIleProSerAsnIleValValLeuAspLysMetProLeuAsnAla 2473
 DB 6127 CTGCGGGAATACATGAGGCGCATCGACCTGTGTCTGGCGCGGATGCCGCTGACGCCG 6186
 QY 2474 AsnGlyLysValAspArgGlyGluLeuSerArgArgAlaLysValValProLysGlnGln 2493
 DB 6187 AACGGCAAGCTGACCGCAAGGCGCTGCCCGCGGATGCCGCTGTGGACGAGTC 6246
 QY 2494 ThrAlaAlaProLeuProThrPheProIleSerGluValGluIleLeuGlyGluGlu 2513
 DB 6247 TACGTGGCGCGCGCA-----AGCATCTGAGCAACAGCTCGCGGGATC 6291
 QY 2514 AlaThrGluValPheGlyMet---LysValAspIleThrAspHisPhePheAsnLeuGly 2532
 DB 6292 TGGCGCGAGGTCTGCAATTGCAACAGGTGGGTGTCGACACAACTTCTGAGCTTGGC 6351
 QY 2533 GlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnArgLeuLysValArg 2552
 DB 6352 GGGCACTCGTGTGGCGCACCCAGGTGATGGCGCTACGCAACACATGCACTGGAC 6411
 QY 2553 IleThrValLysAspValPheAspHisProValPheAlaAspLeuAlaSerValIleArg 2572
 DB 6412 GTCCCGATCAAGTCGATGTTACCCGCGGACACCTGGGTGATCTTCCACGCGCTGAG 6471
 QY 2573 GlnGlyLeuGlyLeuGlnGlnProValSerAspGlyGlnGlyLysAspArgSerAlaHis 2592
 DB 6472 ACCCTCAAGCGCAGAGCGCGCGTGGAAGATGCCCTGTCAATCTCGAGGCGC--- 6528
 QY 2593 MetAlaProArgThrGluThrGluAlaIleLeuCysAspGluPheAlaLysValLeu 2611
 DB 6529 -----CTCAACAGCTCATCTGCGGATCACTTGAAATACTGATT 6567

RESULT 4

US-09-252-991A-6997
 ; Sequence 6997, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 6997
 ; LENGTH: 10023
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-6997

Alignment Scores:

Pred. No.: 2,44e-159 Length: 10023
 Score: 1618.00 Matches: 778
 Percent Similarity: 39.10% Conservative: 454
 Best Local Similarity: 24.69% Mismatches: 1231
 Query Match: 10.03% Indels: 694
 DB: 4 Gaps: 118

US-09-482-788-2 (1-3129) x US-09-252-991A-6997 (1-10023)

65 LeuAspLeuSerAlaIleGlyHisAlaValTyrAspValPro----- 79
 1669 ATGATCCGACGAGC-----GCCGCTTCAACATCCCGCGCGCTCGCGCTG 1716
 QY 80 ---ThrAspIleAspIleSerArgPheAlaLeuAlaTrrLygIuIleValAsnGlnThr 98
 Db 1717 CGCGCGACGCTGGCGAGAGCGCGCTCGCGCGAGCTTCCAGCGCGCTGTGCAACCGCAC 1776
 QY 99 ProAlaLeuArgAlaPheAlaPheThrSerAspSerGlyThrSerGlnValIleLeu 118
 Db 1777 GAAGCGTGGCGACGCGCTTCTCGAGCGGACCGCGCGCTTCCAGCGATGACGAG 1836
 QY 119 LysAspSerPheValPheSerTrpMetCysTrp-SerSerSerSerProAspGluVal 138
 Db 1837 CGCGCGACGATTC-----GCCTGGAGATTCTGTGACCTCGCGCGCTG-GC 1880
 QY 138 ValArgAspGluAlaAlaAlaAla----- 147
 Db 1881 CGAGCAGCAGACGCGCGCGCTCGCGCGAGCGCGGAGCGGAGCGGAGCGCGCTT 1940
 QY 148 -----SerGlyProArgCysValAsnArgPheValLeuLeuGlnAspMetGlnThr 164
 Db 1941 CGACCTGGAAGAGCGCGCTGCTGCGG-----GTACGCTGTGTGCGCTGACGAC 1994
 QY 164 LysCysGlnLeuValTrrThrPheSerHisAlaLeuValAspValThrPheGlnGlnArg 184
 Db 1995 GAGAGCAGACGCTGCGGCTGACCTCGCATCAGATGTCGCGCATGTTGTCGTGAACCT 2054
 QY 184 GValLeu-----SerArgValPheAla----- 191
 Db 2055 GCTGCTGACGAAATTCGCGGCTGTACGCGAGACCTGCGCGCGCGCGCGCGACCT 2114
 QY 191 ----- 191
 Db 2115 GCGCGCGCTGAACTGACCTACGCGGAGTTGCTGCTGCGACAGGAGTGGCTGACGC 2174
 QY 192 -----AlaTyrLysHisGlnLys-----AspThrHisArgPr 202
 Db 2175 GCGCGAGGCGCGCGCGCACTGCGCTTACGCGGGAACGCTGCGGACAGC-----GGCGC 2211
 QY 202 GglnThrProGlnSerSerAspAlaThrAspThrAspSerGlnSerValIle 222
 Db 2232 GGTGCTGGAATCGCCACCGCATCCGCGGACGCGCGCGCGCGCTGCGCGCGCGCG 2291
 QY 222 rMetSerCysGlnAspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnArg 242
 Db 2292 CTACAGCTCGCGGTCGACGAGGCCCTGCGCGCGGCTATCCGCGAGCGCGCGCTG- 2348
 QY 242 PLeuAsnAlaSerValPheProHisLeu-----SerAspHisLeuMetValProAsnPr 260
 Db 2349 CATGAGCGCAGTCTCTTCATGTCGTCGCGCGCGCTCCAGCGCTGCTGCATCCCA 2408
 QY 260 oThrThrThrAlaGlnHisArgIleThrPhePro--LeuSerGlnLysAlaLeuSerArg 279
 Db 2409 CACGCGGACGAGCGAGATCCGCGATCGCGCTGCGCGGACCGCGCGCGCTGAGAC 2468
 QY 279 nSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArgTyrThr----- 295
 Db 2469 CAGAGGCTGTGCGCTTCTTCAACACCTGTGCTGTGCGCGGACCGCGCGCGCG 2528
 QY 296 -----HisSerAspGluAlaLeuPheGlnValAlaValThrG 307
 Db 2529 CAGCGCTTGGCGCGCATTCTCGCGGAGCTCGCGGAGCGACCTCGCGCGCGCGCA 2588
 QY 307 uGlnSerLeuProPheAspLysHisTyrLeuAlaAspGlyThr--TyrGlnThrValAl 326
 Db 2589 CAGAGACCTGCGCTTCCACGAGTGTGCGCGCTGCGGCGCGGCGCGCGCTGTTCA 2648
 QY 326 aProLeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIleSe 346
 Db 2649 GGTGCTGTTCACCAACGAGCGAGCGACCTG-----TCGCGGTGCG 2690

346 rSerTyrAspAspArgLeuGlnHisLeuAlaPhePheGlyLeuArgAspIleArgAsnThr 366
 Db 2691 CGGAGTCCCGCGCGCTGCTCGCGACGAGCTGCGCTGGACAGCGCGCA----- 2739
 QY 366 rGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySe 386
 Db 2740 -----GCCAAGTTTCAGCTGCA----- 2757
 QY 386 rHisValAsnAsnGlyIleAsnGlyPheLeuGlnGlnIleThrGlnSerSerHisPheMe 406
 Db 2757 ----- 2757
 QY 406 tProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlnSerSerGlyAlaLeuLe 426
 Db 2758 -----TCGACAGACGAGAGAGAGACGCTGCGCGCTGCGCTGAC 2792
 QY 426 uValAlaTyr--TyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeuLeuG 445
 Db 2793 CTGAAATTCGACTACCGCGCGACCTTTCGACGAGCGGACGATCCGCGTTTCGCGC 2852
 QY 445 nGlnPheGlnHisLeuLeu-----LysCysLeuGlnSerPr 457
 Db 2853 GCAATTCAGAGCTGCTGCGCGCGCGCGGAGCGCGGAGCGCGCGCTGCTC----- 2904
 QY 457 oLeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGluTyrAspArgAlaGluI 477
 Db 2905 -----GCCATATCGCCCTGTGTGTCGACGCGGACGCGCGCGACCT 2945
 QY 477 eGlnSerTrpAsnSerGlnProLeuGlnValGlnAspThrLeuLeuHisIleGlnMetLe 497
 Db 2946 CGCGGATGGGAGCGCGCGCTGCGAGCGCGCGCGCGCTGCGCGGAGCTGCTGGA 3005
 QY 497 uLysAlaValSerHisSerProThrLysThrAlaIleGlnAlaTrrAsp--GlyAspTr 516
 Db 3006 GCGGCACTGTGACAGTCCCGCGGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCT 3062
 QY 516 rThrTyrSerGlnLeuAspAsnValSerSerArgLeuAlaValHisIleLysSerLeuG 536
 Db 3063 CGGCTACCGCGGACTGACCGCGCGGCGGACCGCGCTGCGCGGACTGCGCGGACGAGG 3122
 QY 536 yLeuArgAlaGlnGlnAlaIleIleProValTyrPheGlnLysSerLysTrpValIleAl 556
 Db 3123 CGTC--GGCGCGGACGTGCGGATGCGATGTCGCGCGGCGGCTTCCGCGGACTGCGGT 3179
 QY 556 aSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIleAspProAsnAspPr 576
 Db 3180 CGGTCTGCTGCGATGCTCAAGCGCGGCGCGCTGCTGCGCGCTGCGCGGACTGAC 3239
 QY 576 oProAlaArgThrAlaGlnValAlaThrGlnThrArgAlaThrValAlaLeuThrSerLy 596
 Db 3240 CAGGAACTGCTGCTGCTGCTGCTGCGCGGACGCGGCTGCTGCTGCTGCTGACCGCAGC 3299
 QY 596 sLeuHisArgGlnThrValGlnLysLeuValGlyArgCysValValValAspAspGlyLe 616
 Db 3300 CATCTGTTGACGCGCTGCTGCGCGGAGCGGCTGACCGCGATGCTGCTGACGACCT 3359
 QY 616 uLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrLysSerGlnAspLeuAl 636
 Db 3360 CAAGCTGCAACTGCGCGCGGCGGACGCGCGGCTGCACTGCGCGGCACTGCTGCG 3419
 QY 636 aTyrValIlePheThrSerGlySerThrGlyAspProLysGlyIleMetIleGlnHisArg 656
 Db 3420 CTAGCTCATTAACCTCGCGCTCAACCGCGCGGCGGAGCGGTGGGCAACCGCACGCG 3479
 QY 656 gAlaPheSerSerCysAlaLeuLysPheGlnAlaSerLeuGlyIleAsnSerAspThrArg 676
 Db 3480 GCGCGTGGCGAGCGCGCTGCAATGATGACGACCGACCTACCGCTTCCACGCGACGAG 3539
 QY 676 gAlaLeuGlnPheGlyThrHisAlaPheGlnAlaCysValLeuLeuGlnIleMetThrThrLe 696
 Db 3540 GCTGATGCAAGAGCGCGGCTGAGCTTTCGACGTCGTGCGGTGAGTGTGCGCGCT 3599

Db 5598 CGGCGCGGTGGCAACCGCATCCGCGCGGAGAGCGAAAGGCTGATCGGCGCTTCTCA 5657
 Qy 1394 nThrgInCymerArgIleAenIleAerNleAerPhThreGlyThrLeuIleAenG 1414
 Db 5658 TACCCAGGTGTGGCGCGCGCTCGAGCAGATGAGTCGCGGAGCTGCTGAGCA 5717
 Qy 1414 nValYValThThrThrAlaAlaPheGluAenGluAerPleProPheGluValVa 1434
 Db 5718 GGTGCGGACACCGTGTATGATGCGGCGGACGACGCTGCGGCTTCCGACGCTGCT 5777
 Qy 1434 lserAlaLeuGluProGlySerArgAerPleuserSerThrProLeuAlaGluLeuPhe 1454
 Db 5778 GGAAGCTTCGACACT---CGGCGAGCGCGCTTACACCGCTGTGTTCCAGGAGATG 5834
 Qy 1454 eAlaValHisSerGlnYValPheLeuGlyArgPheLeuPheGlnGlyLeuGluSerValPr 1474
 Db 5835 CAACGTCAG-----CGCTGGAGTTCAGAGACCGCGCAACTGGC 5876
 Qy 1474 ovalProSerLeuAlaTy-----ThrArgPheAerMetGluPh 1487
 Db 5877 CGGGATACCGTCCAGTACATCCGCAACGATGCGGCGGCGCAAGTTCCGACTCAACT 5936
 Qy 1487 eHleuPheGlnGluThrAerPheSerLeuYsGlySerValAerPheAlaAerGluLeuPh 1507
 Db 5937 TGAAGTACCGACTCGACACGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5996
 Qy 1507 eLywMerGluThrValGluAenValArgValPhePheGluIleLeuArgAenGlyLe 1527
 Db 5997 CGACGACCGCGGATCGCGGATGCGCGGACACTGGAGACACTGCTGGAGGCGCTGCT 6056
 Qy 1527 uGlnSerSerArgThrProValSerIleLeuProLeuThrAerGlyIleValThrLeuG 1547
 Db 6057 GGGCGACCGCGGCGGCGGCTGCGCAATTGCGCTG-----TTCGCGCGCGAGGA 6107
 Qy 1547 uLywLeuAerValLeuAenValYsHleAerTyProArgGluSerSerLeuAlaAs 1567
 Db 6108 GCGGACCAACTGCTGCTCGCGCGGCGCGCGG-----GAGGAGGCGCTTCCAGGA 6158
 Qy 1567 P-----ValPheGlnThrGlnValSerAlaTyProAerPheLeuAlaVala 1583
 Db 6159 CACCTCATAGCGCTGTTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGAC 6218
 Qy 1583 lAerSerSerCywArgLeuThrTyThrGluLeuAerArgGlnSerAerPleLeuAlaG 1603
 Db 6219 CTTCGCGGACAGACCTGAGCTATGCGCAACTGAGTCCGCGCTCAACCTCTGCGGCG 6278
 Qy 1603 yTrPLeuAerArgAerSerMetProAlaGluThrLeuValAlaValPheAlaProAerSe 1623
 Db 6279 GCTCTGCGGAGTACGCGCGCTGCGCGCGGAGTCCGCGCTGCGCTGCGGAGCGTTT 6338
 Qy 1623 rCywGluThrIleValAlaPhePheGlyValLeuYsHleAenLeuAlaTyIleuProLe 1643
 Db 6339 GCTGGAATGATGTGCTCGGCGCTGCGGATCTCTCAAGCGCGCGCTTACGTCGCGCT 6398
 Qy 1643 uAerValAerSerProSerAlaArgValGlnAerPleLeu-----SerGlyLeuSerG 1661
 Db 6399 GGAACCCGGAATATCCGCTGAGCGCTTCGATATCATGATCGAGGACAGCGCGCTGACCC- 6456
 Qy 1661 yProThrIleValIleuGlnIleGlyHleAerThAlaProProAerPleGluValThrAenVa 1681
 Db 6457 -----CTGCTGCTGACCCAC----- 6471
 Qy 1681 lGluPheValArgIleArgAerAlaLeuAerAerSerAerAla----- 1695
 Db 6472 -----GCGGCGCTGTTGAGGCGCTCGGCGGAGCTGCGGCAAGCGCGCTGCTG 6524
 Qy 1696 -----AerGlyPheGluValIleGluHleAerSerThrTywProSerAlaThrSe 1712
 Db 6525 CCTCGAGAGAGACGCGCGCGCTGAGCGCGGAGACCGCGCGCTGAGCGAGCTGAG 6584
 Qy 1712 r-----LeuAlaTyValLeuTyThrSerGlySerThrGlyAerProLeuG 1728
 Db 6585 GGGGCGGACGACCAAGGCTGATCTATCTCGGCTTCAACCGGCAAGCGGAAAGG 6644

Qy 1728 yValMetIleGluHleArgValIleIleArg-----ThrValThrSerGlyCywIlePr 1746
 Db 6645 CGTGGCGGTCTCCACGCGAGATCCGATGCACTGCGCGCGGCTGATCGAGTCTTC-- 6702
 Qy 1746 oAenTyProSerGluThrArgMetAlaHleMetAlaThrIleAlaPheAerGlyAlase 1766
 Db 6703 -GGCATGCGCGCGAGATTTGCAACTGCACTTATTCATTAACATCACTGCTGCGAG 6761
 Qy 1766 rTyGluIleTySerAlaLeuLeuPheGlyArgThrLeuVal----- 1780
 Db 6762 CAGAGCGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6821
 Qy 1781 -----CywAlaAerTywThrThrLeuAerAlaArgAlaLeuYsAerValPhePh 1798
 Db 6822 GTGGGCGCGGAGAAATTCGACGATGATCCGCGGAGGCGCTGAGCATCTCGGCTT 6881
 Qy 1798 eArgGluHleValAerAla-----AlaSerHleValThrSerSerGlnAerValPr 1816
 Db 6882 CACCCGAGCTACGCGGCGGACGCTCGCGGAGTGGCTGGAAGACGAGGCGGCACTTGC 6941
 Qy 1816 oLeuArgValProArgArgLeuSerArgThrLeuMetPhePheLeuValValThrAs 1836
 Db 6942 GCTGCGCATGTG-CATACCGCGCGGCGAGC-----GCTGA 6976
 Qy 1836 pSerThrAlaProAerAlaLeuAerAlaGlnGlyLeuTyGlnGlyValGlnCywTyAs 1856
 Db 6977 CCGCGAGCACCT---GCAACGATTCGCGAGGCTTCCGCGCGCTCG--TTCCTCA 7031
 Qy 1856 nGlyTyGlyProThrGluAenGlyValMet-----SerThrIleTyProIleAerSe 1874
 Db 7032 TGCCTACGACCGACCGAGCGGTGTCATGCGGCTGCGCTGCTGCTGCTGCTGCTGCTG 7088
 Qy 1874 rThnGluSerPheIleAenGlyValProIleGlyArgAlaLeuAerAerSerGlyAlaTy 1894
 Db 7089 ACTGAGAGAGGTCGCCGCGGCGGATCGGATCGGAGCGTGTGCGCGGCGGCGCTTA 7148
 Qy 1894 rValAlaAerProGluGlnGluLeuValGlyIleGlyValMetGlyGluLeuValValTh 1914
 Db 7149 CATCTGATGACGACACTGCGCTGCTGCGCGGCGGCGGCGGCGGCGGCACTTACGTCG 7208
 Qy 1914 rGlyAerGlyLeuAlaAerGlyTySerAerAerAerAlaLeuAerGluAerPheVa 1933
 Db 7209 CGGCGCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7268
 Qy 1933 lHleIleThrValAerAerGlnThrValYsAlaTyArgThrGlyAerArgValArgTy 1953
 Db 7269 GCCCGATCCCTTGGCTGCGGCGGCGGCGGCGGCTGATCCGACCGGCGGCGCTG 7328
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RESULT 5
US-08-222-617A-3
Sequence 3, Application US/08222617A
Patent No. 5882879
GENERAL INFORMATION:
APPLICANT: Veenstra, Annemarie E.
APPLICANT: Martin, Juan P.
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APPLICANT: Von Doehren, Hans
APPLICANT: Palisosa, Harriet
APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Acromonium chrysoeum
FEATURE:
NAME/KEY: CDS
LOCATION: 388..11526
OTHER INFORMATION: /function= "Enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
FEATURE:
NAME/KEY: CDS
LOCATION: 8050..8052
OTHER INFORMATION: /note= "NNN=GCC, AGU, AGC, UCU, UCC, UCA, or UCG;
OTHER INFORMATION: Xaa=Ala or Ser "
US-08-222-617A-3
Alignment Scores:
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Score: 1517.00 Matches: 730
Percent Similarity: 39.70% Conservative: 504
Best Local Similarity: 23.49% Mismatches: 1282
Query Match: 9.41% Indels: 593
DB: Gaps: 124

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| RESULT 6 US-08-222-617A-24 | | | |
| Sequence 24, Application US/08222617A | | | |
| Patent No. 5882879 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Veenstra, Annemarie E. | | | |
| APPLICANT: Martin, Juan P. | | | |
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| APPLICANT: Gutierrez, Santiago | | | |
| APPLICANT: Barredo, Jose L. | | | |
| APPLICANT: Von Doehren, Hans | | | |
| APPLICANT: Palissa, Harriet | | | |
| APPLICANT: Van Liempt, Henk | | | |
| APPLICANT: Montenegro, Eduardo P. | | | |
| TITLE OF INVENTION: A Method for Influencing Beta-Lactam | | | |
| TITLE OF INVENTION: Antibiotic Production and for Isolation of Large | | | |
| TITLE OF INVENTION: Quantities of ACV Synthetase | | | |
| NUMBER OF SEQUENCES: 27 | | | |
| CORRESPONDENCE ADDRESS: | | | |
| ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff | | | |
| STREET: 300 South Wacker Drive | | | |
| CITY: Chicago | | | |
| STATE: Illinois | | | |
| COUNTRY: USA | | | |
| ZIP: 60606 | | | |
| COMPUTER READABLE FORM: | | | |
| MEDIUM TYPE: Floppy disk | | | |
| COMPUTER: IBM PC compatible | | | |
| OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| SOFTWARE: Patentin Release #1.0, Version #1.25 | | | |
| CURRENT APPLICATION DATA: | | | |
| APPLICATION NUMBER: US/08/222.617A | | | |
| FILING DATE: 04-APR-1994 | | | |
| CLASSIFICATION: 435 | | | |
| ATTORNEY/AGENT INFORMATION: | | | |
| REFERENCE/DOCKET NUMBER: 97,157 | | | |
| INFORMATION FOR SEQ ID NO: 24: | | | |
| SEQUENCE CHARACTERISTICS: | | | |
| LENGTH: 11601 base pairs | | | |
| TYPE: nucleic acid | | | |
| STRANDEDNESS: single | | | |
| TOPOLOGY: linear | | | |
| MOLECULE TYPE: DNA (genomic) | | | |
| ORIGINAL SOURCE: | | | |
| ORGANISM: Acromonium chrysogenum | | | |
| FEATURE: | | | |
| NAME/KEY: CDS | | | |
| LOCATION: 388..11526 | | | |
| OTHER INFORMATION: /function= "Enzyme" | | | |
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| LOCATION: 8050..8052 | | | |
| OTHER INFORMATION: | | | |
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| Alignment Scores: | | | |
| Pred. No.: 1.71e-148 Length: 11601 | | | |
| Score: 1517.00 Matches: 730 | | | |
| Percent Similarity: 39.70% Conservative: 504 | | | |

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Query Match: 2
DB: 2

US-09-482-788-2 (1-3129) x US-08-222-617A-24 (1-11601)

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DB 3754
QY 274
DB 3814

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AGTGTGTGCACTACCCCTTCAATTCATCTTCACAGACGCTGTGGACGCTGTGCTCTCACTCT

```


| | | | |
|----|------|--|------|
| Db | 5884 | TTATGCTCAGAGACCTGCGCCGATTAACATGGTCTCTGGCGACCTGGTGGCCATGCGCAAG | 5943 |
| Qy | 980 | LeuProAlaThrAlaThrAlaThrGlyLysIleAspArgArgIleuArgIleMetGlyLysAsp | 999 |
| Db | 5944 | TTCCCGCGTACCGTGAAGGGGAGAGCTGATGCAAGGCGCTTGGCCGGTCCAGAGATACA | 6003 |
| Qy | 1000 | IleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProVal | 1019 |
| Db | 6004 | GTCGAGATGAC-----ATTGGCCACCG | 6027 |
| Qy | 1020 | PheAlaAspThrAlaAlaLysLeuHisSerIleThrValGlnSerLeuGlyIleAspPro | 1039 |
| Db | 6028 | CGTACCGAGGTGAGCCGATCTTACCTGGAGATCTGGTGTGAGCTGTTGGAGATACCGGTC | 6087 |
| Qy | 1040 | AlaThrValAsnValGlyAlaThrPhePheGlnLeuGlyIleAsnSerIleThrAlaIle | 1059 |
| Db | 6088 | GACAGGATCAGCATCTACAGTACTCTTCAAGTCTGGCGCGCGACAGTCTCAAGATGAC | 6147 |
| Qy | 1060 | LysMetValAsnMetAla--ArgSerValGlyMetAspLeuLysValSerAsnIleThr | 1078 |
| Db | 6148 | AAGCTGTCCTTGGTGGCCACTCGGAGCTCTCGATGGCCGTCAAGTGTCCGACATTGTC | 6207 |
| Qy | 1079 | GlnHisProThrIleAlaGlyIleSer----- | 1087 |
| Db | 6208 | AGCCATCCGATATCGAAGCCTTGCTCTACGTGATATACAGGGTTCGACAGAGTCAAG | 6267 |
| Qy | 1088 | -----AlaValIleLysGlyAsp--ProLeuSerThrLeuIleProLysSerThr | 1104 |
| Db | 6268 | GATGTGGCTGTGTGGAGAGGCGCGTCCAGTCTTGAATCCCCCTATCCCT----- | 6318 |
| Qy | 1105 | HisGlnGlyProValGlnGlnSerThrSerGlnGlyArgLeuThrPheLeuAspGlnLeu | 1124 |
| Db | 6319 | -----GCCAGAAAGACTCAATGTCATCAGAGTTC | 6351 |
| Qy | 1125 | -----AspValGlySerLeuThrPyrLeuIleProGlyAlaValArgMet | 1139 |
| Db | 6352 | GGCCATAGCGCGAGATGCTGGCT-----TACATGTGCTTTGGACCTCAGCTCAGCTT | 6405 |
| Qy | 1140 | ArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaIleGlnGlnArgHis | 1159 |
| Db | 6406 | CACCATGATGTCTGTCTCGAATCGCTTGAGAAAGCTCTGGCGGATGTGTCTCGAGACAC | 6455 |
| Qy | 1160 | GluThrLeuArgThr-----ThrPheGlnAspGlnAspGlyValGlyValGln--Ile | 1176 |
| Db | 6466 | GAGGCTCTCCGGACCTTGATCACCAGGACCCAGAAATCTCCGTGGACCTGCCAGAAAGTC | 6525 |
| Qy | 1177 | ValHisGlnLysLeuSerGlnGlnMetLysValIleAspLeu-----CysGlySerAsp | 1194 |
| Db | 6526 | CTCAGCGCGGAAGAGCGCAAAAGCTCTCTGTGTATGTTCTTGGCGCTGACCTCGGAG | 6585 |
| Qy | 1195 | LeuAspProPheGlnValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGlu | 1214 |
| Db | 6586 | ACGGAATGACGGGCGAGATGCCGAGAGTACCGCCACGCGCTTCAAGCTGACAGAGGA | 6645 |
| Qy | 1215 | AlaGlyThrArgAlaThrLeuLeuArgLeuGlyLysAspAsnIleLeu----- | 1231 |
| Db | 6646 | CTCCCGATTCATGACGCTGTACAGGTGTACGTATGGCCGAGGCTCAGCTTGGCC | 6705 |
| Qy | 1232 | ThrIleValMetHisHisIleIleSerAspGlyTyrSerIleAspValLeuArgArgAsp | 1251 |
| Db | 6706 | AGCATGTGCTGCCACATCTGGCGCTTGAACCGGTGTCATGGATGTGTTCACAGAGGAC | 6765 |
| Qy | 1252 | LeuAsnGlnLeuThrSerLeuAlaIleLeuLysAspSerLysAspProLeuSerAlaLeuThr | 1271 |
| Db | 6766 | TTGAGACGCTTCTATGCGCTTCATACGACAGACAAAG-----GCTGCCGCACTGCCA | 6819 |
| Qy | 1272 | ProLeuProIleGlnThrSerAspPheAla--LysThrGlnLysAspGlnPheIleGlu | 1290 |
| Db | 6820 | ACCGTCCGCGTGAATATAGAGATGTCCGATAGACACCGCGGCGCTCTCCGGCGGTAG | 6879 |
| Qy | 1291 | GlnGlnGlnGlnLeu--AsnTyrTrpLysGlnLeuLysAspSerSerProAlaLys | 1309 |

| | | | |
|----|------|--|------|
| Db | 6880 | CAACACCGCTGTTCTCCGGGAACTACTGGGCTGGCAAGCTCAGTGCATGAGGCGCTTTAT | 6939 |
| Qy | 1310 | ILProThrAraPheAlaArgProAlaLeuSerGlyAspAlaGlyCysValHisVal | 1329 |
| Db | 6940 | CTGGTCCCGGATCCGCTCCGACCGCGCCAGTTTGACTATACCGGGAACGATCTTCAGTCC | 6999 |
| Qy | 1330 | ThrIleArgIleGlyLeuTyrrGlnInsSerLeuArgIlePheCysAsnGlnHisAsnThrThr | 1349 |
| Db | 7000 | TCAACTACTCCCGAGACCAACCGCGCAGTGAAGAGCTGGCCAAAGCCGAGGGTTCAAGC | 7059 |
| Qy | 1350 | SerPheValValLeuLeuAlaAlaPheArgAlaAlaHisIrrArgLeuThrAlaValGlu | 1369 |
| Db | 7060 | CTTACACACCGTTGGGGGGCGGCGCTACTTCTTGCTTCTACACGTACACCAACACGCGG | 7119 |
| Qy | 1370 | AspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLeuGluAspIleIle | 1389 |
| Db | 7120 | GATATCACAGATGGTATATCCGCTGGCCACCGTAAACATCCGAGCTTGGATCGGCTGTC | 7179 |
| Qy | 1390 | GlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHisAspThrPheGly | 1409 |
| Db | 7180 | GGCTCTTTGGCACTTGGCTCCCTCTCGGGGTCAACGTCTCAGTCGCGAATTCATGGA | 7239 |
| Qy | 1410 | ThrLeuIleAsnGlnValIleValIeThrThrAlaAlaPheGluAsnGluAspIlePro | 1429 |
| Db | 7240 | ---CTTATCCAGGACAGTGCAGAAAGACTTGTGCATGCCAGATCCATCAGACTTGCCA | 7296 |
| Qy | 1430 | PheGluArgValValSerAlaLeuGlnProGlySerArgPheLeuSerThrProLeu | 1449 |
| Db | 7297 | TTCCAGAGAGATCACCAAGCTTCTTCAATGTG---CAGACATATCCACCGGCATCCCTT | 7353 |
| Qy | 1450 | AlaGlnLeuIlePhe-----AlaValHisSerGlnIleAspLeu | 1462 |
| Db | 7354 | CTCCAGGCGCGGTTCACCTGGGAAACGTACCCGCCAATGTCACAGAGAGACACTGCTT | 7413 |
| Qy | 1463 | GlyArgPheIlePheGlnGlyLeuGlnSerValProValProSerIleAlaIleThrArg | 1482 |
| Db | 7414 | CAGAGATCAAG-----CCGCGCTCGCTCTGCTTGGCGGCG-----AAG | 7455 |
| Qy | 1483 | PheAspMetGluPheHisIleuPheGlnGluThrAspSerLeuIleGlySerValAsnPhe | 1502 |
| Db | 7456 | TTTGATCTCAACGTCACGGTGAAAGAGAGCGCTCAATTCGGCTCAACGTCATTCACAT | 7515 |
| Qy | 1503 | AlaAspGluLeuPheIleCysMetGluThrValGluAsnValValArgValPhePheGluIle | 1522 |
| Db | 7516 | CTTACCAAGCTCTTTCGAGAGAGAACCGTTCAAGGGGTTCAGAAACCTTCATCTCTT | 7575 |
| Qy | 1523 | LeuArgAsn---GlyLeuGlnSerSerArgThrProAlaSerIleLeuProLeuThrAsp | 1541 |
| Db | 7576 | CTTGCACACACTGGCCCAACACAGAGCTTACGACCAAGCCTCTCGAAGCTGTGCGTTGAAGAT | 7635 |
| Qy | 1541 | GlyIleValThrLeuGluIleValLeuAspValLeuAsnValIleHisValAspIleProArg | 1561 |
| Db | 7636 | GGAGGTGTGATCCAGAGCGG-----ACTAACTTCAAGCCCTCAAGCCGGGAGCAGC | 7686 |
| Qy | 1562 | GluSerSerLeuAlaAspValPheGlnThrGlnValSerAlaIleProAspSerLeuAla | 1581 |
| Db | 7687 | GGAATTCATCTCCATGGGCTCTTGCAGAGACATCTGGCTCGACCCCGGACCGCATCGCA | 7746 |
| Qy | 1582 | ValValAspSerSerCysArgLeuThrThrTyrrThrGluLeu---AspArgGlnSerAspIle | 1600 |
| Db | 7747 | ATTGCTGACGGACACAGAGAGTCTCTGACTCCGAACTCAACGCGGGGCAACACAGCTC | 7806 |
| Qy | 1601 | LeuAlaGlyThrLeuArgArgArgSerMetProAlaGluThrLeuValAlaValPheAla | 1620 |
| Db | 7807 | GTACTATTGATCACTCTTCTGCCAGATATTGTAGACAGACACCGCATCGCTCTTTTG | 7866 |
| Qy | 1621 | ProArgSerCysGluThrIleValAlaPhePheGlyValLeuIleValAsnLeuAlaIle | 1640 |
| Db | 7867 | GACAAGAGCATCGATATGTATGTATGTCTCTCTCGACAGTTGGAAAGCGCGGTGCGCATAT | 7926 |
| Qy | 1641 | LeuProLeuAspValValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSer | 1660 |
| Db | 7927 | GTTGCCCTTGAACCGCATATTCGTGTGGAGAGGACTAGCTCATCTTGGAGAAATTAAGT | 7986 |

QY 1661 GLYProThrlleValleuilegLYHlaSPThrlaProProlleuValThlAsn 1660
 Db 7987 GCCAGACGCTCATCACCACTAGAAAGACACG---CCGAGGGAGGAAACAGTGCATAAT 8043
 QY 1681 ValGluPheValArglle-----ArgAspAlaLeuAsnSerAsnAlaSerGlyPhe 1698
 Db 8044 GTTCCANNNTGGCTTGCACAGCCCGAGACCTTACCTGCTTCAACCGACTCAAG 8103
 QY 1699 GluValIleGluHlaSerThrLysProSerAlaThrSerLeuAlaTYrValLeuTYr 1718
 Db 8104 GAAACCCGCAACGTCACGCAAGAACCGTCC-----GACCTCGCATATGTCATCTTC 8157
 QY 1719 ThrSerGlySerThrlArgProLYGlyValMetIleGluHlaArgValIleileArg 1738
 Db 8158 ACCTCGGAGAACACAGCAGCAAGCCGAGGGGTTCTGGTGAGACACAGAGGTAGTCCAG 8217
 QY 1739 ThrValThrSerGlyCysIleProAsnTYrProSerGluThrArgMetAlaHis----- 1756
 Db 8218 ---CTGGCAATTCCTCATCGACGAGTACTTCGCGCAAGACCAACGGGTCTCACGCCGTG 8274
 QY 1757 -----MetAlaThrIleAlaPheAspGlyAlaSerTYrValaSerTYrSerAlaLeuLeu 1774
 Db 8275 CTCTCTGTCGCAACTACGTCCTTCACTCTCTTGAACAGCTCTGCTCTCTGCTCTG 8334
 QY 1775 PheGlyArgThrlleuValCysValAspTYrMetThrlleuAspAlaArgAlaLeuLys 1794
 Db 8335 GGTGGAACAAGCTCATC---ATTCACACAGAGAGGGGTCTCACGACGAGGACTTCTAC 8391
 QY 1795 AspValPhePheArgGluHlaIleValAsnAlaIleSerIleValIleThrSerSerGluAsp 1814
 Db 8392 GACATCGCGCGCAGGAGGAAAGCTATCTCTACGCGGAGACCCCTCGGTGTCGACAG 8451
 QY 1815 ValProleu---ArgValProArgArgLeuSerArgThrlleuMetPhePheLeuVal 1833
 Db 8452 ATTGAGCTCTCCGCTCTGCGCGCAT-----CTTCACATGTCACCGCTGCG 8496
 QY 1834 ValThrlaSerThrlaProAspAlaLeuAspAlaGlnGlyLeuTYrGlnGlyValGln 1853
 Db 8497 GCGAGAGAGTTCACGCTAGTCAGATTGAGAAAGATGCGCTCCGCGGAGG---CAG 8553
 QY 1854 CysTYrAsnGlyTYrGlyProThrlGluAsnGlyValMetSerThrlleTYrProIleAsp 1873
 Db 8554 ATCAACAACCGCTATGGTATCAGTGA---ACGACCGGTATCAACATCATC 8601
 QY 1874 SerThrlleuSerPheIleAsnGlyValProIleGlyArgAlaLeu-----Asn 1889
 Db 8602 ACCACG-----TTCAAGGGCGATGCCCCCTTTACAAAGCACTCTGCCACGGATCCCC 8655
 QY 1890 AsnSerGlyAlaTYrValValaAspProGluGlnGluLeuValGlyIleGlyValMetGly 1909
 Db 8656 GGAAGTCACGTCATACGTCGTAACGACGACTTCAAGGCTCTTCAACGCTGTGGC 8715
 QY 1910 GluLeuValValThrlArgLysArgGlyLeuAlaArgGlyTYr---SerAspLYsAlaLeuAsp 1928
 Db 8716 GACCTCTACTTGGCGGGTGAAGCTGTGCTCGCGGTAACCTCAACGAGATGCCCTTACC 8775
 QY 1929 GluAsnArgPheVal-----HisIleThrlaAsnAspGluThrl 1941
 Db 8776 AAGGAGGATTCATCCCAACCTTTCTACGAGCCGAAACAGGCAAGTACAGTCCGCC 8835
 QY 1942 ValIleAlaTYrArgThrlArgLysAspArgValaArgTYrArgIleGlyAspGlyLeuIleGlu 1961
 Db 8836 CAGAGACTCATCAAGACTGAGATCTGTGGCTTCGCT---GGAACCCCAACATCTCGAG 8892
 QY 1962 PhePheGlyArgMetAspThrlGlnPheLYsIleArgGlyAsnArgIleGluSerAlaGlu 1991
 Db 8893 TATCTCGCGCGCAAGACACGACAGTCAAGCTGAGGGGCTTCGCAATCGAGCTCTCGAG 8952
 QY 1982 IleGluAlaIleLeuLeuArgAspSerSerValaArgAspAlaIleValIleGluGln 2001
 Db 8953 GTGCGGATGCCGTCTAGCATCTCTGCTTTAAGAGGCTCCGTCATCCCAAGTAT 9012

QY 2002 AsnGluAspGluAlaProGluIleLeuGlyPheValValaLeuAsp-HisAsnHlaSerGly 2021
 Db 9013 GACGAGGATGCG-----GAGTATTCACCAAGGCTCAGC 9045
 QY 2021 uAsnAspLYsGlyGlnSerAlaAsnGlnValGluGlyTYrGluAspHlaSerPheGluSerGly 2041
 Db 9046 GCCATGCTGTCTACTACAGCTTCACGCGCGGAACTGTGTGCGAAGCAT----- 9094
 QY 2041 yMetTYrSerAspIleGlyGluLeuAspProSerThrlleGlySerAspPhe---LYsGly 2060
 Db 9095 -----CGAGTATCCGAGACACCTGACCGCAACCTTCCCGCTTAC 9135
 QY 2060 TYrThrlSerMetTYrAspGlySerGluIleAspPheAsp-GluMetHisGluTYrLeuG 2080
 Db 9136 ATGTCCCAAGCATGATCCACGAGTGGAGAGATCTCTCCCGTGAACCTGAATGGAG 9195
 QY 2080 LYsGluThrlaArgThrlleuHlaAspAsn-----ArgSerLeuGlyAsnVal 2096
 Db 9196 CTGACCTGAACAGGCTCTCACACACTCAAGTCTCCGACGCCAGAGCTTACACCGCTCCA 9255
 QY 2096 euGluIleGlyThrlArgLYsSerGlyMetIleuPheAsnLeuAspSerArgLeu-GluSer 2115
 Db 9256 CGAAATTCAGACAGGA-----AACCTTGCCAGCTTGGGCACTC 9297
 QY 2116 TYrValGlyLeuGluProSerArgSerAlaAlaPheValAsnLYsAlaThrlGluSer 2135
 Db 9298 CTCTAGCGCTGCACGACTGCGGCACTTGACGACGACCTGTTGCCGAGCGGACAGC 9357
 QY 2136 IleProSer-----LeuAlaGlyLYsValaLYsValaGlyThrlaThrlaAspIle 2153
 Db 9358 ATCTCTCTCTCCGACTTACGAGTGGTACATTTACCGCGCTTACGCAAGCTCACCGCTC 9417
 QY 2154 GlyGlnValaAspAspLeuHisProAspLeuValaLeuAsnSerValIleGlnTYrPhe 2173
 Db 9418 AAGGACATC---TACCTCCACCGCAGGCTCGAGCCTA----- 9453
 QY 2174 ProSerSerGlyTYrLeuAlaGluIleAlaAsp-----ThrlleuHlaSerProAsn 2191
 Db 9454 ---AGCGAAATGTCCTGACCGACGACGAGATTAAGGTACTCTGCCAGCGCTCTCC 9510
 QY 2192 ValGluArgIlePhePheGlyAspValaArgSerGluAla-----ThrlaAsnGlu 2207
 Db 9511 CTCGAGGAGCGGAGACGAGGCGAGGTGAGGGGACGACCGCTTCTCCCATTCAGGAC 9570
 QY 2208 HisPheLeuAla----- 2211
 Db 9571 TGGTCTCTTCAAGCCCTGATTAACCCGCTTACTGAAACCACTGTTCAACATTGCA 9630
 QY 2211 ----- 2211
 Db 9631 ACCGGGCACTTCCTCGAAGGGCTCCGGGTGCTCTGAAGCTCTGACGAGCGCCAC 9690
 QY 2212 -----AlaArgAlaIleHisThrlleuGly 2219
 Db 9691 GACCTGCTGCTGTGACACTGCAACCGCGGAGAGGATGCGCATGTTCAAGACTTTGGC 9750
 QY 2220 LYsAsnAlaThrlLys-----Asp 2225
 Db 9751 CGTGACTGCGCGCAACTGCTGACTGTGCTAGACCGAGAACTTCAGAGCGGAGAG 9810
 QY 2226 AspValaArgGlnLYsMetAlaGluLeuGlu-----AspMetGluGluGluLeu 2242
 Db 9811 GATGTCCAGAGGCTCTCTGCGAGATCCATTCATTTCACTTCGAGATGAGACCCCTC 9870
 QY 2243 ValGluProAlaPhePheThrlSerLeuLYsAsp-----ArgPheProGlyLeuVal 2259
 Db 9871 TACACAGTGGCTATCATCCAGGTTACAGAGAGGCTCCGCCGAGTGTGGCTGCTC 9930
 QY 2260 GluHisValGluIleuProLYsAsnMetGluAlaVal---AsnGluLeuSerAlaTYr 2278
 Db 9931 CATCAGCTATGATCGACATGAGCTGAGCATTAATTCGAAACCTCGAGGCTCTC 9990
 QY 2279 ArgTYrAlaAlaValaValaHisValaArgGlySerLeuGlyAspGluLeuValaLeuProVal 2298

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Db      9991 TATCATGAGACAGCCTTGTCCTCCAGAGCAGCGTCGACAGTGTGCTGATGCTGTC
Qy      2299 GULUYAASPAAPRTTTLAASPHEGlnAlaenGlnLeuAenGlnYAsp 2318
Db      10051 AGC-----GACTACAAATG---CCACTGTGAGAGGCGCATTTGGAA 10092
Qy      2319 LeuLeuYAspAAspAla-----Ala 2326
Db      10093 GTCTCAGAGAAAGACAGTCCGCGAGCTTGACACCTGCTATCTGATGCGCGGCTG 10152
Qy      2327 lIeMeAlaValSerIYsIleProPheGlu---lIeThraIAPheGluArgInVal 2345
Db      10153 CTCACAGTCGACAGAGAAGTCTCGAGGAAACAGCAACAGCTGCTCCCAAGGCTGCG 10212
Qy      2346 lAsSerLeuAAspSerAenIleAspGluTrpGlnLeuSerThrlleAspSer----- 2363
Db      10213 CCGTGCCTTGACCTCCGCTATGATGATGATCTCTCATGCGCGGCTGCGCTGCA 10272
Qy      2364 ---AlaGluGlyAAspSerSerLeuSerValProAspIlePheArgIleAlaGlyAla 2382
Db      10273 AAGGCGGCGAGGGAT-----GTCCCTCAGCTGCTCAGATGAGAGGCTCACGGG 10320
Qy      2383 GlyPheArgValGlu-ValSerSerAlaArgIleTrpSerGlnAsnGlyAlaLeuAspAl 2402
Db      10321 CGC-----GAGATACTATCGACGCAACTCTGACGCTGACGCGCA-----CAGTC 10365
Qy      2402 aValPheHsHsIleCysCysSerGlnGlyArgThrlleuValAspPheProThraPheHsHsI 2422
Db      10366 GCGTGGTTCACGACGATGACCTTCGAGATCC---CCAAAGTACACGCGCCG--- 10417
Qy      2422 sIleuArgGlySerAspLeuLeuThraAspProLeuGlnArgLeuGlnAsnArgAl 2442
Db      10418 -CTCAGGGCTGCTGCG---ATGTCAGAGAGCG-ATCGTGGGCTGCCGAHATAGGGTGT 10472
Qy      2442 eAlaIleGluValArgIleuArgSerLeuProSerTyMetIleProSerAs 2462
Db      10473 CGGTACCGT-----CCAGCTACGAGATACGCGCGATC 10505
Qy      2462 nIleValValLeuAspLysMetProLeuAsnAlaAsnGlyValValAspArgLysGlu-- 2481
Db      10506 G-----TGCTGCGCCGCGCTGAGCTTCACTACCTTGCTGCGCTGACAGGCTTCTC 10559
Qy      2482 ---LeuSerArgArgAlaLysValValProLysGlnGlnThraAlaAlaProLeuProTh 2500
Db      10560 GGGGGCTCAAGGACTGACGCGCTGCTCATGATGAA----- 10596
Qy      2500 rPheProIleSerGluValGluValIleLeuCysGluGluAlaThrGluValPheGlyMe 2520
Db      10597 -----GACGAGTATCCGCTCGGACTGTGACACAGCGCT---GAGGACTCGGAGC 10643
Qy      2520 cIysValAspIleThraPheAspPheAsnLeuGlyGlyHsIserLeuLeuAlaThrLy 2540
Db      10644 AAGCTCTCATGTGATTTCACTTCTTCACTTGCGGCGCGCATGCTTGC----- 10695
Qy      2540 sIleuIleSerArgIleAspGlnArgLeuLysValArgIleThraValLysAspValPheAs 2560
Db      10696 -----ATGAGTATGATGACAGCTGCGG 10718
Qy      2560 pHisProValPheAlaAspLeuAlaSerValIleArgGlyLeuGlyLeuGlnGlnPr 2580
Db      10719 CCACGGCGCGCAAAATGAATTCGTGCGACAGTTCGTAAC-----ACACTAATGACTT 10772
Qy      2580 oValSerAspGlyGlnGlyLysArgSerAlaHsIleMetAlaProArgThrgluThrG 2600
Db      10773 GATCAAAACACACAGCAGCGAGGACTTCAAGCGACTTCCCTCCGTCGATCGAGATC 10832
Qy      2600 uAlaIleLeuCysAspGluPheAlaLysValLeuGlyPheGlnValGlyIleThraPAs 2620
Db      10833 CAGC-----TTCAACCCCTTATTTTGTCTTGAGAGGCGCAGACGACGCG 10877
Qy      2620 n-----PhePheAspLeu-----GlyGlyHsIserLeuMetAlaThrLyLe 2634

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Db      10878 CGCTCCGCTTCTCTGCTCCACCTGCGAGGCGGAGCGGAGACTTACTTCCAAACAT 10937
Qy      2634 uAlaValArgIleGlyHsIAspLeuAspThrlleValSerValLysAspValPheAspHs 2654
Db      10938 TGTCAAGGCTTCTCCGAACCGC----- 10959
Qy      2654 sProValLeuPheGlnLeuAlaIleAlaLeuAspAsnLeuValGlnSerLysThraenG 2674
Db      10960 -----AATCTTGCTGTTCACAACTATTCACGCGAGAGAGAAAGCGCTCCG 11006
Qy      2674 uIleValGlyLysArgIleMetAlaGlyLys-----SerProPheGlnLeuLeuPheTh 2692
Db      11007 GACCATC-----GAGCGCTGCGCGAGTACTCTGCTCCACATCCGATCCAGCGCC 11060
Qy      2692 rGluAspProGluGluPheMetAlaSerGluIleLysProGlnLeuGlnGluI 2712
Db      11061 GAGAGGGCCATACACATCTCTGCGCTGAGATTTCGAGGCAATCCTGCTGAGAGCGGC 11120
Qy      2712 eIleGlnAspIleTyProSerThrglnMetGlnLysAlaPheLeuPheAspHsThrl 2732
Db      11121 AAGCATTTAGTCGCGAGGCTCACAAGATTCGACGCTGCACTTATGATCG----- 11175
Qy      2732 rAlaArgProArgProPheValProPheTyrlleAspPheProSerThrs----- 2749
Db      11176 -----TACTTGACATCCGCTCCGCTCAAGGCCAT 11207
Qy      2750 ---GluProAspAlaAlaGlyLeuIle----- 2757
Db      11208 CGGCCAATCGACGATGCTGCGCTTGAGACCCCATATACACGCTTACACCGCTGCGC 11267
Qy      2758 ---LysAlaCysGlnSerLeuValAsnHsIleuAspIlePheArgThraI 2774
Db      11268 GAGAGCTTACAGACGCTGATCTCTCACTATATCATATGACCTGTTCAAGGCTAAC-- 11325
Qy      2774 eAlaGluAlaSerGlyGluLeuTyrgluValLysSerCysLeuAspLeuProIleG 2794
Db      11325 ----- 11325
Qy      2794 nValIleGluThryAspAsnIleAsnThraIAsnGluPheLeuAspGlu---Ph 2813
Db      11326 -----GAGACGAAATGACAGCATGCGCAATGCGACGACAGCGCTGTATGATGCTT 11378
Qy      2813 eAlaLysGluProVal 2818
Db      11379 TGCCACGTGCTTGTG 11394

RESULT 7
US-09-252-991A-71
; Sequence 71, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 71
; LENGTH: 7527
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-71

Alignment Scores:
Pred. No.: 9.66e-148 Length: 7527
Score: 1506.50 Matches: 552
Percent Similarity: 44.41% Conservative: 338
Best Local Similarity: 27.54% Mismatches: 859

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QY 1372 111eglyThrProileAlaenArGaenArProgluLeuGluluepIleilegIleCysph 1392
D 5904 CCGCGGGGCTACTATCCCAACCGCAACCGCGGAGGTGAGGCGCTGATCGGCTTCTT 5963
QY 1392 eValaenThrGlnCysenArGileanIleAenRhiAenThrPhegluThreul 1412
D 5964 CCGTCAATACCCAGGCTGCTGCGCTGCGTCAATGCTGCGCTGCTGCGCTGCTGCT 6023
QY 1412 eaenGlnValaAlaenThrThrThrAlaIaPheGlnuAenGlnuAenIleProPhegluAr 1432
D 6024 GGGCGCGGCTGAGGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6083
QY 1432 gValaValaIaenArIleuGlnProgluIaenArPheSerArPheSerArProleuAlaIle 1452
D 6084 ATGGGTGATGCTGCTGCGAGCC---GAACGCAATCTGACGCAACGCGCTGTTCCAGGT 6140
QY 1452 uIlePheAlaValaIaIaSerGlnuAenPhegluAenPhegluAenGlnuAen 1472
D 6141 GATGTATTAACCCAGGAGC-----GGCGAGCGCGAGGATGCCAAGTCGATGG 6188
QY 1472 rValProvalProSerArPheAlaTyr-----ThrArPheAenPheGluPheH 1488
D 6189 TTGGACATGAGAGGTTTGGCTGAGAGCGGTGCTGCGCGCAAGTTCGACCTTGGCTTCA 6248
QY 1488 sleuPheGlnGluThraPheSerleuAenPheValaIaenPheAlaIaenPheleu 1508
D 6249 TACCTGGAAACCCCGGAGCGCTTGGGCGCGCGCTGACCTGACGCAACGCGCTTCA 6308
QY 1508 eMetGluThraValaGlnuAenValaIaIaValaPhePheGlnuIleuAenGlnuAen 1528
D 6309 GGGCGGAGCGCTGAGCGGAGCGGCGGCGGATGGCAGAACCTGCTGCGCGGATGCGA 6368
QY 1528 nSerSerArGluThraProvalSerIleleuProleuThraPhegluIleValaThreuglu 1548
D 6369 GAACCGCGGAGCGCGCTGCACTGCTGCGGATGCTGATGCGGAGAGCGGCGCGCTT 6428
QY 1548 sleuAenValaIaenAenValaIaIaIaPheValaPheValaPheValaIaenPhe 1568
D 6429 CCGGAAAGCGTGAAGCGCACTGCTGCGGATGCGGATGCGGAGCGGCGCGCTT 6488
QY 1568 lPheGlnThrGlnuAenValaIaIaPhePheSerleuAenValaIaIaPheSerleu 1588
D 6489 GTTCGAGGAGCGGCTGAGCGGAGCGGCGGCGGCGGCTGCTGCGCGGAGCGG 6548
QY 1588 gleuThrThrThrGlnuAenPheValaIaIaIaPheAlaPheAlaPheAlaIaIaIa 1608
D 6549 CCGGACTGAGCGGAGCGGCTGAGCGGAGCGGCGGCGGCGGCTGCTGAGCGG 6608
QY 1608 gSerMetProAlaGluThraIleuValaIaIaIaPheAlaPheAlaPheAlaIaIa 1628
D 6609 CCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6668
QY 1628 lAlaPhePheGlnuAenValaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1648
D 6669 GGGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6728
QY 1648 oSerAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1668
D 6729 CGAGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6788
QY 1668 yHISArPheAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1688
D 6789 GCACCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6834
QY 1688 pAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1708
D 6835 -----GATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6878
QY 1708 o-----SerAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1724
D 6879 GGATATTATCTGATGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCT 6938

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QY 1724 yArGProLeuGlyValaMetIleGlnuIaIaIaIaIaIaIaIaIaIaIaIaIa 1744
D 6939 CAAGCCCAAGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 6996
QY 1744 sIle-----ProAenThrProSerArGluThraPheMetAlaIaIaIaIaIaIa 1762
D 6997 CAGCAGGCGGCTATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 7055
QY 1762 eaenGlnuAenThrGlnuIleThrSerAlaIaIaIaIaIaIaIaIaIaIaIaIa 1782
D 7056 CAGCGTGTGCGTGTGGAAGTCTTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCT 7115
QY 1782 lArGlyMetThrThrleuAenAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1802
D 7116 CCGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 7175
QY 1802 lAenAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1818
D 7176 CAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 7235
QY 1818 gValaProArGluIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1838
D 7236 CTCTGACAGCGCTGAAGC-----ATGTTTGCAGCGGCGGAGCG 7277
QY 1838 rAlaProArPheAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1848
D 7278 GCTGCGG-----GCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCT 7331
QY 1848 uTyrglnGlnuValaGlnuPheGlnuIleuPheGlnuIleuPheGlnuIleuPhe 1868
D 7332 C-----TATAACCTTTATGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCT 7373
QY 1868 rIleTyProIleAenPheThrGlnuSerPheIleAenGlnuValaProIleGlnuAla 1888
D 7374 CACTG-----ACCTGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCT 7427
QY 1888 uAenAenSerGlyAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 1908
D 7428 CGCCCAACTGCGTGAATCTTGTATGCGCAACTGAGCGGAGCGGAGCGGAGGCT 7487
QY 1908 tGlyGlnu 1911
D 7488 CCGGAGGATG 7497

RESULT 8
US-09-710-279-759
: Sequence 759, Application US/09710279
: Patent No. 6703492
: GENERAL INFORMATION:
: APPLICANT: KIMBERLY, WILLIAM JOHN
: TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
: FILE REFERENCE: PUS480US
: CURRENT APPLICATION NUMBER: US/09/710,279
: CURRENT FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/164,258
: PRIOR FILING DATE: 1999-11-09
: NUMBER OF SEQ ID NOS: 4472
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 759
: LENGTH: 6968
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: nucleic acid sequence
US-09-710-279-759

Alignment Scores:
Pred. No.: 1,41e-139 Length: 6968
Score: 1429.00 Matches: 576
Percent Similarity: 41.62% Conservative: 462
Best Local Similarity: 23.10% Mismatches: 1030
Query Match: 8.86% Indels: 426

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Db 1882 AACACGATGGTTAACGTCATCTTTATTTAAATCAAAATGCTACGACGATTCGAAACA 1941
Qy 744 LeuAlaThrLeu-----ValLeuValGlyGluGlnMetSerSerSerValAsnAlaIle 761
Db 1942 CTGAACATCTTAACTTATTTACTTATTTGTCGGGAAGTG-----TTAAATGCTAAA 1992
Qy 762 TyrAlaProLybLeu-----GlnLeuLeuAsnGlyTyrGlyGln 774
Db 1993 TGGGTTCACTTATTAATTCGCGTACGTCATCTCAAAATTAATCAATGTTATGACCG 2052
Qy 775 SerGluSerSerSerIleCySphAlaSerAsnMetSerThrGluProAsnAsnMetGly 794
Db 2053 ACAGAGAAATACAAACA-----TTTACTCAACCTTTTCGAGT---CCACAAGACATCCCT 2103
Qy 795 ArgAlaVal-----GlyAlaHisSerTyrValIleAspProAsn 807
Db 2104 TCACGATACCTATGTTGTTACCTATTAAGTGAACGACAGTTATGTCATCGCAAGT--- 2160
Qy 808 AspIleAsnArgLeuValProIleGlyAlaValGlyGluLeuValIleGluSerProGly 827
Db 2161 -----AATCGTATTTGTCGGTACGTCGTCAGTGAATGTCATTTGTCGTCAGGT 2214
Qy 828 IleAlaArgAspTyrIleValProProProProGlu-----LysSerPro 842
Db 2215 TTAGCAAAAGGTTATTTAAATCAACCTTAACCTTACCTGACGTTTATTCAGTCACCT 2274
Qy 843 PhePheThrAspIleProSerTyrProAlaAsnThrPheProAspGlyAlaLybLeu 862
Db 2275 TTTAACATGGAATG-----CTT 2292
Qy 863 TyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIleValCysLeuGlyArg 882
Db 2293 TATCGAAGCGGTGATTTAGTTCGTCCTCAAGAAAGATGCTATATGTTATATAGTCGT 2352
Qy 883 IleAspSerGlnValLybIleArgGlyGlnArgValGlyGluGlyAlaIleGluThrHis 902
Db 2353 ATCGATACGCAAGTTAAATACGCGGTTTAAATGAATATATGCAAAATTTGAAAAACA 2412
Qy 903 LeuArgGlnGlnMetProAspAspLeuThrIleValAlaGluAlaThrLybArgSerGln 922
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Db 2470 -----GATAAACAATAGTGCATATGATGACATCGCAATTA----- 2508
Qy 943 ProSerAspAlaHisIleLeuAspHisAspAlaThrIleAlaIleAsnIleLybLeuGlu 962
Db 2509 -----AAATCAACAGCTCAATTAATAAGATTTTAAGT 2541
Qy 963 GlnValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGluLeuProArg 982
Db 2542 GAAACATTTACTGATATATGATATCTGTCGATTTTGAAGGTGATCGATATCTATC 2601
Qy 983 ThrAlaThrGlyLybIleAspArgArgArgLeuArgIleMetGlyLybAspIleLeuAsp 1002
Db 2602 ACCATGAAATGGGAAATAGATGTCGTCATTA-----CCTGAAATTAATCTA 2649
Qy 1003 LybGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAsp 1022
Db 2650 AAGAAATATAGAAATTAATGTAACCAAGT-----AACGAT 2665
Qy 1023 ThrAlaIleLybLeuHisSerIleTyrValGlnSerLeuGlyIleAspProAlaThrVal 1042
Db 2686 ATTGAACGACACAGTTTCCCGATTTTGAAGAGATTTTACATGTTGAT-----CAGATA 2739
Qy 1043 AsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLybMetVal 1062
Db 2740 GGTGTTAAAGATATATTTCTTGAACGTAGGACACCTCTTGAAGCAACATTTAGTTGTA 2799
Qy 1063 Asn---MetIleAspSerValGlyMetAspLeuLybValSerAsnIleTyrGlnHisPro 1081
Db 2800 AACCGATTAAGAAAGGTTAAAAAAGCTTTAAAGTAGTGATTTAAAGAAATGCGCT 2859

Qy 1082 ThrLeuAlaGlyIleSerAlaVal-----LysGlyAspProLeuSerTyrThr 1098
Db 2860 ACTGTAGACGACCTGGACAAACAATGGAAGACGTGCAAAATGAT-----GCTATGAA 2913
Qy 1099 LeuIleProLybSerThrHisGluGlyProValGluGlnSerTyrSerGlnGlyArgLeu 1118
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Qy 1119 TyrPheLeuAspGlnLeuAspValGlySerLeuTyrTyrLeuIleProTyrAlaValArg 1138
Db 2974 TATCTTTTAGAAGGCAATCTTAAAGACAGTGTATTAACATTCATCTTATGAGCA 3033
Qy 1139 MetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaLeuGlnArg 1158
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Qy 1159 HisGluThrLeuArgThrPheGluAspGlnAspGlyValGlyAlaGlnIleValHis 1178
Db 3094 CATGAATATATTACCAACAAATATGTAATGATGACAAATGAACGTAATTCGCG 3153
Qy 1179 GlnLybLeuSerGlnGluMetLybValIleAspLeuCybGlySerAspLeuAspProPhe 1198
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Qy 1199 GluValLeuAsnGlnGluGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTyrArg 1218
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Qy 1219 AlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisIle 1238
Db 3265 GTTAATATATATACATGACCAACAAGATTA---TTATTTAGATCACTCAATAGT 3321
Qy 1239 IleSerAspGlyTyrPheIleAspValIleuArgArgAspLeuAsnGlnLeuTyrSerAla 1258
Db 3322 ATTAATCATGTATGACATACAGATTTTACTTCTGATTTGAACGTTATATCCAAAT 3381
Qy 1259 AlaLeuLybAspSerLybAspProLeuSerAlaLeuThrProLeuProIleGlnTyrSer 1278
Db 3382 -----AAATCACTTACCTGAACCTTAAGCTTCAGTATMAA 3414
Qy 1279 AspPheAlaLybTyrGlnLybAspGlnPheIleGluGlnGlyGlnLeuAsnTyrTyr 1298
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Qy 1358 PheArgAlaAlaHisTyrArgLeuThrAlaValGluAspAlaValIleGlyThrProIle 1377
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Qy 1378 AlaAsnArgAsnArgProGluLeuGluAspIleIleGlyCybAspPheValAsnThrGlnCyb 1397
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 QY 1457 HisSerGlnIleAspLeuGlyArgPheLeuPheGlnGlyLeuGlnSerValProValPro 1476
 DB 3946 AATAATGAACAACATCATCGAATTTTGGACATAGTCATGACATTTGACACATATTCC---CCT 4002
 QY 1477 SerValAlaIleThrArgPheAspMetGlnPheHisLeuPheGlnGlnIleThrAspSerLeu 1496
 DB 4003 CACTCAACAACACTAATTTGATTTGTCATTATTATTAAGAAGAACAGTCAAGTACTAT 4062
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 DB 4063 GTGCTCAATTTGAATATATATACAGATTATATTAACAAGACCATTCATCATTTGCT 4122
 QY 1517 ArgValPhePheGlnIleLeuArgAsnGlyLeuGlnSerSerArgThrProValSerIle 1536
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 DB 4585 TCC-----TCACTATATCCAGTATTAATTAAGATATTGATGATAC 4626
 QY 1692 AspSerAsnAlaAspGlyPheGlnVal-----IleGlnHisAspSerThr 1706
 DB 4627 ACTGAATAATTAAGTAAATATATGATGATGATGATGATGATGATGATGATGATGAT 4680
 QY 1707 LysProSerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyArgPro 1726
 DB 4681 -----ATGTATCATATTTATTCATCTGGAACACAGGAAGGCT 4719
 QY 1727 LysGlyValMetIleGlnHisArgValIleIleArgThrValThrSerGlyCysIle--- 1745
 DB 4720 AAGGCAAGTATCATGAAACAAGTAAATATTAATTAATTAATTAATTAATTAATTAATTAAT 4770
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 QY 1763 AspGlyAlaSerTyrGlnIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCysVal 1782
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DB 4891 ACATCAAGTGAAGCGACCAATACAGATTTTATTAAGAAAGTTAATTTCCAAAGAAAATATC 4950
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 DB 4951 ACCATGCGACT-----ATTCACATTCAG 4974
 QY 1823 LeuSerArgThrLeuMetPhePheLeu-----ValValThrAspSerThrAlaPro 1840
 DB 4975 GTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5034
 QY 1841 AspAlaLeuAspAlaGlnGlyLeuTyrGlnGlyValGlnCysTyr---AsnGlyTyrGly 1859
 DB 5035 ACTCCAGCATTTGTCAACATTTTCAACATTTGATGATGATGATGATGATGATGATGATGATGAT 5094
 QY 1860 ProThrGlnAsnGlyValMetSerThrIleTyrProIleAspSerThrGlnSerPheIle 1879
 DB 5095 CTTTCGAAAATACAGTTATACATCTTTGTGATATACCAAAAGGTGACGCCATACCA 5154
 QY 1880 AsnGlyValProIleGlyArgAlaLeuAsnAspSerGlyAlaTyrValValAspProGln 1899
 DB 5155 TCGACTATTCGATGGGAAACCGTTAGCTAATGTTGATTTTATTTATGATGCTA---GCC 5211
 QY 1900 GlnGlnLeuValGlyIleGlyValMetGlyGlnLeuValValThrGlyAspGlyLeuAla 1919
 DB 5212 GGTAACTATGTCGCGTGTGATTTCCAGGTGAATTAATGATGATGATGATGATGATGATGATGAT 5271
 QY 1920 ArgGlyTyrSerAspLys---AlaLeuAspGlnAsnArgPheValHisIleThrValAsn 1938
 DB 5272 TCAGGATATTTAAACAGACCCGAACTTTCTGTAAGAAATTTATTAATTAATTCCTTTGGG 5331
 QY 1939 AspGlnThrValLysAlaTyrArgThrGlyAspArgValArgTyrArgIleGlyAspGly 1958
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 QY 1959 LeuIleGlnPhePheGlyArgMetAspThrGlnPheLysIleArgGlyAsnArgIleGly 1978
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 DB 5557 GAAGATGAAGTCAATTTTACAAACATTTAATCAATAT-----TTGCCTAATATACATG 5610
 QY 2039 GlnSerGlyMetTyrSerAspIleGlyGlnIleAspProSerThrIleGlySerAspPhe 2058
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 QY 2059 LysGlyTyrThrSerMetTyrAspGlySerGlnIleAspPheAspGlnMetHisGlnTyr 2078
 DB 5662 -----AAGTGAATGAGTCAAGATTAACCTGTACCTTAATGATGACAAATAAT 5706
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 QY 2099 GlyThrLysSerGlyMetIle-----LeuPheAsnLeuAspSerArgLeuGlnSer 2115
 DB 5758 -----AGCGAGGTGGAGCGATCGCTATGATGATGATGATGATGATGATGATGATGAT 5796
 QY 2116 TyrValGlyLeuGlnProSerArgSerAlaAlaPheValAsnLysAlaThrGlnSer 2135
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Db      5824 CTAGATGCTATGCTGATGATCAAACTA-----AAA 5856
Qy      2156 ValAspAepLeuHisProAepLeuValLeuAenSerValIleGlnIyrPheProSer 2175
Db      5857 TCAAATGGCATACAC-----ATTACATGCAAGATGATATCA---TTTAAACT 5904
Qy      2176 SerGlnIyrLeuAaGlu-----IleAaSerThrLeuIle--- 2187
Db      5905 GTTCGTTATATGCTATATCAACAGAAAAGCCAGACACTACACAGAGATATTCACA 5964
Qy      2188 ---HisLeuProAenValGlnArgIlePhePheGlyAspValArgSerGlnAaIleThrAsn 2206
Db      5965 GATCATTCTACCAATTAATCAATCTTGGTT-----GAAAGACGATACCAACTAAATCA 6018
Qy      2207 GlnHisPheLeuAaIleAaGlnAaIleHisThrLeuGlyAspAaIleThr----- 2223
Db      6019 CAACACTTAACGCAATATCTCTAGGTCATGATGCTAATCTGCTAATGCTGCAACAGGTTCTCA 6078
Qy      2223 ----- 2223
Db      6079 GCGCATATTAAATGATGAATGCAAGATGATGCTGATCAAAATTACATGATATGTCAGA 6138
Qy      2224 LysAspAepValArgGlnIyrMetAaIleGlnLeuGlnAspMetGlnIleGlnLeuVal 2243
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Qy      2244 GluProAaPhePheThrSerLeuLysAspAepPheProGlyLeuValGlnHisValGlu 2263
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Qy      2281 AlaAlaValValHisValArgIleSerLeuGlyAspGlnLeuValLeuProValGlnLys 2300
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Qy      2301 AspAepTrpIleAspPheGlnAaIleAsnGlnLeuAsnGlnIyrSerLeuGlyAspLeuLeu 2320
Db      6331 GATGATCAAAACATTTTTCGATGTCATAGTAAAGTACACAGCATTAATGATTTGCT 6390
Qy      2321 LysSerSerAspAlaAlaIleMetAaIleValSerIleIleProPheGlnIleThrAlaPhe 2340
Db      6391 AAGCATTAATAAGCAATTAATCTATATATCAACGATA----- 6429
Qy      2341 GluArgGlnValValAaSerLeuAenSerAsnIleAspGlnIyrGlnLeuSerThrIle 2360
Db      6430 -----AGTGGGTCACGGTA 6444
Qy      2361 ArgSerSerAaGlnIyrAspSerSerLeuSerValProAaPhePheArgIleAaGly 2380
Db      6445 TTGGAATACATCAACAGCATATTAATTTCTGAAAAAAGATTAATATAA-----GGC 6498
Qy      2381 GluAlaGlyPheArgValGlnValSerSerAaIleArgIleIyrSerGlnAaGlyAlaLeu 2400
Db      6499 CAGGTTA---TTTACATCACCATACACTAAAGTAAGTTATATAGCGAGATTAAGGTGTA 6555
Qy      2401 AspAlaValPheHisHisCysCysSerGlnIleArgIleValLeuAaPhe-----Pro 2418
Db      6556 GAAGCGGTTATGAAGGTTTAGCAGCTCAAGATTATTAAGAAATTCGACAAAGTCT 6615
Qy      2419 ThrAspHisHisLeuArgGlySerAspLeuThrAsnArg 2432
Db      6616 TCTACTGACCATTAATAATGAAAAATTTAACAACTAATGCT 6657

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RESULT 9
US-08-956-171E-206/c
; Sequence 206, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi

```

```

; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
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; ATTORNEY/AGENT INFORMATION:
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; INFORMATION FOR SEQ ID NO: 206:
; LENGTH: 29555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-956-171E-206
Alignment Scores:
Pred. No.: 2,9e-138 Length: 29555
Score: 1428.00 Matches: 646
Percent Similarity: 39.61% Conservative: 458
Best Local Similarity: 23.18% Mismatches: 1028
Query Match: 8.85% Indels: 657
DB: Gaps: 109
US-09-482-788-2 (1-3129) x US-08-956-171E-206 (1-29555)
Qy      194 LysHisGlnLysAspThrHisArgProGlnIyrProGlnIyrSerSerAspAlaThrAspThr 213
Db      27274 AAGCATTCATTAATAAGCAAGCTTATATCAACGATATTTGATGATGATGATGATGATCAATA 27215
Qy      214 AspSerGlnSerValSerValSerMetSerCysGlnAspAaIleValSerAaIleThr 233
Db      27214 GATATGGCATGCTGGCT---GTTAGTGTATATTAGCTAATCATTAATGATGATCAACA 27158
Qy      234 His-----PheTrpGlnThrHisLeu---AsnAspLeuAaAaSer 246
Db      27157 CATGATGTCACATTAGTATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 27098
Qy      247 ValPheProHisLeuSerAspHisLeuMetValProAsnProThrThrAlaGlnHis 266
Db      27097 ATTTGGCGC-----TTTACCTTAAACATCGATGCAACAAAGATGATGATGCA 27053
Qy      267 ArgIleThrPheProLeuSerGlnLysAlaLeuSerAsnSerAaIleCysArgThrAla 286
Db      27052 CGTTTACAAACAGATTTTAATAATGCTGTCGCAAAATATGTCGCAATTACAGTGGCG 26993

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QY 287 LeuSer1LeuLeuSerArgTyrThrHisSerAspGluAlaLeuPheGluAlaValThr 306
 DB 26992 AGCTCTCGCTT-----TCACTAGACACTATTTT----- 26963
 QY 307 GluGlnSerLeuProPheAspLysHisTyrLeuAlaAspGluTyrGlnThrValAla 326
 DB 26963 ----- 26963
 QY 327 ProLeuArgValHisCysGlnSerAsnLeuArgAla-----SerAspValMetAspAla 344
 DB 26962 -----CATGTGATATCATCATATGATGCTGTGTGTAATGATGTTATTTGAGGAT 26915
 QY 345 LLeSerSerTyrAspAspArgLeuGluHisLeuAlaProPhe----- 358
 DB 26914 GTTACATCAATATACATGATGACACATACATCTTTAGCCGATATGAAATTTTCCACATCA 26855
 QY 359 ---GlyLeuArgAsp1LeuArgAsnThrGlyAspAsnGlySerAlaAlaCysAspPheGln 377
 DB 26854 CACGGGTTCAAAATTTATATATAC-----AGTCACAGATATGATTTGCTC 26810
 QY 378 ThrValLeuLeuValThrAspGlySerHisValAsnAsnGlyLeuAsnGlyPheLeuGln 397
 DB 26809 TCATATGACAGCGCTGAGTGAC-----TTAGTTCGAAATATTATTATTG 26768
 QY 398 Gln1LeThrGlySerSerHisAspMetProCysAsnAsnArgAlaLeuLeuHisCys 417
 DB 26767 CAATATTAAGTCAAAATATGCA-----AATTAACGA----- 26738
 QY 418 GlnMetGlySerGlyAlaLeuLeuValAlaTyrTyrAspHisAsnVal1LeuAspSer 437
 DB 26738 ----- 26738
 QY 438 LeuGlnThrThrArgLeuLeuGlnGlnPheGlyHisLeuLeuLeuCysLeuGlnSerPro 457
 DB 26738 ----- 26738
 QY 458 LeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGluTyrAspArgAlaGlu1Le 477
 DB 26737 -----ACAACGTGAGATGAACCTTAATTTGATGACAGACGTGATATCACTATTAT 26687
 QY 478 GluSerTyrAspSerGlnProLeuGluValGlnAsp-----ThrLeu1Le 492
 DB 26686 GACGATATCATTTAAGTTGGCTGAGATGATGATGACGCAACAGTTGTAACCTTATT 26627
 QY 493 HisHisGluMetLeuLysAlaValSerHisSerProThrTyrThrAla1LeuGlnAlaTyr 512
 DB 26626 GAGCAACA-----GTTGAAACAACGCCGAATCATGTCCGTGGCAA---TTT 26582
 QY 513 AspGlyAspTyr---ThrTyrSerGluLeuAspAsnValSerSerArgLeuAlaValHis 531
 DB 26581 GACGGAGTGTTTATACATATCAACATTAATGATGACGCGGCAATGATTTAGCACACCGT 26522
 QY 532 IleLysSerLeuGlyLeuArgAlaGlnGlnAla1Leu1LeuPro-----Val 546
 DB 26521 -----TTGAAACAACGATAGTGCTTGACCTAATGATCGTGCTGCTC 26477
 QY 547 TyrPheGluLysSerLysTyrVal1Leu1SerMetLeuAlaValLeuLysSerGlyAsn 566
 DB 26476 ATAGCTGAAAAAATTTGATGAGATGATATAGCCGATGATAGTGTTGGAAGCTGGTGGG 26417
 QY 567 AlaPheThrLeuLeuAspProAsnAspProValArgThrArgAlaGlnVal1Val1ThrGln 586
 DB 26416 GCTTATGTCGCAATTTGATGCAACTATTCAGAGATGTCAGAGATGATTTTAAAAAGAT 26357
 QY 587 ThrArgAlaThrValAlaLeuThr---SerLysLeuHisArgGluThrValGlnLysLeuVal 606
 DB 26356 GTAAAGCGCTAAAGTTGTAATATACGATCAACAGCTTTATATGAAATGTTAAACAAATAT 26297
 QY 606 1-----GlyArgCysValValValAspAspGluLeu 617
 DB 26296 AATCACATGATTTGATATAGATAGCGCTGGAATAATTTGATATATC----- 26251
 QY 617 uGlnSerValSerAlaSerAspPheSerSerLeuThrLysSerGlnAspLeuAlaTyr 637

DB 26250 -----TTTCTAATATGTAACACGTTA---GAAGATCATGCTTA 26217
 QY 637 rVal1LePheThrSerGlySerThrGlyAspProLysGly1LeuMet1LeuHisArgAl 657
 DB 26216 TGTATTTTACACGTGGGACACATGTTAAACCTTAAGGACACATATTCGACCGACG 26157
 QY 657 aPheSerSerCysAlaLeuLysPheGlyAlaSerLeuGly1LeuAsnSerAspThrArgAl 677
 DB 26156 TATTGTCGCTTGCTGCATCA---AATCATTTATGTAACCTTTAAATGAAGACAGACGAT 26100
 QY 677 aLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGlu1LeuMetThrThrLeu1 697
 DB 26099 TTGTATTATCAGAACTATAGCTTTGATGCTGCACATTTGAATATATGTCGATTCGT 26040
 QY 697 eAsnGlyGlyCysValCys1LeuProSerAspAspArgMetAsn-----Ser1LeuP 715
 DB 26039 CAATGGTGGAACCTGATTTGCTTAATAAAGAACATTTATTAATTCATATACCGGTAGA 25980
 QY 715 oSerPhe1LeuAsnArgTyrAsnValAsnTyrMetMetAlaThrProSerTyrMetGlyTh 735
 DB 25979 ACAATTAATCAATGAATAATGACCTTTAATCTATGCTGTAACCTCTCATATTATTAATCA 25920
 QY 735 rPheSerProGluAspValProGlyLeuAlaThrLeu-----ValLeuValGlyGlu1 753
 DB 25919 GATTGCTAGTGAACGATAGAGATATGTAACGCTTAAGATATTATTAATGCTGAGAGA 25860
 QY 753 mMetSerSerValAsnAla1LeuPalaProLysLeu----- 766
 DB 25859 AGTA-----TTGAACTGAAGTGGGTGATTTGCTTAATCAAAAACCGAACATCC 25809
 QY 767 -GlnLeuLeuAsnGlyTyrGlyLysSerGlySerSer1LeuCysePheAlaSerAsn 786
 DB 25808 TCATATTAATTAATGATTAATGACCAACTGAATAACACTTTTCAACAGACGATTAATAT 25749
 QY 786 tSerThrGlu---ProAsnAsn-----MetGlyArgAlaVal---GlyAlaHisSerTyr 802
 DB 25748 ACCTAACAAAGTCCAAATGATGATTCCTATGTTAAACGATTCGGGTATCATGTTTA 25689
 QY 802 pVal1LeuAspProAsnAsp1LeuAsnArgLeuValPro1LeuGlyAlaValGlyGluLeuVal 822
 DB 25688 TATCATGCAAGGC-----GAGCGTCGCTGCGGTGATTCCTGGAATAATATG 25638
 QY 822 1LeuGlySerProGly1Leu1LeuArgAspTyr1Leu1ProProProProGluLysSerP 842
 DB 25637 TACAAGTGGCTTTGGGTAGCTGACAGTTATTTAAATCAACCGAATGACAGACATTA 25578
 QY 842 oPhePheThrAsp1LeuProSerTyrTyrProAlaAsnThrPheProAspGlyAlaLysLe 862
 DB 25577 ATTTATCAAAAGAT-----TCAAATATA-----AATCAAGCTGAT 25545
 QY 862 uTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySer1LeuValCysLeuGlyArg 882
 DB 25544 GTATAGAGAGTGTGATATCGTTGTTGTAACCGGATGCGCAACATGATATTATTATATCG 25485
 QY 882 g1LeuAspSerGlnValLys1LeuArgGlyGlnArgValGluLeuGlyAla1LeuGlnThrHis 902
 DB 25484 AAGGACAACAAGTTAAGATTGAGAGGTTTATGATTAATGATTCAGAGTTGAG----- 25430
 QY 902 sLeuArgGlnGlnMetProAspAspLeuThr1LeuAlaGluAlaThrTyrArgSerGly 922
 DB 25429 -----CATGCGTCGACGGTATACA 25410
 QY 922 nSerAlaAsnSerThrSerLeu1Leu-----PheLeu1Leu1 935
 DB 25409 AGCTATTAATAAGACAGTTGTATTGTTCAAAATCATGATCAAGATCAGATATATCGTT-- 25352
 QY 935 ySerSerTyrPheGlyAsnArgProSerAspAlaHis1LeuLeuAspHisAspAlaThrLys 955
 DB 25351 -----GCTTATTA-----GAAGCGATGCATCAATTAATCAATATAAGATTAA 25308
 QY 955 sAla1LeuAsn1LeuLeuGlnGluGlnValLeuProArgHisSer1LeuProSerPheTyr1 975

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|----|-------|--------------------|--|-------------------------|-------|--|
| Db | 25307 | ATCA----- | -CAATTAGCTAGACCTTAACCGAGTACATGATACAGATTAA | TTTCAT | 25257 | |
| Qy | 975 | ECYMECLUGLULEUPROA | RGTHRALATHRGILYSLLEAPRATGARGLEURGI | 1 | 995 | |
| Db | 25256 | GCATATGAGCAAAATTC | CTATTACTATTAATGGGAATTTGATMAAGCAATTCCTAT | 25197 | | |
| Qy | 995 | EMETGILYASAPRI | LEUENAPRYSGLINTHNGINYLALILEVALGINGLALAEPROI | 1 | 1015 | |
| Db | 25196 | CATG----- | -GACTATGTCGAT----- | ACCGATCC | 25173 | |
| Qy | 1015 | APROI | AEPROVALPHEALAEPRTHRALALALYSEUHI | SESEIETRPVALGINSEIPE | 1035 | |
| Db | 25172 | CTAATGTAACCGAGTA | ACAGTACAGTACCAGAACCTTGCTATGCCAATTTTTCAGATATTTT | 25113 | | |
| Qy | 1035 | UGLITLEAPPROALATH | VALAENVALGIYALATHRPHENGLULEUGILYASNSE | 1055 | | |
| Db | 25112 | ACATGTGGAAT----- | -CAAGTAGGTATTCATGATTAATTTCTTGATTTAGTGCGCATTC | 25059 | | |
| Qy | 1055 | RIETHRALILELYSE | MECVALLAN--MECALAASERVALGIMECASPLEULSVIA | 1074 | | |
| Db | 25058 | ATYMAAGCAACGTTAG | AGTGGATCGGAATCGGAATAGAGCATCTACCTGGAAAAAGATTACAAAT | 24999 | | |
| Qy | 1074 | ISEA | ANILETRYGINHISPROTHLEUVALAGILYILESER--ALAVALLIEGLIYAE | 1093 | | |
| Db | 24998 | TGGGATTTATTAACAA | AGCCACTGATTTTGAACATACGACAAAGCATTCCTAAGTTCA | 24939 | | |
| Qy | 1093 | PROLEUSERTRYTHREU | LEIPROLYSETRTHISGLUGLYPROVALGLUINSETRY | 1113 | | |
| Db | 24938 | AGAACA | MAAATCATATGAGATTCAGAAACCTATATGTTAAAGATTAATGCTGACGTC | 24879 | | |
| Qy | 1113 | RSEGINGLYARGLEUTR | PHLEUENAPGINLEUAPVALGILYSELEUTRTRYLEUI | 1133 | | |
| Db | 24878 | TGCACMAAGGATGAT | TATTTATTTATGMAATCAACACATMAAGATACGGTGTATACCT | 24819 | | |
| Qy | 1133 | EP | PROTYLAVALARMECARGILYPROVALAENVALAPALAEUARGARGLAEUUI | 1153 | | |
| Db | 24818 | ACCTTTTATGAGCGG | CTTATCATACAACTTATATGTCATTCGACAAACAGCTGCA | 24759 | | |
| Qy | 1153 | AALAEUGLUNARHIS | GLUTHREUARGTHRPH-----GLUENAPGLNAB | 1170 | | |
| Db | 24758 | GC | GTATTGATAGCGGACATGATTTTACGAACCAATATATGTTGTGATGATGATGAG-- | 24701 | | |
| Qy | 1170 | PGILYALGILVALGIN | LEVALHISGLUYSEUSERGILUIMELYEVALLIEASPLE | 1190 | | |
| Db | 24700 | ----- | -GTTCCACAACGATATGTGGCAGATGTGACAGTT----- | 24668 | | |
| Qy | 1190 | UCYEGLYSERASPLEU | APROPHEGILUVALLEAENGLINGLINTHR----- | 1206 | | |
| Db | 24667 | ----- | -GACTTTGAAGAGTTTACACGCATTTTACGAGTACACACAGA | 24627 | | |
| Qy | 1207 | ----- | -ThrProPheAenLeuSeSeSeGluAlaGlyTyrPArgLath | 1220 | | |
| Db | 24626 | AATCATGCGCAATTTG | ATAGACCTTTTAAATTTGGAAAACCAAGCAATTAATAGAGTGAG | 24567 | | |
| Qy | 1220 | RL | EUENARGLEUGILYASAPRHSILIELEUTHRILEVALMECHISILIELESE | 1240 | | |
| Db | 24566 | ATACATTTAGAAAGT | CCCTTACATGATAC--CTCTTATGATACCATCATATCTATTAA | 24510 | | |
| Qy | 1240 | RA | SGILYTRIPSERILEASPVALLIEUARGAARPLEUENGLINTHRYSERLALALAE | 1260 | | |
| Db | 24509 | TGACGGATGATGATTA | TATACATTAATGAATGATCTTAAAGCCATTTATCAACATAAATTT | 24450 | | |
| Qy | 1260 | ULYASAPSERLYSAP | PROLEUSERLALAEUTHRPROLEPROILEGLINTYSEASAPH | 1280 | | |
| Db | 24449 | A----- | -TTGTTAACCACTTAATTTGCATATTAAGACATTA | 24417 | | |
| Qy | 1280 | EALALYETR | GINLYSAPGINPHEILEGLINGILYSGILNEUASNTYTRPLYSLY | 1300 | | |
| Db | 24416 | TAGTGAGTGATGTG | CGCATCGTATATGACGAAACATATAGCAA-----TATGTGTTATTC | 24363 | | |
| Qy | 1300 | SGILNEULYASAPSER | PRO--ALALYSLIEP | ROTHRAPHPEALARGPROLALAE | 1319 | |
| Db | 24362 | TCAATTTCAAAATGA | ATGATCTTATTTTAACTTATTAACGACAGCATTAATGATGACCAAAATYT | 24303 | | |

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|----|-------|--|-------|
| QY | 1319 | uLeuSeCgLYaerAlaegLYcyvSvAlhSvAlThrIleAerGcLYuLeuTYgLISeRie | 1339 |
| Db | 24302 | TAAACCAAAATGAGCAATGATGTCATTTTAAATGAATCAACAATATGACAGCAGCTACT | 24243 |
| QY | 1339 | uArGAlaPheCySaenGluhISeAenThrThSeRSePheValIValLeuLeuAlaIaPheAr | 1359 |
| Db | 24242 | TCAAAGATATGTGAAGAAAGCATCAAAATTACATTTTATATGTTCTTTATAGAGTGTGCAT | 24183 |
| QY | 1359 | gAlaIaIhIeTYrArGLeuThrAlaValIGluAraIaValIleGlyThRProIleAlaIs | 1379 |
| Db | 24182 | GACGTTGTGAAGTAAATGCTCGAAAAGATGATGTGTGTCGTGAAGTATGATGCTGC | 24123 |
| QY | 1379 | nArGAsnArGProGluLeuGluAerIleGlyCySpheValAenThrGInCySeMeAr | 1399 |
| Db | 24122 | GCGATGCGATTAAGAGCAGCGACGAATGCTGAGCAGCTTTGCTAAATACGTTGATATAG | 24065 |
| QY | 1399 | gIleAenIleAerPhISeIeAerThRPhGlyThrLeuIleAenGluValIyLeAlaThrTh | 1419 |
| Db | 24062 | AGGGCAACCGCTCACCTGATTAATATGTGGACACAGCTTTTAAACAAGAGTTAGGAATGAG | 24003 |
| QY | 1419 | rThAlaIaIaPheGluAenGluAerIleProPheGluATGArValISeValIleuGInAr | 1439 |
| Db | 24002 | TTTGGAGCGATACAGATCAAGAAATACCATTGCAATGTTTATGTAATGACATTAGTCA | 23943 |
| QY | 1439 | oGlySeArGArPLeuSeSeRThRProLeuAlaGInLeuIlePheAlaValhISeGcI | 1459 |
| Db | 23942 | A---TCACATGATGCTCCACGGAATCCATATTATGTGATGTCATGTGTACTCAAAACAA | 23886 |
| QY | 1459 | nIySe-----AerLeuGluArGPhelySeRheGInGlyLeuGInSeArValProVa | 1475 |
| Db | 23885 | TGAACCAATCATGCTCATTTTGGCGATAGTAAATTAAACACATTTCA----- | 23833 |
| QY | 1475 | lProSeLyAlaIaTYrThRArGPhAerPMeGcIuPhehISeuPheGInGluThRAsPe | 1495 |
| Db | 23836 | -CCCAATTCAGTACGGCGGAATTTGATTTATCTTCATTCATTAAGAAAGATGCGATGA | 23778 |
| QY | 1495 | rLeuIyGlySeValaIaenPheAlaAerGcIuLeuPheLySeMetGluThValIGluAenVa | 1515 |
| Db | 23777 | CTATACATCAATATTCAGATATATATCCGATTTATATCATCTCGAAACAGTTCGTACAT | 23718 |
| QY | 1515 | lValArGValPhehGluIleuArGAsnGlyLeuGInSeArSeArThRProValSe | 1535 |
| Db | 23717 | GGGTATCAATGTRATG---ATTATGATGATTTATTTTGAAGCATCAAGATACACTACA | 23663 |
| QY | 1535 | rIleLeuProLeuThRAspGlyIleValIhRleuGInLyLeuAerPValIleuAenVal-- | 1554 |
| Db | 23660 | AATTTGATATATCAAAACGGC-----ACGAGAGAACTCTTAAATGGGTCAATACGCA | 23607 |
| QY | 1555 | -----LyhIhISeValaerPyRProArGcIuSeRSeLeuAlaAerValPheGInh | 1571 |
| Db | 23606 | TGTTAACGATGAGATGCTTATATGCTCCGGGAAATTAATCATATCAATAGTACTTTATGA | 23544 |
| QY | 1571 | rGInValSeValaTYrProAerSeRSeIeAlaValaIaAerSeSeCyArGLeuThRY | 1591 |
| Db | 23546 | AGTTGTCTCACGACAAAGATATCATGTGGCGTACGATCAAGATATTTGACATGACGTA | 23487 |
| QY | 1591 | rThGluLeuAerArgInSeRAspIleLeuAlaGlyTrPLeuArGArGSeMeAr | 1611 |
| Db | 23486 | TGAACCACTTACGCAACTATGTGATGCAATGTGGCACATGCTCTTCAAAATGCTGTGG | 23427 |
| QY | 1611 | oAlaGluThRleuValaIaValaPheAlaProArGSeCyGluThrIleValaIaPhePh | 1631 |
| Db | 23426 | CAATGCGTCAACGGGTTGCTTTTACAGAACTAGTTTGAATATGATTTGCGCGCATGTT | 23367 |
| QY | 1631 | eGlyValleuIyAlaAenLeuAlaTYrIleuProLeuAerPValArGSeProSeRAlaAr | 1651 |
| Db | 23366 | GGCGACAGTTAAAGTATGAGTCACTTATATACCTATACGATATGATTTCCGATTAACG | 23307 |
| QY | 1651 | gValIGluAerIleuSeRcIyLeuSeRcIyProThrIleValLeuIleGly-----hI | 1669 |
| Db | 23306 | ACAAGTGCAATTTTGGAGATGCTAAAGTAACTGACGATCATGTCTTACGGCGCTGAAT | 23244 |

QY 1669 sAepThrAlaProProAspIleGluValThrAsnValGlu---PheValArgIleArg-- 1687
 Db 22446 TGAAGACATTACAGTCAATTCGAAATTCGTAAGCTTTCTTGAATCAAAAGCA 22187
 QY 1688 -----AspAlaLeuAsnSerSerAsnAlaAspGlyPheGluValIleGluH1 1703
 Db 22186 AATGAAACATATGATGATTTACATGCAATCAACTGAAACACAGCGGTGTAGATTA 22127
 QY 1703 sAepSerThrLysProSerAlaThrSerLeuAlaValValLeuLysThrSerGlySerTh 1723
 Db 22126 TGGG-----ATGATGCTATTTACATCTGGATGAC 22094
 QY 1723 rGlyArgProLysGlyValMetIleGluH1ArgValIleIleArgThrValThrSerG1 1743
 Db 22093 CGGGATGCCATTAAGCGGTGCCATACAGCAACGAAATTTGTGATTTATGATGCA-- 22036
 QY 1743 yCysIleProAsnLysProSerGluThrArgMetAla-----HisMe 1757
 Db 22035 -----TGGTCACATGCAATTCGCAATTAAGCCACATGAAATTTTTCGCAACA 22989
 QY 1757 rAlaThrIleAlaPheAspGlyValAseryrGluIleTyrSerAlaLeuLeuPheGlyAr 1777
 Db 22988 TGCATAATTTGTTTGTGATCATCAGTTATGAGATTATTTGTTGTTTAAATGCTCA 22929
 QY 1777 gThrLeuValCysValAspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValPh 1797
 Db 22928 TAGCTTGTATTCACAGTAGAGAGAACCGTTAAACCAAGACAGTTACCAACATCAT 22869
 QY 1797 ePheArgGluH1ValAsnAlaAspSerHisValThrSerSerGlnAspValProle 1817
 Db 22868 TAATTAAGCATCTGTGTCAGCTGTCGTCG----- 22841
 QY 1817 uArgValProArgArgLysSerLysrGlyThrLeuMetPhePheLeu-----ValValTh 1835
 Db 22840 ----ATTCCGTATCAGATGTGTAGTGTATGAGAACCTTTATATGAAAAAGTTGATTA 22785
 QY 1835 rAepSerThrAlaProAspAlaLeuAspAlaGln-----GlyLeuTyr 1849
 Db 22784 AGCGCGGCAACATGACGCAATCCCTTGTAAATATATGAGACAGATTGTGCAGCTA 22725
 QY 1849 rGlnGlyValGlnCysTyrAsnGlyTyrGlyProThrGluAsnGlyValMetSerThrI1 1869
 Db 22724 T-----TTCAATGCGCTATGAGACATCTGAGTCAACAGTATCATCATCGTA 22680
 QY 1869 eTyrProIleAspSerThrLysSerPheIleAsnGlyValProIleGlyArgAlaLeuAs 1889
 Db 22679 TTGGTCAATCATCTGTGTGATTTGATATCTGAGACAGATTCCAATTCGCAACCCCTTATC 22620
 QY 1889 nAsnSerGlyAlaTyrValValAspProGluGlnGluLeuValGlyIleGlyValMetG1 1909
 Db 22619 TAAATCCAAAGTGTATTTATATGCA--GATGCTTTGTATGCGGTATTTGTATGCCAGG 22563
 QY 1909 yGluLeuValValThrGlyAspGlyLeuAlaArgGlyTyr----- 1922
 Db 22562 CGAGTTGTGATTTGACGAGTGTATGAGATGAGATATATTAATGTCGCAAAATTAAT 22503
 QY 1923 -SerAspLysAlaLeuAspGluAsnArgPheValHisIleThrValAsnAspGlnThrVa 1942
 Db 22502 GGCTGATTA--TGGCAAAATATATCATTT-----GGTAAAGG 22467
 QY 1942 lLysAlaTyrArgThrGlyAspArgValArgTyrArgIleGlyAspGlyLeuIleGluPh 1962
 Db 22466 AAGGTGTATCATATGTGTATTTAGACCTTAT--ACATCTGATGTCMAATTTGAATT 22410
 QY 1962 ePheGlyArgMetAspThrGlnPheLysIleArgGlyAsnArgIleGluSerAlaGluI1 1982
 Db 22409 TTTAGAGAAATATGATTAACAAGTAAAGTTAACGGGTACCGTATTAACCTTGATGAAT 22350
 QY 1982 eGluAlaAlaLeuLeuArgAspSerSerValArgAspAlaAlaValValLeuGlnGlnAs 2002
 Db 22349 TGAATAATGATATATGCTATTCGTGTATATATGATTTGTGTGATTAACAGATGCTCACTT 22290
 QY 2002 nGluAspGlnAlaProGluIleLeuGlyPheValValAlaAspHisAspHisSerGluAs 2022

Db 22289 TGATAGCAT-----GATATATTTGAATGCTTATATGTCGAGAGCAACAGATGCAACA 22236
 QY 2022 nAspLysGlyGlnSerAlaAsn-----GlnValGlnGluIlyrGlnAs 2036
 Db 22235 GGAATTTGAACCAATATTTAAATATGATCAGCTGCTAAGTATATGATTCCTTAAGACTATAC 22176
 QY 2036 pHisPheGluSerGlyMetTyrSerAspIleGlyGluIleAsp----- 2050
 Db 22175 GCATATGATGTATATGCCATTAAACAGATGACAGATGACAGCTGATACAGCGTTGCCAA 22116
 QY 2051 -ProSerThrIleGlySerAspPheLysGlyTyrThrSerMetTyrAspGlySerGluI1 2070
 Db 22115 TCCATCACTTAAACAGATTAATAAGTATAGTATAGCAACCTCTATGAATGAATGAGCA 22056
 QY 2070 eAspPhe--AspGluMetHisGluIlyrPheLysGlyIlyrThrArgThrLeuHisAspAs 2089
 Db 22055 GACATTTGTTGATGATTTTGGAGAGAGTATGAAACAAATGATGTCGCTGTGACAT-- 21998
 QY 2089 nArgSerLeuGlyAsnValLeuGluIleGlyThrGlySer-----GlyMetIleLeuPh 2107
 Db 21997 -----GATTTCTTAACTTGSTGTACTCTATTAGAGCGATGTATGTT 21951
 QY 2107 eAsnLeuAspSerArgLeuGluSerTyrValGlyLeuGlu-----ProSerArgSe 2124
 Db 21950 CTCGCAATTTAAACGATTTGCGCATATATTCATAGCAGACATTAACCATATATAAAC 21891
 QY 2124 rAlaAlaAlaPheValAsnLysValaThrGluSerIleProSerLeuAlaGlyValAlaLy 2144
 Db 21890 CGTGCAGACAGATTGTAAATATATGATACCAAAATCAACATCACTTA----- 21845
 QY 2144 sValGlnValGlyThrAlaThrAspIleGlyGlnValAspAspLeuHisProAspLeuVa 2164
 Db 21844 -----GTGCATTAACCGATTAACCTT----- 21824
 QY 2164 lValLeuAsnSerValIleGlnIlyrPheProSerSerGluTyr--LeuAlaGluIleAl 2183
 Db 21823 -----TCGGAATTAACAAAGATTTGATGTCTCGTTATTAACCTTGCGTATTTAGA 21774
 QY 2183 aAspThrLeuIleHisLeuProAsnValGlnAlaGlyIlePhePheGlyAspValArgSerG1 2203
 Db 21773 GGAATGCTTAAGTATGATCGACTCTAGAAATATACATTAATGCTGCG----- 21728
 QY 2203 nAlaThrAsnGluHisPheLeuAlaAlaArgAlaIleHisThrLeuGlyLysAsnAlaTh 2223
 Db 21727 -GGGACAGCT-----TTTATAGTGTCTTATCTGATTTGAATCTA----- 21689
 QY 2223 rLysAspAspValArgGlnLysMetAlaGluLeuGluAspMetGluGluLeuLeuVa 2243
 Db 21688 -----CAAGATACAGATCATGCAATTTATGTTTCATATACGTCGATATATGAGGAATAGC 21633
 QY 2243 lGluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGluH1sValG1 2263
 Db 21632 ATGATTAAGTGTATGATCGAAATTTAAATGATTTATTTTCA-----GAAAGAGCGGTGA 21579
 QY 2263 uIleLeuProLysAspMetGluAlaValaLaengLysLeuSerAlaTyrArgTyrAlaAlaVa 2283
 Db 21578 AATTAATGTTATCAAACTTAAGTCACT----- 21551
 QY 2283 lValHisValArgGlySerLeuGly-----AspGluLeuValLeuProVa 2298
 Db 21550 -----CTTGATATTTGAGTGTATGATGATGATGATGATTTTATACAGA 21510
 QY 2298 lGluLysAspAspTrpIle-----AspPheG1 2307
 Db 21509 AAACATGATATCATTAATTCATCAGATGCTCTGACAGATCACTTGCTGATATGATGA 21450
 QY 2307 nAlaAsnGlnLeuAsnGlnLysSerLeuGlyAspLeuLeuLysSerAsp----- 2324
 Db 21449 ATTTGAAAAGTAAATGTTCAAGCTACTGTTGATGTCATACGTTTGGCAACAACATCA 21390
 QY 2325 -AlaAlaIleMetAlaValSerLysIle----- 2333

Db 25637 TACAGTGGCTTGGCTTACGTGATTTAATCAGCAATTTGACAGCATTA 25578
 Qy 842 ophetheThAspIleProSerTrpTyProAlaAsnThrPheProAspGlyAlaIysle 862
 Db 25577 ATTTATCAAAAGAT-----TCAAAATATA-----AATCAGCTGAT 25545
 Qy 862 uTyArgThGlyAspLeuAlaArgTyAlaSerAspGlySerIleValCysLeuGlyAr 882
 Db 25544 GTATTAGAGTGTGATATCGTTCGTTTGTTTACCCGATGCGCAACATTAATTATATTCG 25485
 Qy 882 gIleAspSerGlyValIysIleArgGlyValArgValGluLeuGlyAlaIleGluThrH 902
 Db 25484 AAAGCAAAACAGTTAGATTAAGATTCAGAGGTTTGGATGAGTTGCAGAGGTGAG----- 25430
 Qy 902 sleArgGlnGlnImerProAspAspLeuThrIleValIleValGluAlaThrIysArgSerG 922
 Db 25429 -----CARGCGCTCGAGCTATATCA 25410
 Qy 922 nSerAlaAsnSerThrSerLeuIleAla-----PheLeuIleG 935
 Db 25409 AGGTATTATTAAGACAGTTGTTATTTCAAAATCATGATCATGATCATGATATCGTT-- 25352
 Qy 935 ySerSerTrpPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrLy 955
 Db 25351 -----GCTTATTTAT-----GAAGCGATGATACATTCATCATATTAAGATTA 25308
 Qy 955 sAlaIleAsnIleLeuLeuGlnGlnValIleuProArgHisSerIleProSerPheTyri 975
 Db 25307 ATCA-----CAATTAGCGATGACCTTACCGGAGTACATGATACAGATTAATTTAT 25257
 Qy 975 eCyMeLeuGlnLeuProArgThrAlaThrGlyIleAspArgArgArgLeuAla 995
 Db 25256 GCATATTGACCAATTCCTATTACTATTAAATGGGAAATTAAGATTAAGAGCATTTGCTAT 25197
 Qy 995 eMeGlyLeuAspIleLeuAspIlyGlnThrGlnGlyAlaIleValGlnGlnAlaProAl 1015
 Db 25196 CATG-----GACTATGTCGAT-----ACGCGATGC 25173
 Qy 1015 aProIleProValPheAlaAspThrAlaAlaIleLeuHisSerIleTrpValGlnSerle 1035
 Db 25172 CTATGTAGCAACCGATGACGATACCGAAACCTTGCTATGCGCAATTTTGGAGATATTTT 25113
 Qy 1035 uGlyIleAspProAlaThrValAsnValGlyAlaThrPhePheGluLeuGlyGlyAsnse 1055
 Db 25112 ACATGTGCAAT-----CAAGTAGCTATTCATGATTAATTTCTTGAATTAGCTGCCATTC 25059
 Qy 1055 rIleThrAlaIleLeuMetValAsn---MetAlaArgSerValGlyMetAspLeuIysVa 1074
 Db 25058 ATTAAAGCAACGTTAGTGTGATGCGATGAGGCACTTCTGGGAAACGATTACAAAT 24999
 Qy 1074 lSerAsnIleTyrglnHisProThrLeuAlaGlyIleSer---AlaValIlyGlyAs 1093
 Db 24998 TGGTGAATTTTCAAAAGCACTGATTTGAATTTGACGACACAGCAGTTGGTAAAGTTCA 24939
 Qy 1093 pProLeuSerTyThrLeuIleProIlySerThrHisGlnGlyProValGlnGlnSerTy 1113
 Db 24938 AGAACAACACTAGTACGATGTTCCAGAAACTAGTAAAGATGATTAATGTCGACCTC 24879
 Qy 1113 rSerGlnGlyArgLeuThrPheLeuAspGlnLeuAspValGlySerLeuTrpTyriLeu 1133
 Db 24878 TGCCAAAGAGGATGATTTATTTATGGAATCAACATTAAGATTCGCGTATTAACGT 24819
 Qy 1133 eProTyAlaValAlaArgMetArgGlyProValAsnValAspAlaLeuArgAlaLeuAl 1153
 Db 24818 ACCTTTATTTATGGCGGTTATCATCAGAACTTAATGTAGCTCAATTTGGACAGAGAGTCA 24759
 Qy 1153 aAlaLeuGlnGlnArgHisGluThrLeuArgThrPhe-----GluAspGlnAs 1170
 Db 24758 GCGTTTGATAGCGGACATGATGATTTTACGAACAATATTTGTTAGTATGATGAG-- 24701
 Qy 1170 pGlyValGlyValGlnIleValHisGlyIleLeuSerGlnGlnMetIysValIleAspLe 1190
 Db 24700 -----GTTGCAACAACGATTGTCGACATGTCAGTT----- 24668

Qy 1190 uCyGlySerAspLeuAspProPheGluValLeuAsnGlnGlnThr----- 1206
 Db 24667 -----GACTTTGAGAAAGTTAACACGCAATTTACGATGAAACAAG 24627
 Qy 1207 -----ThrProPheAsnLeuSerSerGlnAlaGlyTyTrpArgAlaTh 1220
 Db 24626 AATCATGCGCCAAATTTGAGCACCTTTTAAATTTGAAAAACCAAGTCMAATTTGAGTGA 24567
 Qy 1220 rLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValIleMetHisIleIleSe 1240
 Db 24566 ATACATTAGAAAGCCCTTACATGCATAC---CTCTTTATGATAGACGATCATATCTTAA 24510
 Qy 1240 rAspGlyTyPseTrIleAspValLeuArgAspLeuAsnGlnLeuTySerAlaAlaLe 1260
 Db 24509 TGACGGTATGAGTAATATCAATTAATGAATGATCTTAAACGCACTTATATCAACATAATT 24450
 Qy 1260 uTyAspSerLeuAspProLeuSerAlaLeuThrProLeuProIleGlnTySerAspH 1280
 Db 24449 A-----TTGTTACCACTTAAATTCMAATTAATAAGACTA 24417
 Qy 1280 eAlaTyTrpGlnIleAspGlnPheIleGlnGlnIleuAsnTyTrpIlybly 1300
 Db 24416 TATGAGTGAATGCCATGCCATGATATGACGAACATAGACA-----TATGTTATTC 24363
 Qy 1300 sGlnLeuIleAspSerSerPro---AlaIysIleProThrAspPheAlaArgProAlaLe 1319
 Db 24362 TCATTCMAAAGATGAAGTACCTATTTTAACTTACCGACAGACTATGTTAGACCAATAT 24303
 Qy 1319 uLeuSerGlyAspAlaGlyCysValHisValThrIleAspGlyGluLeuTyGlnSerle 1339
 Db 24302 TAAACCAACAATGAGCAATGATGTCATTTACAAATGAATCAACAATGAGACGACTACT 24243
 Qy 1339 uArgAlaPheCysAsnGlnHisAsnThrThrSerPheValIleuLeuAlaIleAsp 1359
 Db 24242 TCAAAAGTATGTAAGAAAGCATCAAAATTAATCTGATTTATGATGATGATGATGAT 24183
 Qy 1359 gAlaAlaHisTyArgLeuThrAlaValGluAspAlaValIleGlyThrProIleAlaAs 1379
 Db 24182 GAGTTGTTAAGTAGATATGCTCGAAAGATGATGTTGTTGCGTAGTGTGATGATGC 24123
 Qy 1379 nArgAsnArgProGluLeuGlnAspIleIleGlyCysPheValAsnThrGlnCysMetAr 1399
 Db 24122 GCGTATGATTAAGCAACGAGCAAGGAAATGCTAGGCACTTTGCTAAATCGTGTATATAG 24063
 Qy 1399 gIleAsnIleAspHisIleAspThrPheGlyThrIleuLeuAsnGlnValIysAlaThrTh 1419
 Db 24062 AGGCAACCGTCACCTGATTAATATGCGACACAGTTTATACAGAGCTTAAGAAATGAG 24003
 Qy 1419 rThrAlaAlaPheGluAsnGluAspIleProPheGluAspValIleSerAlaLeuGlnPr 1439
 Db 24002 TTTGAGAGCATACGACATCATCAAGAAATACCATTCGATGTTTGAATGACTTAGATCA 23943
 Qy 1439 oGlySerArgAspLeuSerSerThrProLeuAlaGlnLeuIlePheAlaValHisSerG 1459
 Db 23942 A---TCAATGATGAGCCGTCAGCAATCCATTAATTTGATGATGTTAGTACAAACAA 23886
 Qy 1459 nIys-----AspLeuGlyArgPheIlyPheGlnGlyLeuGlnSerValProVa 1475
 Db 23885 TGAACCAATCATGCTCATTTTGGCATAGTAAATTAACACACATCA----- 23837
 Qy 1475 lProSerLeuAlaTyThrArgPheAspMetGluPheHisIleuPheGlnGlnIleThrAspSe 1495
 Db 23836 -CCCAATCAGTACGCGCAAAATTTGATTAATTTTATTCATCATGTAAGAAGATGCGCATGA 23778
 Qy 1495 rLeuIyGlySerValAsnPheAlaAspGluLeuPheIlyPheMetGlnIleValGluAsnVa 1515
 Db 23777 CTATACATCAATCAATAGAGATTAATACGATTTATATCACTAGAAACAGTTGTCATCAT 23718
 Qy 1515 lValArgValPhePheGluIleuArgAsnGlyLeuGlnSerSerArgThrProValSe 1535
 Db 23717 GCGTAAATCAATGATATG---ATTATGATGATTTATTTTGAAGCATCAAGATACACTACA 23661

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|----|-------|---|-------|
| Qy | 1535 | rTlLeuProLeuThraSpIglYleValThrLeuGluYbLeuAspValLeuAspVal-- | 1554 |
| Db | 23660 | AAATTGTGATATACCAACGAC-----ACGAGAGAACTTTAAATTTGGTCAATACGCA | 23607 |
| Qy | 1555 | -----LysHisValAspTyrProArgGluSerSerLeuAlaAspValPheGlnth | 1571 |
| Db | 23606 | TGTTAAAGCATCGAATGCTTATATGTCGCCGGAATAATATCATATCAAGTACTTTAATGA | 23544 |
| Qy | 1571 | rGlnValSerAlaTyrProAspSerLeuAlaValAlaAspSerSerCysArgLeuThrTy | 1591 |
| Db | 23546 | AGTTGTCTCACAGCAACAGTAATCATGTTGGCTGACATCAATGAATTTGCATGACGTGA | 23487 |
| Qy | 1591 | rThrGluLeuAspArgGlnSerAspIleLeuAlaGlyTyrPheLysArgArgSerMetTr | 1611 |
| Db | 23486 | TGAACATTTACGCAACATATGTGTGATGTCATGGCCACATGCTCTATCAATGTCGTGG | 23427 |
| Qy | 1611 | oAlaGluThrLeuValAlaValPheAlaProArgSerCysGluThrIleValAlaPheh | 1631 |
| Db | 23426 | CAATGTGTCAACGGGTTCCTTTGTTTACAGAACTGATTTTGAATGATTTCCGCGCATGTT | 23367 |
| Qy | 1631 | eGlyValLeuLysAlaAsnLeuAlaTyrLeuProLeuAspValArgSerProSerAlaAr | 1651 |
| Db | 23366 | GGCAGCAGTTAAAGTAGTGCGATCTCTATATACCTATGATGATATTTCCGATTAACG | 23307 |
| Qy | 1651 | gValGlnAspIleLeuSerGlyLeuSerGlyProThrIleValLeuIleGly-----Hi | 1669 |
| Db | 23306 | ACAAGGTGCATATTTTGAGAGATGCTAAAGTAAGTACGTGCATGCTATTCGCGCTTGAAAT | 23247 |
| Qy | 1669 | sAspThrAlaProProAspIleGluValThrAsnValGlu---PheValArgIleArg-- | 1687 |
| Db | 23346 | TGAACACACATTACACGTCTTCATCTTCAATTTGAAATTCCTAAAGGCTTTGTGTGATCAAAAGA | 23187 |
| Qy | 1688 | -----AspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGluI | 1703 |
| Db | 23186 | AAATGAACAAATATGATGATTTATACATGCGCATCACTGAAACACAGCGCATGTTAATGA | 23127 |
| Qy | 1703 | sAspSerThrLysProSerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerTh | 1723 |
| Db | 23126 | TGAC-----ATGATGTCATTTATTAACACATCTGGTACGAC | 23094 |
| Qy | 1723 | rGlyArgProLysGlyValMetIleGluHisArgValIleIleArgThrValThsSerG | 1743 |
| Db | 23093 | CGGATGCTTAAAGGGGTGGCATACACAAACGAATTTGTGAATTTAGTGCATGCA-- | 23038 |
| Qy | 1743 | yCysIleProAsnTyrProSerGlnThrArgMetAla-----HisMe | 1757 |
| Db | 23035 | -----TGCTCACTGAAATTTGCATTAAGCGCAATTAAGCATATTTTGGACA | 22988 |
| Qy | 1757 | AlaThrIleLeuAlaPheAspGlyAlaSerTyrGluIleTyrSerAlaLeuLeuPheGlyAr | 1777 |
| Db | 22988 | TGCAAATATTTGTTTGTATGCATGACATTAAGAGATTATTTGTTTGTAAATGGTCA | 22928 |
| Qy | 1777 | gThrLeuValCysValAspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValh | 1797 |
| Db | 22928 | TACCTGTGTATTCACATATGAGAGAAACGTGTTAAATCCAGAACAGTTTCAACAACTCAT | 22869 |
| Qy | 1797 | ePheArgGluHisValAsnAlaAlaSerHisValThrSerSerGlnAspValProle | 1817 |
| Db | 22868 | TAAATACATCTGTGTACGCGTGGCTG----- | 22844 |
| Qy | 1817 | uArgValProArgArgLeuSerArgThrLeuMetPhePhePheLeu-----ValAlaTh | 1835 |
| Db | 22840 | -----ATTCGGTTACAGATGTGTAGTGTATGAAGACTTTTATTTGAAAAGTTGATTAAC | 22785 |
| Qy | 1835 | rAspSerThrAlaProAspAlaLeuAspAlaGln-----GlyLeuTy | 1849 |
| Db | 22784 | AGCGGGGCAACTAGTACGCGATCTTTGTTTAAATATATTGAGAACGATTTGGACGGA | 22725 |
| Qy | 1849 | rGlnGlyValGlnCysTyrAsnGlyTyrGlyProThrGluAsnGlyValMetSerThrI | 1869 |
| Db | 22724 | T-----TTCAATGCTGTATGACATCTAGACTCAACAGTATATCATCATCGTA | 22688 |
| Qy | 1869 | eTyrProIleAspSerThrGluSerPheIleAsnGlyValProIleGlyArgAlaLeuAs | 1889 |

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|----|-------|---|-------|
| Db | 22619 | TTGGTCACATCATTTGGTGGTATTTGATACCTGAGACGATTCSCATTTGGCAACCCCTTATC | 22622 |
| Qy | 1889 | naenSerGIyAlaTyValValAspProGluGlnLeuValGIyIleGIyValMetGI | 1909 |
| Db | 22619 | TAAATCCAAAGTGAATATATATGCA---GATGGTTGTTATATGCGGATTTGGATATGCGAG | 22653 |
| Qy | 1909 | yGIuLeuValValThrGIyAspGIyLeuAlaArgGIyT | 1922 |
| Db | 22562 | CGAGTTTGATGATTCAGAGTGATAGTTTGAAGATAGATATATTAACTGCCAAATTAAAT | 22503 |
| Qy | 1923 | -SerAspLyAlaLeuSerGIyAsnArgPheValHisIleThrValAsnAspGIuThrVal | 1942 |
| Db | 22302 | GGCTGATAAA---TGCGAAATATATTCATTT-----GGTAAAG | 22466 |
| Qy | 1942 | LyValAlaTyArgThrGIyAspArgValAlaArgTyrArgIleGIyAspGIyLeuIleGIuPh | 1962 |
| Db | 22466 | AAAGTTGTATCATATAGTGTGATTTAGACGCTTAT---ACATCGATAGGTCAATTCATTT | 22410 |
| Qy | 1962 | ePheGIyArgMetSerThrGIuPheLyIleArgGIyAsnArgIleGIuSerAlaGIuI | 1982 |
| Db | 22409 | TTTGGAAAGATATGATTAACAAATGAAAGTTAACCGGGTACCGGTATTAACCTGATTAAT | 22355 |
| Qy | 1982 | eGIuAlaIleLeuLeuArgAspSerValAlaArgAspAlaIleValIleuGlnIle | 2002 |
| Db | 22349 | TGAAATGCAATATTAATCTATTCGTGGTATATGATGTGTGTGTTAAACGTATGTCATTT | 22290 |
| Qy | 2002 | nGIuAspGIuAlaProGIuIleuGIyPheValIleAspHisAspHisSerGIuAs | 2022 |
| Db | 22289 | TGATATGCCAT-----GATATATTTGAATGCTTTATATGTCGAGACCAACAAAGTGGAA | 22233 |
| Qy | 2022 | naSpLyGIyGlnSerAlaAsn-----GlnValGIuGIyTyrGlnAs | 2036 |
| Db | 22235 | GGATTTGAACCAATATTTAATATGATGACGTGCTTAATATGATTCCTTAAGACTATAAC | 22170 |
| Qy | 2036 | PhIePheGlnSerGIyMetYrGexAspIleGIyGluIleAsp----- | 2050 |
| Db | 22175 | GCATATGCAATTTGATGCCATTAAACCAAGTAACAAGGTGGATTAACCGCTTGGCAAA | 22118 |
| Qy | 2051 | -ProSerThrIleGIySerAspPheLyGIyTyrThrSerMetYrAspGIySerGlnI | 2070 |
| Db | 22115 | TCCATCACTATACAAAGCTATAAAGGTATACGAAACCTCAATGAATATGAGA | 22055 |
| Qy | 2070 | eAspPhe--AspGIuMetHisGIuTyrPheGIyGluThrThrArgThrLeuHisAspAs | 2089 |
| Db | 22055 | GACATTTGGTATGATATTTGGAAGGATATGAACAAATATGATGTCGGTGTGACGAT-- | 21998 |
| Qy | 2089 | naYrSerLeuGIyAsnValLeuGIuIleGIyThrGIySer-----GlyMetIleLeuPh | 2107 |
| Db | 21997 | -----GATTTCTTAAACTGGTGTGTACTCATTAAGCGCATGTATCTTGT | 21951 |
| Qy | 2107 | eAsnLeuAspSerArgLeuGIuSerTyrValGIyLeuGIu-----ProSerArgSe | 2124 |
| Db | 21950 | CTCCCATTTAAACGATTTGGCCATCATATTTAAATGACGACATTTACCATATATAAC | 21891 |
| Qy | 2124 | rAlaAlaIlePheValAsnLyAlaThrGluSerIleProSerLeuAlaGIyLyValAlaLy | 2144 |
| Db | 21890 | CGTCCGACAGATTTGTTATATATATGTAACAAATCAACATATCTTA | 21845 |
| Qy | 2144 | sValGlnValGIyThrAlaThrAspIleGIyGlnValAspAspLeuHisProAspLeuVa | 2164 |
| Db | 21844 | -----GTTCGATTAACCGGATTAATCTT----- | 21824 |
| Qy | 2164 | lValLeuAsnSerValIleGlnIlyrPheProSerSerGIyTyr--LeuAlaGIuIleAl | 2183 |
| Db | 21823 | -----TCGGAATTAACAAAGATTTGATATGCTCGTTAAACTTGGGATTTTAA | 21774 |
| Qy | 2183 | aAspThrLeuIleHisIleuProAsnValGlnArgIlePhePheGIyAspValArgSerGI | 2203 |
| Db | 21773 | GGATATGCTAAAGTCATGACGCTACGGAATAACATATGACGTGGC----- | 21728 |
| Qy | 2203 | naIleThrAsnGIuHisPheLeuAlaIleArgAlaIleHisIleThrLeuGIyLyAsnAlaTh | 2223 |

SEQ ID NO 627
 LENGTH: 7215
 TYPE: DNA
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-627

Alignment Scores:

| Pred. No.: | 3,54e-139 | Length: | 7215 |
|------------------------|-----------|---------------|------|
| Score: | 1425.50 | Matches: | 581 |
| Percent Similarity: | 41.42% | Conservative: | 459 |
| Best Local Similarity: | 23.14% | Mismatches: | 1040 |
| Query Match: | 8.84% | Indels: | 431 |
| DB: | 3 | Gaps: | 94 |

US-09-482-788-2 (1-3129) x US-09-134-001C-627 (1-7215)

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QY 68 GlnSerAlaIleGlyHisAlaVal-----TyrAspValProThrAspIleAspIle 84
DB 106 CATCAAGTTCAGAAACAGCGGTGACATCTGGTAAAGTTAAGTCGCGCATTTGAGTTA 165
QY 85 SerArgPheAlaLeuAlaTrpLysGluIleValAsnGlnThrProAlaLeuArgAlaPhe 104
DB 166 CGTAGTTAATGATGATGATTTAGATGCTGTTCAAGTCAACCTGTGTGCGTACA--- 222
QY 105 AlaPheThrSerAspSerGlyLysThrSerGlnValIleLeuLysAspSerPheValPhe 124
DB 223 CAGTTTGTCAGATGATTTTATCAACTCAAGATAATTAAAGATTTTTCATT 282
QY 125 SerTrpMetCysTrpSerSerSerSerProAspGluValAlaArgAspGluAla 144
DB 283 -----ATTGAAATTTAAAGAAAGTTAAATGAAATGTCGAAACATAGATTTA 327
QY 145 AlaAlaAlaSerGlyProArgCysAsn-----Arg 154
DB 328 GAAGCATCTTTACACGTAATTTAAATCTTACCATTCAATCAATTAACCTGTGTTAAT 387
QY 155 PheValLeuLeuGlnAspMetGlnThrLysCysGlnLeuValTrpThrPheSerHis 174
DB 388 TTTAAGATTTTCAATTCTTGAT-----GAAGCCCTACTACTTTAGATTTCACGCT 441
QY 175 AlaLeuValAspValThrPheGlnAlaArgValLeuSerArgValPheAlaAlaTyrLys 194
DB 442 ACTAATTTTAAATGAAGTCAATTAACCTCATTTTTCACAAATTAATATCGCTTAAC 501
QY 195 His----- 195
DB 502 CACTCTTTAAAGAAAGTAATAGTATCTCGAATTTTAAATGATGATTAAGAAATGAAT 561
QY 196 ---GluLysAspThrHisArgProGluThrProGluSerSerAsp-----AlaThr 211
DB 562 CAAGAATGATGATAAATCAAGTGTGTGTCATCAAGCACTTCAACCGATTGAATGCA 621
QY 212 AspThrAspSerGlnSerValSerValSerMetSerCysGluAspAsnAlaValSer 231
DB 622 GACGGGATGATTAATACCTTCACTACCTGTTAAGAAATCATGATGAAAAAAGAAATGTGT 681
QY 232 AlaThrHisPheTrpGlnThrHisLeuAsnAspLeuAsnAlaSerValPhe----- 248
DB 682 TCTTTCAT-----GCAGAACTAACCATCTTTAGACATGATGATGATGATGAT 722
QY 249 ProHisLeuSerAspHisLeuMetValProAsnProThrThrAlaGluHisArgIle 268
DB 733 ATTTACTTACCGCATCTTTTAAAGTCAGCTCTTTCATGATGACGTTA-----GGATC 786
QY 269 ThrPheProLeuSerGlnLysAlaLeuSerAsnSerAlaIleCysArgThrAlaLeuSer 288
DB 787 CATTTTTCATGATGATATAAATAATACGAAATATGATGATTTTAAACACAGACATGCGC 846
QY 289 IleLeuLeuSerArgTrpThrHisSerAspGluAlaLeuPheGluAlaValThrGluGln 308
DB 847 CCACTTAATTTAAGATTAATGATCAAGATGAC--GTGCTAAAGATATGATGATGATGT 903
QY 309 SerLeuProPheAspLysHisTyrLeuAlaAspGlyThrTyrGlnThrValAlaPro--- 327

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DB 904 TCCGCTCTACTTGAAGAGCTTCAAAATGTGTGTCGCTCTTT---GTTGTCAACCTAAA 960
QY 328 ---LeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIleSer 346
DB 961 GCAGTACAAATTAATAGTATGAAACAGATGATTCATATTGAAAAAAGTACAAACAATTT-- 1017
QY 347 SerTyrAspAspArgLeuGlnHisLeuAlaProPheGlyLeuArgAspIleArgAsnThr 366
DB 1018 -----GAGCTTAATCATATATGT-----CATCATATACATCGCTTA 1053
QY 367 GlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySer 386
DB 1054 TACAAATGAACATCATCATTCGCGGATTTAGATTTTATTCCTCATGTCGAGATGTTT 1113
QY 387 HisVal-----AspAsnGly----- 391
DB 1114 GATATAGTTTATATATGACAAAGTTTATGATGATTTAATCTGTACATACGTTAGTCAATTA 1173
QY 392 IleAsnGlyPheLeuGlnGlnIleThrGluSerSerHisPheMetProCysAsnAsnArg 411
DB 1174 ATTAATGCGATTTATATGCAATTTACAA-----ATTCGA 1209
QY 412 AlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuLeuValAlaTyrTyrAsp 431
DB 1210 TCATTTATTAATTAAGATATTAAGTAAACACAGTATCGCTCAGATTTAGCTAATATTAATGAC 1269
QY 432 HisAsnValIleAspSerLeuGlnThrThrArgLeuLeuGlnGlnPheGlnHisLeuIle 451
DB 1270 ATCAAT-----CTTCAAAAATGATGACTT----- 1293
QY 452 LysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGlu 471
DB 1294 -----AATTATAGTAGGTCTTAATAAACCGCTG 1323
QY 472 TyrAspArgAlaGluIleGluSerTrpAsnSerGlnProLeuGlnValGlnAspThrLeu 491
DB 1324 GTTGAAAGATTCGA----- 1338
QY 492 IleHisIleGluMetLeuLysAlaValSerHisSerProThrLysThrAlaIleGlnAla 511
DB 1339 -----CCTCAAGTGCACCAACATCCCATGATGATTTGGTTCATATAT 1380
QY 512 TrpAspGlyAspTrpThrTyrSerGluLeuAspAsnValSerSerArgLeuAlaValHis 531
DB 1381 GAACAAACGATCGATGACATATCATCATTTAAATCAATGTCGATCTTTTACGATATAGA 1440
QY 532 IleLysSerLeuGlyLeuArgAlaGlnAlaIleIleProValTyrPheGluLysSer 551
DB 1441 TTGCGTTTAAATCATGACATGAAACCTAATGATATGATGTGTCATTAATAGCAAGACGAC 1500
QY 552 LysTrpValIleAlaSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIle 571
DB 1501 TTGAAGATGATTTTGAAGATTTGAGGATCTTGAAGACGTGTCAGAGTACATCAACAAAT 1560
QY 572 AspProAsnAspProProAlaArgThrAlaGlnValValThrGlnThrArgAlaThrVal 591
DB 1561 GATCCGATATATCTGGAAGAAAGATGATTAATTAATTAAGAGACGCAAAACCTAAAGCG 1620
QY 592 AlaLeuThrSerLysLeuHisArgGluThrValGlnLysLeuValGlyArgCysValVal 611
DB 1621 GTTGTAACA-----TATGCTACATCATTTCAATCAAGCTTTTACCTCAAA----- 1662
QY 612 ValAspAspGluLeuLeuGlnSerValSerAlaSerAspAspPheSerSer----- 628
DB 1663 ATGATATATGATATGATGATGATGAT--TCAGAGAAACATGATATTTGATTAACCCGAGAGGC 1719
QY 629 LeuThrLysSerGlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspPro 648
DB 1720 ATTAATTTTCAAGATATCGCTTATGCTATGCTATATACATACAGAAACGATCTGTAACCT 1779
QY 649 LysGlyIleMetIleGluHisArgAlaPheSerSerCysAlaLeuAspPheGlyAlaSer 668

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QY 2086 LeuHisAspAsnArgSerLeuGlyAsnValLeuGluIleGlyThrGlySerGlyMetIle 2105
 Db 123 CTCTCTGACACAGCCAGCCGGAAGAGTCTCGAGATCCGAACTGGTACCGGATGGTG 182
 QY 2106 LeuPheAsnLeuAsp-----SerArgLeuGlySerTyrValGlyLeuGluProSerArg 2123
 Db 183 CTTTTCATCTGGGCAAGGTGAGGAGCATACAGAGCATCGGCTTGAGCCCTGGCGC 242
 QY 2124 SerAlaAlaAlaPheValAsnValAsnValAsnValAsnValAsnValAsnValAsnVal 2143
 Db 243 TCCGTCACCTGCGGCTTAAACAAGCAATCTTCCCAAGCCTGGAGGAGAGCGCC 302
 QY 2144 LysValGlnValGlyThrAlaThrAspIleGlyGlnValAspAspLeuHisProAspLeu 2163
 Db 303 CAGATCAGCTTGGAACCGCCGAGAGTGAAGTCCATCAATGAGACTGCGTCCGAGTCTC 362
 QY 2164 ValValLeuAsnSerValIleGlnTyrPheProSerSerGlyTyrLeuAlaGluIleAla 2183
 Db 363 GTTGATATCACTCGGCTCCGCAATCTTCCCAAGTCAGAAATATCTCGCTGAGCTGACG 422
 QY 2184 AspThrLeuIleHisLeuProAsnValGlnArgIlePhePheGlyAspValArgSerGln 2203
 Db 423 GCCAATCTGATTCGACTGCGCGCGTCAGACGCTATTTCTTCGCGCAGATGAGAACCTAT 482
 QY 2204 AlaThrAsnGlnHisPheLeuAlaAlaArgAlaIleHisPheLeuGlyLysAsnAlaThr 2223
 Db 483 GCACCAATTAAGGACTCTTGTGGGACGAGCAGATCAATCCCTAGGAGTCCAAATGCAATCT 542
 QY 2224 LysAspAspValArgGlnLysMetAlaGluLeuGluAspMetGluGluGluLeuVal 2243
 Db 543 AAGGCCATGGTTCGACACAGAGTGGCCCAAGCTTGAAGATACAGAGAGAGTTCCTTGT 602
 QY 2244 GluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGluHisValGlu 2263
 Db 603 GACCCGCTCTTCTTCCACGAGCTGAGCAGACATTCCTCAGCAAAATCAAGCAGCTGAG 662
 QY 2264 IleLeuProLysAsnMetGluAlaValAsnGluLeuSerAlaTyrArgTyrAlaAlaVal 2283
 Db 663 ATTCTCCCAAGAGGATGGCCGCGCAGCCAACTCACTTCAACGATATGCTGCTGT 722
 QY 2284 ValHisValArgGly-----SerLeuGlyAspGlu-----LeuVal 2295
 Db 723 ATTCACTGGGAGCCAGCAGATGCCGAATGGGAGATACGATACGATAGCATGGCTGTC 782
 QY 2296 LeuProValGluLysAspAspTyrIleAspPheGlnAlaAsnGluLeuAsnGlnLysSer 2315
 Db 783 AAGGATATCGATCCGAAGGCTGGGTGACTTCGCGCGCAGAGATGAGACCGTCAAGCT 842
 QY 2316 LeuGlyAspLeuLeuLysSerSerAspAlaAla-----IleMetAlaValSerLysIle 2333
 Db 843 CTCTTCAGCTCTCTCGACGAGCCGCAACGTGGCGATGACCTTGTGCGCTGATTAACATC 902
 QY 2334 ProPheGluIleThrAlaPheGluArgGlnValAlaIleSerLeuAsnSerAsnIleAsp 2353
 Db 903 CCATACAGCAGACCATATGAGAGCCCATCTGTCTCACTTGAACATGACGAGAGAC 962
 QY 2354 -----GluTyrPheLeuSerThrIleArgSerSerAlaGlu 2365
 Db 963 GGCACCTTCAGATCGACAGCAGCGCTG---ATATCGCCCACTCAATCAGCGGCGAAG 1019
 QY 2366 GlyAspSerSerLeuSerValProAspIlePheArgIleAlaGlyGluAlaGlyPheArg 2385
 Db 1020 GAATGCCCTGCTCTTCAGTGGCGCATGATGAGATGATGAGGAGATCGGCTTCCAA 1079
 QY 2386 ValGluValSerSerAlaArgGlnTyrSerGlnAsnGlyAlaLeuAspAlaValPheHis 2405
 Db 1080 GTTGAACACAGCTGGGCTGACACACACTCCACAGCGGCGGAGCTCATGCTGTTTCCAC 1139
 QY 2406 -----HisCysCysSerGlnGlyArgThrLeuValAsnPheProThr 2419
 Db 1140 CGATCGAAAAACCAAGACAC-----TCGGGTGATGTCATGTTCCAGTTCCTCACT 1190

QY 2420 AspHis-HisLeuArgGlySerAspLeuLeuThrAsnArgProLeuGlnArgLeuGlnAs 2439
 Db 1191 GAAACACAGGGGGCGGTCTTTCAGCAGCTCATAGATCCGCGCTACACTGGTTGAG 1250
 QY 2439 nArgArgIleAlaIleGluValArgGluArgLeuAspSerLeuLeuProSerTyrMetIle 2459
 Db 1251 CCGCGGCTGAGAGCAAGGTCCGCGAGCGGCTGACATCGCTGCTTCATCGTACATGAT 1310
 QY 2459 eProSerAsnIleValAlaLeuAspLysMetProLeuAsnAlaAsnGlyLysValAspAr 2479
 Db 1311 TCCCTCTCGATCATATGCTGATCAAGATGCTCTCACTCAAGCGGCAAGGTGAGTCG 1370
 QY 2479 GlyGluLeuSerArgArgAlaLysValValPro-LysGlnGlnThrAlaAlaProLeuP 2499
 Db 1371 CAAAGAGCTCGCTCGACAGCCCGGCTCATCCCAACATTCGCCCAAGCAGCTTGAGCTT 1430
 QY 2499 roThrPheProIleSerGluValGluVal-IleLeuCysGluGluAlaThrGluValPhe 2518
 Db 1431 TGTGGCGCGCAGCAGCAAGATGAGAGTGGCTTCTGCGCAAAATTAACCGATCTACTA 1490
 QY 2519 GlyMetLysValAspIleThrAspHisPhePheAsnLeuGlyGlyHisSerLeuLeuAla 2538
 Db 1491 GGGGTCAAGGTCCGCAATTCACAGCAACTTCTTGAGTGGCGGCGCATTCGCTGGCC 1550
 QY 2539 ThrLysLeuIleSerArgIleAspGlnArgLeuLysValArgIleThrValLysAspVal 2558
 Db 1551 ACBAATGAGCGCAGCTCTTAAGTCCGACACTGAGCCGCGTCTCATCTGGAAGCAGATC 1610
 QY 2559 PheAspHisProValPheAlaAspLeuAlaSerValIleArgGlnGly 2574
 Db 1611 TTGACACAGCAGTACTTGCTGATCTTGCTGCTTCTTATTCGTAAGGC 1658

RESULT 13
 US-08-222-617A-26
 ; Sequence 26, Application US/08222617A
 ; Patent No. 5882879
 ; GENERAL INFORMATION:
 ; APPLICANT: Veenstra, Annemarie E.
 ; APPLICANT: Martin, Juan F.
 ; APPLICANT: Garcia, Bruno D.
 ; APPLICANT: Gutierrez, Santiago
 ; APPLICANT: Barredo, Jose L.
 ; APPLICANT: Von Doehren, Hans
 ; APPLICANT: Palises, Harriet
 ; APPLICANT: Van Lierp, Henk
 ; APPLICANT: Montenegro, Eduardo P.
 ; TITLE OF INVENTION: A Method for Influencing Beta-lactam
 ; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
 ; TITLE OF INVENTION: Quantities of ACV Synthetase
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,617A
 ; FILING DATE: 04-Apr-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; REFERENCE/DOCKET NUMBER: 97,157
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11444 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

858 AspglyAlaIyLeuLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIle 877
Db 2400 -----ATGACAAAGACCGGTGACCTGCGCGCTGCGACGCGAGGTT 2447
Gly 878 ValCysLeuGlyValArgIleAspSerGlnValLeuIleArgGlyGlnArgValGluLeuGly 897
Db 2448 GAGTATCTCGGACCGCGACGATTTCCAGATCAAACTCGAGGTATTCGAATTTGAACCTGGT 2507
Gly 898 AlaIleGluThrHisLeuArgGlnGlnMetProAspAspLeuThrIleValIleGluAla 917
Db 2508 GAATTTGAACAGATGCTGCTATGATACCTAGGTCGCGACCGATTAGTGTGCCAA 2567
Gly 918 ThrLeuArgSerGlnSerIleAsnSerThrSer-----LeuIleAlaPheLeuIleGly 935
Db 2568 AGCTTCGCAACGCTCCAGAGAACTACCAAGAGACCTCGTGGTTATTTAGTTGT 2627
Gly 936 SerSerTyrPheGlyValAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrLeu 955
Db 2628 GATAGC-----GCCTCAGTGTCCGAGGACAGCTCTGTCATTT----- 2666
Gly 956 AlaIleAsnIleLeuLeuGlnValLeuProArgHisSerIleProSerPheTyrIle 975
Db 2667 -----TTAGAGAAAGAACTGCTCGATGATGATGATCCACGCGGTGGTA 2711
Gly 976 CysMetLeuGlnLeuProArgThrAlaThrGlyLeuIleAspArgArgArgLeuArgIle 995
Db 2712 CAGCTTCGCAATCCAGTGAATGTGAACGGGAGCGGACCTACGCGCTTGCAGGCC 2771
Gly 996 MetGlyLeuAspIleLeuAspLeuGlnThrGlnAlaIleValGlnGlnAlaProAla 1015
Db 2772 GTCGAT-----ATCTCAATTCACGAGAGTG 2798
Gly 1016 ProIleProValPheAlaAspThrAlaAlaLeuLeuHisSerIleTyrValGlnSerLeu 1035
Db 2799 CGTTCGACCTTCGAGCGGATGAGAAATGCGCTCGGAGAAATCTGGCGGACGTTTG 2858
Gly 1036 GlyIleAspProAlaThrValAsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSer 1055
Db 2859 GAGAGCCCGCAGAGATCGCTCTCGCAACAGACACTTCTCGCGCTAGAGGGGACAGC 2918
Gly 1056 IleThrAlaIleLeuMetValAsnMetAlaArgSer-----ValGlyMetAspLeu 1072
Db 2919 ATCACTGATCACTCACTGATCGCTCGCATCGCAACAGACAGACTCGTCGACGATC 2978
Gly 1073 LysValSerAsnIleTyrGlnHisProThrLeuAlaGlyIleSerAlaValValLeuGly 1092
Db 2979 TCCGTGAAGATGTTTTCACAAAGACCTTGAGCGCATGGCAGACCTTTACAGAAC 3038
Gly 1093 AspProLeuSerTyrThrLeuIleProLysSerThrHisGlnGlyPro-----Val 1109
Db 3039 AGCAGACAGAGAAATGCCAACAAC-----CATAGGCGCGGACAGAGCTGCTT 3089
Gly 1110 GlnGlnSerTyrSerGlnGlyArgLeuTyrPheLeuAspGlnLeuAspValGlySerLeu 1129
Db 3090 GAGGAGAAATCGACACAGCAATATCTATCTGCAAAAGCTTTCAGAGGGGCTTGTC 3149
Gly 1130 Trp-----TyrLeuIleProTyrAlaValArg 1138
Db 3150 TACCATTACTCTAGAGATGAAACAATCCGACGCGCTATGTAATGACGCTGTTCCG 3209
Gly 1139 MetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaIleGlnGlnArg 1158
Db 3210 TACAAACACCAATGCTCTCCAGATCTGTTCAAGAGACCTTGAAAGCATGCACGACGTC 3269
Gly 1159 HisGluThrLeuArgThrThrPheGlu-----AspGln 1169
Db 3270 TTTCAGCGCTGCGGCTGCTCTCATGTGAAAGAGGTTTCCAACTGCTGATCAG 3329
Gly 1170 Asp-----GlyValGlyValGlnIleValHis 1178
Db 3330 GATTCACCAATTTGACGTGGCGTTCTCTACTTACCAACGACGTTGCGCGGCTGCTGAG 3389
Gly 1179 GluTyrLeuSerGlnGluMetLysValIleAspLeuCysGlySerAspLeuAspProPhe 1198

Db 3390 GACCGGAAATTTGAGACATTCGCG----- 3413
Gly 1199 GluValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTyrArg 1218
Db 3414 -----CGCCAAACCTTACGAGAGATTTCAAGCTGAGTTGGCAGACTGTTCCG 3464
Gly 1219 AlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisIle 1238
Db 3465 GTCTATCTGATTTAAACACAGCGGAATCGTTACCGTCTTTTACAGCTCCATCATGCA 3524
Gly 1239 IleSerAspGlyTyrPheSerIleAspValLeuArgArgAspLeuAsnGlnLeuTyrSerAla 1258
Db 3525 ATCCGATGATGTTGAGTCTGACACTCTGTTGAAAAGGTTACAGACAGACTCTGCAA 3584
Gly 1259 AlaLeuLeuAspSerTyrAspProLeuSerAlaLeuThrProLeuProIleGlnTyrSer 1278
Db 3585 CTGCTCATGCG-----GACAACTCATCTTCGTCATGATGATACCT----- 3626
Gly 1279 AspPheAlaLysTyrGlnLysAspGlnPheIleGlnGlnLysGlnLeuAsnTyrTyr 1298
Db 3627 -----TACACTGCAACCGGAGTATCTCCAGCTCACCGTGAAGATCACCTTCATTTGG 3683
Gly 1299 LysLeuGlnLeuLysAspSerSerProAlaLysIleProThrAspPheAlaArgProAla 1318
Db 3684 GCGGATGATGTTCA-----AAGATCAACGACGCGTGTATGAAAGCGC 3728
Gly 1319 LeuLeuSer-----GlyAspAlaGlyCysVal----- 1327
Db 3729 TTGTTGAACGAGCGAGCTGTTACAAAGTCAGCTGCGACAGATGACGAGGTGACGAG 3788
Gly 1328 -----HisValThrIle-----AspGlyGluLeuTyr-----GlnSerLeuArgAlaPhe 1342
Db 3789 CAGCGACACTGTCACATTTGCTCTCTGAGAGAGCATGCTGACAGACCTTCGTCAGACC 3848
Gly 1343 CysAsnGlnHisAsnThrThrSerPheValValLeuLeuAlaAlaPheArgAlaAlaHis 1362
Db 3849 TGTCTCGGCCAGAGGTATTAACCTTAACATTCGATTCGCAATTTGTTGGACGCGTGTG 3908
Gly 1363 TyrArgLeuThrAlaValGluAspAlaValIleGlyThrProIleAlaAsnArgAsnArg 1382
Db 3909 CAGCGTTATGCGCGTGGACCCACACCATTAACGCGGACGCACTTTCTGGAAAGAACCTG 3968
Gly 1383 ProGluLeu-----GluAspIleIleGlyCysPheValAsnThrGlnCysMetArgIle 1400
Db 3969 CCACTTGGGAATTAACAGACAGATTTGTCGTATATCAACT-----TACCGCTG 4022
Gly 1401 AsnIleAspHis-----HisAspThrPheGlyThrLeuIleAsnGlnValLys 1416
Db 4023 GTACTGATCATTCGACGTTCAAGATTAAGACAATATGAGGCCATTCGAGATGTGCAG 4082
Gly 1417 AlaThrThrThrAlaAlaPheGluAsnGluAspIleProPheGluArgVal---ValSer 1435
Db 4083 GCCAAGGTAAACGTCAAGAACCGCGGCGCAATGTGCACTGGCGGCTTGCACAAAC 4142
Gly 1436 AlaLeuGlnProGlySerArgAsp-----LeuSerSerThrProLeuAlaGln 1451
Db 4143 GACTTAAAGCAGCATTTATTCGATTTCTTATTCGTGCTTAAAACTACCGAAATTGGAC 4202
Gly 1452 LeuIlePheAlaValHisSerGlnLysAspLeuGlyArgPheLysPheGlnIleLeuGln 1471
Db 4203 AAATCGGAAACATTTAGACACAGACTGAACTGGGGATTCGATTGAAAGCGGACGTAG 4262
Gly 1472 SerValProValProSerLysAlaTyrThrArgPheAspMetGluPheHisLeuPheGln 1491
Db 4263 AACGTGAATTAATCACTGCTGTCATCGCGCG----- 4295
Gly 1492 GluThrAspSerLeuLysGly-----SerValAsnPheAlaAspGluLeuPheLys 1508
Db 4296 GAAAGTCAGAGCACTGGCGGATTCACAGTATTCGCTACGCGCAGAGCTATTTGAG 4355
Gly 1509 MetGluThrValGluAsnValAlaArgValPhePheGluIleLeuArgAsnGlyLeuGln 1528

QY 2095 -----ValLeuGluIleGlyThrGly 2101
 Db 6516 CTGTGACAGGATCAGCGAACCGGATCTATCTTCAGAAAGTATTGATCCCGATGAAGCC 6575
 QY 2102 SerGlyMetIleLeuPheAsnLeuAspSer----- 2111
 Db 6576 CAGGGATGTTCTCCGTCAACGTGACACAGCAAGCAGGTGAGCGGCTGACCAAGAG 6635
 QY 2111 ----- 2111
 Db 6636 ATAGCCAGTCTATCCAGCATGTTTCCGCTCGATGATGAACTGCTTGAGAGCCCGC 6695
 QY 2112 -----ArgLeuGluSer----- 2115
 Db 6696 ATCTTAACCTCAATCCCGCGGCTGATCTCATTCGCGTTCCACATACCTGCTTC 6755
 QY 2116 -----TyrValGlyLeuGlu 2120
 Db 6756 GATGCAATGTCATTGAAAGTCTTCAGCAAGAGCTTCGGGCTTGTACGAGCGCTCCAG 6815
 QY 2121 ProSerArgSerAlaIle----- 2126
 Db 6816 AAAACCAAAAGTGCAGCAACTTACCAAGCCCTCAAGCGCATGACAAAGAAATACGGCTC 6875
 QY 2126 ----- 2126
 Db 6876 TACCATGCCCGGAGCTGTCTGGCATGCGATGCGCAACCTGTACAGCTTTGGCTGGG 6935
 QY 2126 ----- 2126
 Db 6936 AAATCATTTGGCTTGGAAACCATTTGACAGTATCAGGACCGCCACGCTCTGTGCAATTC 6995
 QY 2127 -----AlaPheValAsnLysAlaThrGluSerIlePro 2137
 Db 6996 AAATGACAGCGTACACGACTCATGAACTGACAGAAAGAAACGGAACCTGAGG 7055
 QY 2138 SerLeuAlaGlyLysAlaLysValGln-----Val 2147
 Db 7056 GGGGTGCGAAAGTTCGACAGTCAAGTCTGACGTGCTGTGTTGCTTATTTGCGTT 7115
 QY 2148 GlyThrAlaThrAspIleGlyGlnValAsp-----Asp 2158
 Db 7116 ATCTGAGCTCTGTACGCGAACAGTCCGATGTTTCCGTGGGTATCCAGTCAAGCACCA 7175
 QY 2159 LeuHisProAspLeuValIleLeuAsnSerValIleGlnTyrPheProSer----- 2175
 Db 7176 AGCGATCTCTAG-----TTCAAATCGGTCAATGATTTCTGTCAACCTTGTGGTG 7226
 QY 2176 -----SerGluTyrLeuAlaGlu 2181
 Db 7227 CTAAAGGTGATATTCTCAGTCAAGCATTTGCGGCTCATCAGAAAGGTATATGAAGAG 7286
 QY 2182 IleAlaAspThrLeuIleHisLeu----- 2189
 Db 7287 CTGTGTGACCGCAACTGCACCAAGACATGCCGTTCCAGAGAGTACGAAAGCTGTGACG 7346
 QY 2190 -----ProAsnValGlnArgIlePhePheGlyAspValArg 2201
 Db 7347 GTGGATATATGACCCAGCCGCGCATTCGCTGTACAGAACGTGTC-----AACTTCGAA 7400
 QY 2202 SerGlnAlaThrAsnGluHisPheLeuAlaIleArgAlaIleHisThrLeuGlyLysAsn 2221
 Db 7401 TCCCGTCCGAACGAGAACACATGCGAGGTCCGAGAGTGAAGAGTGCCTTGCACTTCAAT 7460
 QY 2222 -----AlaThrLysAspAspValArgGlnLysMet 2231
 Db 7461 CAATACCGCGCGGTTCAGCCGCGATTCGTTGCGAAAGTTTCATCTGAACGCAACGCTC 7520
 QY 2232 AlaGluLeuGlnLysPheMetGluGluLeuLeuValGluProAlaPhePheThrSerLeu 2251
 Db 7521 ACGGAATTG-----GAGTCGGAGTTTGAAGATCACTTCAACTATGCGACCAAGCTTA 7571
 QY 2252 -----LysAspArgPheProGlyLeuValGluIleLeuProLysAsnMet 2269

Db 7572 TTCACAAAAGCAGATCCAGGCTTTTTCATACCTATGATGATCTC-----CTG 7622
 QY 2270 GluAlaValAsnGluLeuSerAlaTyrArg-----TyrAlaAlaValHis 2285
 Db 7623 CGCCAGCTGTCCAGTCAAGTGAAGAGATCAATGAGATACGAGCTGTGCTTA-- 7679
 QY 2286 ValArgGlySerLeuGlyAspGluLeuValLeuPro----- 2297
 Db 7680 GTTCGCCGACAGAGATGGCGATCTGCACTTGCAATTGGCAGACGTCCTTGGAGAG 7739
 QY 2297 ----- 2297
 Db 7740 ACTGTAGAGAGCAGAAAGTAGCGTGTGTAACAGGCTTTGAGCGCGAAGCTTCTT 7799
 QY 2298 -----ValGluLysAspAspTyrIleAspPhe----- 2306
 Db 7800 GCCGACAGAGAAAGTCCGCTGTGACAGGAGATAGACACTTATGTTACTTAACTTAAAC 7859
 QY 2307 -----GlnAlaAsnGlnLeuAsn----- 2312
 Db 7860 GGGCAGGCTTACCAAGCTCGCCCGGTACATACAGTCCGTCCTGTATGGGGCAGACGAC 7919
 QY 2313 -----GlnLysSerLeuGlyAspLeuLysSerSerAspAlaAla 2326
 Db 7920 GGAATAGCTTTGATGCTGGAAGAAAGATATCAGACATTAAT-----TGC 7964
 QY 2327 IleMetAlaValSerLys-----IleProPheGluIleThr----- 2338
 Db 7965 ATTCTGCGATTTGGAGGCGTGTGACATACATGCTGCTTGGATCGACTTACCAACC 8024
 QY 2339 -----AlaPheGluArgGlnValAlaLaseLeuAsnSer 2350
 Db 8025 GAGCGCTCCAGCTGATTCGTGAGAGATTAAGCGAAGCTCTCTTGTCACCTCCAGT 8084
 QY 2351 AsnIleAspGluTyrGln-----LeuSerThrTle 2360
 Db 8085 CATGCTTCGAATATGTAACCCATGCGCGAGAGTATTGCACTGCACGCCGCGCATC 8144
 QY 2361 ArgSerSerAlaGluLysAspSerSerLeuSerValProAspIlePheArgIleAlaGly 2380
 Db 8145 GAGACGCGGTGACCGAACAGTCAAGCTGTGACTGCCCAATTTGCTACGCTCGGCAT 8204
 QY 2381 GluAlaGlyPheArgValGluValSerSerAlaArgGlnTyrSerGlnAsnGlyAlaLeu 2400
 Db 8205 CTAGCG-----TATTAATCTTACTTACAGGCACTTCGAGTAAGCCAAAGGAGCTTA 8258
 QY 2400 ----- 2400
 Db 8259 GTTAGCAAAAGCAGTCTTCTTCTACGCGATGCCCTCCGGAGGGTATTTCCGTCGA 8318
 QY 2401 AspAlaValPheHisHis----- 2406
 Db 8319 GACTGTACCAAGCATGAGCGTCTGCTCTGTCCTCAACTGCTTTCGACTTCGCTC 8378
 QY 2407 -----CysCysSerGlnLysArgThrLeuValAsnPheProThrAsp-- 2420
 Db 8379 GAACAACTGTGTGTCGGGTCTCAGCGGACACAAAGTATGCTTCCCTCCAGCTGAGTTC 8438
 QY 2421 -----HisIleLeuArgGly 2425
 Db 8439 GTGCGAGATGATGATTTTACAGATGGCCAGACGACGACGCTCTCCCTATCTCAGCGGC 8498
 QY 2426 Ser--AspLeuLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgAlaIle 2444
 Db 8499 ACACATCTTACTGTGAGAAAGATGATCTGGCAGCACTGGACCATCTGCGAGTTTACC 8558
 QY 2445 -----GluValArgGluArg----- 2449
 Db 8559 GCCCGGGCGAAGAGCTTACGCCACCCAGTACGAAAGTATGCGCGCGCATTCACAGGT 8618
 QY 2449 ----- 2449

Db 8619 CCATCTACAAATGCTTGTGTCACCGAGACACGGTGTACAAATTAATCGCGAATTC 8678
 Qy 2450 -----LeuArgSerLeuLeuPro-----SerTyr 2457
 Db 8679 ACAAGCAATTCGATATTGGAATGCTCTTCGGGAATGCTCCCTGGTACCCGAGCTAT 8738
 Qy 2458 MetIleProSerAenIleValIleuAspIleMetProLeuAenIleAenIleValIleVal 2477
 Db 8739 GTCTGACCGCG-----GCACCTTCAGCCCTCCCTTCGATGCTGTGCGA----- 8783
 Qy 2478 AspArgIleGluIleuSerArgArgIleValIleValIleProIleGlnIleIleIleIlePro 2497
 Db 8784 -----GACCTATCTTCCCGCGACACGGTACCGGTGTATTCACAACT 8834
 Qy 2498 LeuProThr-----PheProIleSerGluValIleGluValIleLeuCys 2511
 Db 8835 CTTCATACGATACGACATTCATTCACACCTTTCGCAAGAGAGAGACATCGCATG 8894
 Qy 2512 GluGluIleThrGluValPhe----- 2518
 Db 8895 GGGCGCTTCGCGCGCTCTACAGACCGCGACCTGTGATCGCTTCAACCTCAG 8954
 Qy 2519 ----- 2520
 Db 8955 CACGACCGCAGCTGGAATACCTAGAGAGCGATCTGCATCAATGATGAGGGATAC 9014
 Qy 2521 LysValAspIleThrAsp----- 2526
 Db 9015 CGGATCGAGATTCTGAGATTGACAGACTCTCACTCCCGGTCCCGGAGGT 9074
 Qy 2527 -----HisPheAenIleuGlyIleHisSerLeu 2537
 Db 9075 GCAGTCGTCGCAAGTATGAGAACACGATACCTATCCGAGCCGCTCTCTGTGTC 9134
 Qy 2538 Ala-----ThrIleLeuIleSerArgIleAsp-----GlnArgLeuIle 2550
 Db 9135 GGTACTATACACGACCAATGAAACAGTATCGAAGCCGATATTCATCTTCATGAAA 9194
 Qy 2551 ValArgIleThrValIleAspValPheAspHis-----Pro 2562
 Db 9195 GCAAGGTTCCACGATCATGATGTCGCAAGGACCTGTGTGAGAGGCGACCTGCT 9254
 Qy 2563 ValPheIleAspLeuIleAspValIleArgGlnIleuGlyIleuGlnIleProValSer 2582
 Db 9255 GTACAGCATTAACGGAAGCTGACGTCGCGAGA-----TTCGCGAGATTATACAC 9305
 Qy 2583 AspGlyIleGlnIleAspArgSerAlaHisMetIleProArgIleIleIleIleIle 2602
 Db 9306 GACTCCGCG-----CAGTCTCTGACAGCCCAAGAACATTAATGAGGCCAAG 9356
 Qy 2603 LeuCysAspGluPheAlaIleValIleuGlyPheGln-----ValGlyIleThrAspAspPhe 2621
 Db 9357 ATGTGACGACTGTGGGAATCCGCTTGGGAATGAGGATGCGGTATACAGACGACTG 9416
 Qy 2622 PheAspIleuGlyIleHisSerLeuMetAlaThrIleLeuAlaValArgIleGlyHisArg 2641
 Db 9417 TTCAACGAGGTGGCGACACATCATCTTCGATCTCGGCGCCAGATTCAACACAG 9476
 Qy 2642 LeuAspThrThrValSerValIleAspValPheAspHisProValIleuPheGlnLeuAla 2661
 Db 9477 GTGGCGTCAAGATCACCGTTCGGATATATTGAACAT-----CGTACCGCC 9524
 Qy 2662 IleAlaLeuAspAenIleuValIleuSerIleThrAenIleValIleGlyIleArgGluMet 2681
 Db 9525 CAGAGCCTCATATACATGCTTTCATGAGACCTC-----GACCG 9566
 Qy 2682 AlagIleIleSerProPheGlnIleuPheThrGluAspProGluIleuPheMetAlaSer 2701
 Db 9567 AGTAATGTGACTAGTCCGA-----ACGAAACAAGGCGCGATCGCGAGGCG 9617
 Qy 2702 GluIleIleProGlnIleuGluIleGlnIleIleIleGlnIleIleIleIleIleIleIleIleIle 2721
 Db 9618 CCCTACTGCG-----ATTCAAGACTGGTTTGTTCAAAGCT 9656

Qy 2722 MetGlnIleValPheLeuPheAspHisThrThrAlaArgProArgProPheValProPhe 2741
 Db 9657 CTCAGCATCCGATGATGATGATACACT-----TTC 9689
 Qy 2742 TyrIleAspPheProSerThrSerGluProAspAlaIleGlyIleuIleIleValIleCysGlu 2761
 Db 9690 TACGTC-----CGAACGCAAGCTGAGATGATGATTCCTTAAGCCGCTGTGACAG 9740
 Qy 2762 SerIleValAsnHisLeuAspIlePheArg-----ThrValPheAlaGluIleAspGlyIle 2780
 Db 9741 GACTTGCAACAGATACAGATGATTTCCGATCGACGATCAAGGCGAGAGAGCGGATTC 9800
 Qy 2781 LeuTyrGlnValIleuSerCysLeuAspLeuProIleGlnValIleGlyIleIleThrGluAsp 2800
 Db 9801 GTGACGCTCTTCTGAGGACTTCTCTCCGACCACTTCGGGTGCGTGAACGTAAAGAT 9860
 Qy 2801 ---AsnIleAsnThrAlaThrAenGluPheLeuAsp-----GluPheAlaIle 2815
 Db 9861 GTTGACGGGTCCGCGCCGCTCAACGATATGATGAGGAGTGGGAGTCTGCTCAACCTT 9920
 Qy 2816 GluProValArgLeuGlyHisProLeuIleArgPheThrIleIleIleGlnThrIleSer 2835
 Db 9921 GAGAACGACCCATTGCTTC-----ATTGCTACTCATGAGGATGATGAGACCATCC 9974
 Qy 2836 MetArgValIleMetArgIleSerHisAlaLeuTyrAspIleLeuSerLeuGluHisVal 2855
 Db 9975 GCGCGAGTGTGTTCCCTCCCTTACCATATGCGCATGACCGCTGACGCTGAGATCCTT 10034
 Qy 2856 ValArgIleLeuHisMetLeuTyrAenGlyArgSerLeuLeuPro----- 2871
 Db 10035 GTCCGTGACCTTGAGACGCTGTACCGAATGAAAGCTTCGGAACGAGGACGACCTTTC 10094
 Qy 2872 HisGlnPheSerArgTyrMetGln---TyrThrAlaAspGlyArgIleSerGlyIleGly 2890
 Db 10095 CGGCACTGCTCAAGCCATCCAAATTCAGAGCGCTCAGCTTGAAGGAACT--- 10151
 Qy 2891 PheTyrArgAspValIleGlnAenThrProMetThrIleLeuSerAspThrValIle 2910
 Db 10152 ---TGGAATTAAGCTCGTATGAAACAGCTTCAGAGATATCCCAATTCGCTACG----- 10202
 Qy 2911 AspGlyAsnAspAlaThrCysIleValAlaLeuHisLeuSerIleIleValIleIleProSer 2930
 Db 10203 -----TCAACCGGTTCGCGCGCTGAGCGCTGAGCAAGATTGAGC---CTTGAG 10247
 Qy 2931 GlnValLeuArgIleIleSerAenIleIleThrGlnAlaThrValPheAenAlaCys 2950
 Db 10248 AAGACA----- 10253
 Qy 2951 AlaLeuValLeuSerArgIleuSerAspSerIleAspVal---ValPheGlyArgIleVal 2969
 Db 10254 GCTCACTGATTCAGAGAGATGATTCAGACAGATGTCTCCGTGACGACTCCCTCTG 10313
 Qy 2970 SerGlyArgGlnIleuProValIleuTyrGlnAspIleValIleGlyProCysThrAenAla 2989
 Db 10314 ACTTCA---GTTGATTTGGGCTCAACATATGCTCAACCGGCCA-----AGTATG 10364
 Qy 2990 ValProValArgAlaHis 2995
 Db 10365 GTTACGATCGAGGACAT 10382

RESULT 14
 US-08-222-617A-1
 ; Sequence 1, Application US/08222617A
 ; Patent No. 5882879
 ; GENERAL INFORMATION:
 ; APPLICANT: Veenstra, Annemarie E.
 ; APPLICANT: Martin, Juan F.
 ; APPLICANT: Garcia, Bruno D.
 ; APPLICANT: Gutierrez, Santiago
 ; APPLICANT: Barredo, Jose L.
 ; APPLICANT: Von Doehren, Hans
 ; APPLICANT: Palisae, Harriet

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APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: Quantities of ACV Synthetase
CORRESPONDENCE ADDRESS:
ADDRESS: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
NAME/KEY: CDS
LOCATION: 264..11600
OTHER INFORMATION: /function= "enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
US-08-222-617A-1

Alignment Scores:
Pred. No.: 6 46e-130 Length: 12364
Score: 1342.50 Matches: 748
Percent Similarity: 36.31% Conservative: 525
Best Local Similarity: 21.33% Mismatches: 1244
Query Match: 8.32% Indels: 992
DB: 2 Gaps: 136

US-09-482-788-2 (1-3129) x US-08-222-617A-1 (1-12364)
QY 258 ProAsnProThrThrThrAlaGluHisArgIleThrPheProLeuSerGlnValAlaLeu 277
DB 532 CCAGCTCCAGCGCATGATGAGTGCATGCTGGT---TCGGTACGCGAGCGCTCGT 588
QY 278 SerAsnSerAlaIleCysArgThrAlaLeuSerIleLeuSerArgTrpThrHisSer 297
DB 589 ACCAGAGCGCTTGATGATGATGCTCC-----CTGTTGAGTACATGCGCGCTCC 636
QY 298 AspGluAlaLeuPheGluAlaVal-----ThrGluGlnSerLeuProPheAspIleHis 315
DB 637 AAGAGCTGTCCTAAGACCGCGGTGTGAGCGGTGATCCGTCATTAA-TTCTCCGTGCAC 695
QY 316 TyrLeu-----AlaAspGlyThrTyrGlnThrValAlaProLeuArgValHis 331
DB 696 CAGATGCTGAAGGGTTTGAAGATGACACACACATGACCGCTCTGTG-----CAC 749
QY 332 CysGlnSerLeuAlaGlnAlaSerAsp-----ValMetAspAlaIleSerSer 347
DB 750 CGTACGACGAAATTTTTCGCAATTTCTTCGCAATCTCGGTGATGCTCCCAATGTCAC 809
QY 348 TyrAspAspArgLeuGluHisLeuAlaProPheGlyLeuArgAspIle-----Arg 364

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DB 810 CATGAGAAACAGACCGATGCTCCGTGCGCAGCGCGTCCAGATGCAAGCGCGCGC 869
QY 365 AsnThrGlyAspAsnGlySerAlaIleCysAspPheGlnThrValLeuLeuValThrAsp 384
DB 870 GGTCCGAGAGAGTCACTGACTGCGATTGAC-----TCGCG 908
QY 385 GlySerHisValAsnAsnGlyIleAsnGlyPheLeuGlnGlnIleThrGlnSerSerHis 404
DB 909 TCAAGTCTCGTAAATGGGTTATTGACTTACTGTCTGACGCTTGTGCAATGCAAGCAT 966
QY 405 Phe---MetProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlnSerSerGly 423
DB 969 GCTGATTCATGTTTCCACTTCCCTC----- 998
QY 424 AlaLeuLeuValAlaTyrTyrAspHisAsnVal-----IleAspSer 437
DB 999 GCAGTATGATGGGTGATGATGCGCAACCTCTCGTACTGTGCGTTTCTCGCATGT 1058
QY 438 LeuGlnThrThrArgLeuLeuGlnGlnPheGlyHisLeuIleLeuSerCysLeuGlnSerPro 457
DB 1059 CTCTTCAACAGACAGACGATATGCAATTTTACCGATGCCCTAAACATCTTGTCCGCGAA 1118
QY 458 Leu-----AspLeuSerSerMetAlaGluValAsnLeuMetThrGluTyrAspArg 474
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QY 494 HisGlnMetLeuLeuValAlaValSerHisSerProThrThrThrAlaIleGlnAlaTrpAsp 513
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DB 1299 CGAGAGCTCACTTACGCGCAGCTCAATGCGCAAGCAACAGCTCGCAGCATCTCGT 1358
QY 534 SerLeuGlyLeuArgAlaGlnGlnAlaIleIleProValTyrPheGlyLeuSerLeuTrp 553
DB 1359 TCCATTGGTATCCCTGCCCGCAGCAG---CTAGTGCATGTTCTTGTAGTAAGCGAGAG 1415
QY 554 ValIleAlaSerMetLeuAlaValLeuLeuSerGlyAsnAlaPheThrLeuIleAspPro 573
DB 1416 CTCAATTGTTACATCTCGCGGTGTGAATCCGACCGCGCTTACGTCGCGCATGACCCG 1475
QY 574 AsnAspProProAlaArgThrAlaGlnValValThrGlnThrArgAlaThrValAlaLeu 593
DB 1476 ACTTATCCGATGAGCGAGTCCGCTGCTGCTGTGATGACACCAAGCAGCGGCATGATC 1535
QY 594 ThrSerLeuHisIleArgGluThrValGlnLeuVal-----GlyAspCys 609
DB 1536 GCCCATGATCAACATGTGAGAGGCTCCACGAGAGTCAATCGCGATGAGAACTTATGC 1595
QY 610 ValValValAspAspGluLeuGlnSerValSerAlaSerAsp----- 624
DB 1596 ATTATCCGTGAGCGCTGTGTGGCTCTCTGCTAGGATTCCTAAATTCGCCCGCG 1655
QY 625 -----AspPheSerSerLeuThrIleSerGlnAspLeuAlaTyrValIlePheThr 641
DB 1656 CATTAATGAGACACCTAACCCCTCAC---AGCAGAGAGTCTGCGTATGATGACTTACAC 1712
QY 642 SerGlySerThrGlyAspProLeuGlyIleMetIleGlnHisIleArgAlaPheSerSerCys 661
DB 1713 TCTGGACCACTGGTTTCCCAAGGGCATTTTAAACAAACACCAATGTGTGTAAAGT 1772
QY 662 AlaLeuLeuPheGlyIleSerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGly 681
DB 1773 ATTAACGACCTGTCTGCAAGTACGGGCTG-----GCCGGG 1808
QY 682 ThrHis-----AlaPheGlyAlaCysLeuLeuGlu----- 691

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| | | | |
|----|------|---|------|
| Db | 1809 | CAGACCCAGAACCATTTCTGCTTTTCTCCGGCTGCGGTTCCAGACGGCTGTTCCAGAC | 1868 |
| Qy | 692 | lIleethrThrLeuIleAsnGlyGlyCysValCysIleProSerAspAspArg--- | 710 |
| Db | 1869 | ACGGTCATGGACCTCGTAAATGGCCATCTCTCCGATGATATCAATGACGTGGAAATAT | 1928 |
| Qy | 711 | ---MetAsnSerIleProSerPheIleAsnArgTyrAsnValAsnTrpMetMetAlaThr | 729 |
| Db | 1929 | GATGCCGATAGCGCTCTCTCCCTTCATACGACACACACATCATCTACTCTCAATGGTACT | 1988 |
| Qy | 730 | ProSerTyrMetGlyThrPheSerProGluAspValProGlyLeuAlaThrLeuValLeu | 749 |
| Db | 1989 | GCCCTGCTCTTGCAGAGTAGTACGACTTTTCCGACTCCCATCATCGATACGATATACCTG | 2048 |
| Qy | 750 | ValGlyGlyGlnMetSerSerSerValAsnAlaIleTrpAlaPro---LysLeuGln | 767 |
| Db | 2049 | GTGGGTGGAACCTGCACGAAGCCCGGTATGTGGCGCTGCCACGCGTTCAGAAATCCG | 2108 |
| Qy | 768 | LeuLeuAsnGlyTyrGlyGlnSerGlnSerSerIle-----CysPheIla | 783 |
| Db | 2109 | ATCTCTAACGAGTATGGTTTATCCAGTACAGCTTTGTAAACGGCCCTCAAGATTTTGCAC | 2168 |
| Qy | 784 | SerAsnMetSerThrGluProAsnAsnMetGlyArgAlaVal---GlyAlaHisSerTrp | 802 |
| Db | 2169 | CCGGAGTCGACCCCTTAAGACACGAGCTGGGGAGACCGGTGGCGAAGCTCAAGCTAC | 2228 |
| Qy | 803 | ValIleAspProAsnAspIleAsnArgLeuValProIleGlyAlaValGlyGlyLeuVal | 822 |
| Db | 2229 | ATCTCTCAATCCATCC-----CTTAAAGTGTCCGATTTGAGCTACCGGTGAGATTTGCAT | 2282 |
| Qy | 823 | IleGluSerProGlyIleAlaArgAspTyrIleValProPro-----ProProGluLys | 840 |
| Db | 2283 | ATCGAGGGGTTGGGATTTCCAGAGGAGTACCTCAACGCCGCCGAACTCAGCCGACCGC | 2342 |
| Qy | 841 | -----SerProPhePheThrAspIleProSerTrpTyrProAlaAsnThrPhePro | 857 |
| Db | 2343 | TTTCATTTCCCAACCCCTTCCAAACGATTTGCCAGAAAGCAGCTCCGGATACACGCTG--- | 2399 |
| Qy | 858 | AspGlyAlaLysLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIle | 877 |
| Db | 2400 | -----ATGTACAAACCGGTGACCTGGCCGCTGGCTTCCGAACGGGAGGTT | 2447 |
| Qy | 878 | ValCysLeuGlyArgIleAspSerGlnValLysIleAsnGlyGlnArgValGlnLeuGly | 897 |
| Db | 2448 | GAGTATCTCGGACCGGACAGATTTCCAGATCAAACTGACGAGGTATTCGAATTGAACCTGT | 2507 |
| Qy | 898 | AlaIleGlyThrHisLeuAsnArgGlnGlnMetProAspAspLeuThrIleValIleVal | 917 |
| Db | 2508 | GAATTTGAGACAGTCTGGCTATGTAACCTTAGGGTCCGGACCAAGTTATGCTGTCCAA | 2567 |
| Qy | 918 | ThrLysArgSerGlnSerIleAsnSerThrSer---LeuIleAlaPheLeuIleGly | 935 |
| Db | 2568 | AAGCTCCCGCAACCGTCCAGAGAACTCAACAGCAGCCTCGTGGGTTATTAAGTTGT | 2627 |
| Qy | 936 | SerSerTyrPheGlyAsnArgProSerAspAlaHisIleLeuAspPheIleAspAlaThrLys | 955 |
| Db | 2628 | GATAGC-----GCTCAGTGTCCAGGAGACCTGCTGCATTT----- | 2666 |
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| Db | 2712 | CAGCTGTGCAGATCTCCAGTGAATGTGAACGGAAAGCGCACTACCGGCTTCCGGCC | 2771 |
| Qy | 996 | MetGlyLysAspIleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAla | 1015 |
| Db | 2772 | GTCCGAT-----ATCTCAATTTCCACGAGAGTG | 2798 |
| Qy | 1016 | ProIleProValPheAlaAspThrAlaAlaLysLeuHisSerIleTrpValGlnSerLeu | 1035 |
| Db | 2799 | CGTTCCGACTTTCAGAGCGATACGGAATTCGCTTCGGGAAATTCGGGCGGACGTGTG | 2858 |

| | | | |
|----|------|--|------|
| QY | 1036 | GIYLILeaPrOlaLthPrVaLaenValGLYLaLthRhehheGluLeuGLYVaenSer | 1055 |
| Db | 2859 | GGAGCCGCCAGAGATCGCTCTCCGACGACAACTTCTCCGCTTAAGAGGAGCACAGC | 2918 |
| QY | 1056 | ILethrLaLeLysMetValAsnMetLaArgSer-----ValGlyMetAspLeu | 1072 |
| Db | 2919 | ATCACTCGCATCCAACTGATCGCTCGCATCCGACAAAGCAACGACTCGTGATGATC | 2978 |
| QY | 1073 | LysValSerAsnIleTYRGLnHisProThiLeuLaLeLYLLeSerAlaValValLyGly | 1092 |
| Db | 2979 | TCCCTGCAGAGTGTGTTTGGCAACAGGACCTTAGCGGCATGGAGCACTTTCACAGAC | 3038 |
| QY | 1093 | AspProLeuSerTYRThrLeuIleProLYsSerThrHisGlyPro-----Val | 1109 |
| Db | 3039 | AAGCAGCAGGAGAAATCGACAAACCC-----CATGAGGGCGCGACAGAGCTCTT | 3089 |
| QY | 1110 | GlulnSerTYRserGLnGLYVaLgLeuTrpPheLeuAspGLnLeuAspValGlySerLeu | 1129 |
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| QY | 1130 | Trp-----TYRLeuIleProTYRAlaValArg | 1138 |
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| QY | 1139 | MetArgGLYProValaenValAspAlaLeuArgTrgAlaLeuAlaLeuGLnArg | 1158 |
| Db | 3210 | TACAAACACCACTGTCTCCAGATCTGTTCAGAGACCTCGAAGCATGACAGACAGATCC | 3269 |
| QY | 1159 | HisGLnThrLeuAspGlyThrTrpPheGlu-----AspGLn | 1169 |
| Db | 3270 | TTTCCAGCGCTCGCGCTCGGTTCTCATGGGAAAGAGGTTTCCAGTCTCGATCAG | 3329 |
| QY | 1170 | Asp-----GlyValGlyValGlnIleValHis | 1178 |
| Db | 3330 | GATCACACCATTTGACCTGGCGTTCTCTCTACTTTCACGACGTTGGCGGGGCTGTCAG | 3389 |
| QY | 1179 | GLYLYsLeuSerGLnGLnMetLYsValIleAspLeuCYsGLYSerAspLeuAspProPhe | 1198 |
| Db | 3390 | GACCGGAAATTGAGAAAGCTGGCG----- | 3413 |
| QY | 1199 | GLYValLeuAsnGLnGLnThnTrpProPheAsnLeuSerGLYValAGLYTrpArg | 1218 |
| Db | 3414 | -----GCCCAAGACCTTAACGGAAGATCTCAAGCTGATGTGGCAGACCTTCCG | 3464 |
| QY | 1219 | AlaThrLeuLeuArgLeuGLYVaLAspAspHisIleLeuThrIleValMetHisHisIle | 1238 |
| Db | 3465 | GTCATATCGATTAAACACAGAGAAATCGCTTCCAGCTGCTTTCACGCTCCATCATGCA | 3524 |
| QY | 1239 | ILeserAspGLYTrpSerIleAspValLeuArgAspLeuAsnGLnLeuTYRSerAla | 1258 |
| Db | 3525 | ATCTCATATGTTGAAGTCTGCCACTTGTTCGAAAAGTTCTCAGAGACTTACTGCA | 3584 |
| QY | 1259 | AlaLeuLYsAspSerLYsAspProLeuSerAlaLeuThrProLeuProIleGLnTYRser | 1278 |
| Db | 3585 | CTGCTGCATGGG-----GACAACTCATCTTCGCCATGATGACCT----- | 3626 |
| QY | 1279 | AspPheAlaLYstrpGLnLYsAspGLnPhelLeuGLnGLnLYsGLnLeuAsnTYRTrp | 1298 |
| Db | 3627 | ---TACATCTGCACCCAGCGGATATCTCCACGCTCACCGTAGATCACTTCGACTTTGG | 3683 |
| QY | 1299 | LYsValGLnLeuLYsAspSerSerProAlaLYsIleProThrAspPheAlaArgProAla | 1318 |
| Db | 3684 | GCCGGTGTGTTCAA-----AAGTCAACGAACGGTGTGATATGAACGCC | 3728 |
| QY | 1319 | LeuLeuSer-----GlyAspAlaGLYCYsVal----- | 1327 |
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| QY | 1328 | -----HisValThrIle-----AspGLYGLnLeuLYR---GlnSerLeuAspAlaPhe | 1342 |
| Db | 3789 | CAGCGACACCGGACAAATGTCTCTCTCTGAGAGACGATGGCTAGACAACTTTCGTCAAC | 3848 |

Dh 5931 CAGTCTGGCTCCCTGGCTACATGTCCTCTCTCATTTCTGTCAGCAAGTTCCC 5990
Qy 2017 -----HisPheHisSerGlu 2021
Dh 5991 GTCACTCTAGTGAATAATAGACCAAGGCTTTGCCCGAGCGAGAAAGAGCGAG 6050
Qy 2022 AsnAspIysGlnSerAlaSerGlnValGlnGly-----TyrGlnAsp 2036
Dh 6051 ATTGACGTGTGCGCGCGCGGTAGTGAATCGAACGCTCTTGTGTGACATCTGGCGGAA 6110
Qy 2037 HisPheGlnSer-----GlyMetTyrSer----- 2044
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Qy 2044 ----- 2044
Dh 6171 GACAGCTTAAGACGAAAGCTTCTTCATGATTCAGAGTCTTTAACCGCGCGTC 6230
Qy 2044 ----- 2044
Dh 6231 TCAGTCAGCGCCCTTTTCTGTACCGGACAGTTGAAAGCCAGACGACTTGATCTGAAAC 6290
Qy 2045 -----AspIleGlyGlnIleAspProSerThrIleGlySer----- 2056
Dh 6291 GATGCTGCAATGTGCAAGAAATTACTCCATAGATTGCAATGATACGACAGATGATCCC 6350
Qy 2057 -----AspPheIysGlyTyrPheSerMet 2064
Dh 6351 GTGTCCCGTCCCGAGAGACACTCTCTTCATCCAGCAATTTGAGATGAGCAAGCAATGCA 6410
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Qy 2085 ThrLeuHisAspAsnArgSerLeuGlyAsn----- 2094
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Qy 2095 -----ValLeuGlnIleGlyThrGly 2101
Dh 6516 CTGTGACAGATCACGACCGGATCTTCTTACAGAAAGTATGATGCCGATGAAAGCC 6575
Qy 2102 SerGlyMetIleLeuPheAsnLeuAspSer----- 2111
Dh 6576 CAGGCGCATGTTCTCCGTCAACGTGACACAGCAAGGAGTGAAGCGGTGACAGAG 6635
Qy 2111 ----- 2111
Dh 6636 ATAGCCAGTCTATCCAGCATGTTTCCGCTCGATGATGAACTGCTGGAGAGCCCGC 6695
Qy 2112 -----ArgLeuGlnSer----- 2115
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Qy 2116 -----TyrValGlyLeuGln 2120
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Dh 6816 AAAACCAAAAGTGCAGGAACTTACCAAGCCCTCAAAAGCGAGTACAAAGAAATACGCGCTC 6875
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Dh 6936 AAATCTATTGGCTTGAACCATTCGACCTGATCAAGGACCGCCACGCTCTGTGCAATTC 6995
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Dh 6996 AAATACGACGGTGAAGCATCTCAATGAACTGAGCAAGAAAGAAACGGAACCTGAGG 7055

Qy 2138 SerLeuAlaGlyIysAlaIysValGln-----Val 2147
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Qy 2148 GlyThrAlaThrAspIleGlyGlnValAsp-----Asp 2158
Dh 7116 ATCTAGCCCTCGTACCGGAAACAGTCCGATGTTTCCGTGGGTATCCCACTACGCCACCA 7175
Qy 2159 LeuHisProAspLeuValIleAsnSerValIleGlnTyrPheProSer----- 2175
Dh 7176 ACCGATCTCAG-----TTCCAATGGGTGATTGATTTCTTCGCAACCTTGTGGTG 7226
Qy 2176 -----SerGlyTyrLeuAlaGln 2181
Dh 7227 CTAAAGGTGATATTTCTCAGTCAGCCATTTCGGGCTCATCAGAAAGGTATGAAAGAG 7286
Qy 2182 IleAlaAspThrLeuIleHisLeu----- 2189
Dh 7287 CTGTGAGCGCCCACTGCACCAAGACATGCCCTTCCAGGAAGTACGAAAGCTGTGACG 7346
Qy 2190 -----ProAsnValGlnArgIlePhePheGlyAspValArg 2201
Dh 7347 GTGGATTAATGACCCAGCGCGCATCCGCTGTACAGAACGTGTT-----AACTTCGAA 7400
Qy 2202 SerGlnAlaThrAsnGlnIlePheLeuAlaIleArgAlaIleHisThrLeuGlyIysAsn 2221
Dh 7401 TCCGTCGCAACCGAAGAACATGTCAGGTCCGAGATGAAAGATCGCTTGATTCAT 7460
Qy 2222 -----AlaThrIysAspAspValArgIleIysMet 2231
Dh 7461 CAATACCGCGCGTTACGCCCTGAGATTCCTGTCGAAAGTTCGATCTGAAAGCAAGCGTC 7520
Qy 2232 AlaGlnLeuGlnIleAspMetGlnGlnIleLeuValGlnProAlaPhePheThrSerLeu 2251
Dh 7521 ACCGAAATG-----GAGTCGGGATTGAGAGTCAACTCAATGATGACCAAGCTTA 7571
Qy 2252 -----LysAspArgPheProGlyLeuValGlnIleValGlnIleLeuProIysAsnMet 2269
Dh 7572 TTCACAAAGACGATCCAGCGGTTTTCGATACCTATGAGATGCTC-----CTG 7622
Qy 2270 GlnAlaValAsnGlnLeuSerAlaIysArg-----TyrAlaAlaValHis 2285
Dh 7623 CGCCAGCTGCCAATGACTGACAG-AGGATCAATGAGATACCGACGTGTCGTTA-- 7679
Qy 2286 ValArgGlySerLeuGlyAspGlnLeuValLeuPro----- 2297
Dh 7680 GTTCGCCGACAGAGATGCGATCTGCACTTGCAATGGCACAGTCCCGCTTGGGACG 7739
Qy 2297 ----- 2297
Dh 7740 ACTGCTGAGAGCAGAAAGTACGCTGTGAAACAGAGCTTTGAGCGGAGCTTCCCTT 7799
Qy 2298 -----ValGlnIysAspAspTyrIleAspPhe----- 2306
Dh 7800 GCCGACAGAAAGTTGCCGTGCTGACAGGAGATAGACACTTATGCTGATCTTAAAC 7859
Qy 2307 -----GlnAlaAsnGlnLeuAsn----- 2312
Dh 7860 GGGCAGGCTTACCAAGCTCGCCGCGTACATACAGTCCGCTGCTGTATGGGCGACAGAC 7919
Qy 2313 -----GlnIysSerLeuGlyAspLeuLeuIysSerSerAspAlaAla 2326
Dh 7920 GGAATAGCTTGTATGCTGAAAAGATATCGACACCATTAAT-----TGC 7964
Qy 2327 IleMetAlaValSerIys-----IleProPheGlnIleThr----- 2338
Dh 7965 ATTCTGCGATTTGAAAGCGGTGTGACGATACAGTCCCTTGTGATTCGACTTACCAACC 8024
Qy 2339 -----AlaPheGlnArgGlnValValAlaSerLeuAsnSer 2350
Dh 8025 GACGCGTCCAGCTGATTTCTGAGAGATTAAGAAAGCAAGCGCTGCTTGTGCACTCCAGT 8084

QY 2351 AsnIleAspGluTrpGln-----LeuSerThrIle 2360
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Db 8085 CATGCTTCGAATGTGAAGCCCATGGCGGAGAGTGAATTGCAGTCAGTCCGCCGCATC 8144
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Db 8145 GAAACCGCGGTCCACCAACAGTCAAGCTGCTGACCTGCCAACAAATTGCTACCTCGGCAT 8204
QY 2381 GluAlaGlyPheArgValGluValSerSerAlaArgIleTrpSerGlnAlaGlyAlaLeu 2400
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Db 8205 CTAGCG-----TATATATCTTACTTACGACCTTCGGTAAGCCAAAGGAGTCTTA 8258
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QY 2401 AspAlaValPheHis----- 2406
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Db 8319 GACTGTACCAAGCATGCGCTGCTGTCCTGTCACATACGTCTTCACTTCTCCGTC 8378
QY 2407 -----CysCysSerGlnGlyArgThrLeuValAsnProThrAsp--- 2420
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Db 8379 GAACAACTGTGTGTGCTCGTCTCAGCGACACAAAGCTGATCTCCCGACGTGAGTTC 8438
QY 2421 -----HisHisLeuArgGly 2425
::: :::
Db 8439 GTGCGAGATGATATTTTACAGATGGCCAGACGCGCTCTCTCTTCTTCTCAGCGC 8498
QY 2426 Ser---AspLeuLeuThrAsnArgProLeuGlnArgLeuAlaAsnArgIleAlaIle 2444
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Db 8499 ACACCATCTTACTCTGAGAGATCGATCTGACGACATGACCATCTGACAGTTGTTACC 8558
QY 2445 -----GluValArgGluArg--- 2449
::: :::
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QY 2449 ----- 2449
Db 8619 CCCATCTACAAATCCATATGTGTGTACCGACCAACGAGTGTACAAATATTCGGGAATTC 8678
QY 2450 -----LeuArgSerLeuLeuPro---SerTyr 2457
::: :::
Db 8679 ACAACGATTCGATATTTGAGAAATGCTCTCGGGAAGTGTCTCCCTGTGATCCGAGCTAT 8738
QY 2458 MetIleProSerAsnIleValIleValAspIleMetProLeuAsnAlaAsnGlyVal 2477
::: :::
Db 8739 GTGCTGACCGCG-----GCACTTACGCCGCTCCCTTCCATGCTGTGCGA----- 8783
QY 2478 AspArgIleGluLeuSerArgArgAlaValValProIleGlnIleThrAlaAlaPro 2497
::: :::
Db 8784 -----GAACTTATCTTGTCCGCGCGACACGCTTACGCGGTATATTCACCAACCT 8834
QY 2498 LeuProThr-----PheProIleSerGluValGluValIleLeuCys 2511
::: :::
Db 8835 CTTCTAAGCATCAGGATTCATTTCCCAACCTTTTCTGCAAAAGAGAGACATCGTATG 8894
QY 2512 GluGluAlaThrGluValPhe----- 2518
::: :::
Db 8895 GGGCGCTTCGCGGCTCTTACAAAGCCGCGACCTGTTGATCGCTTCAACCGTCAAG 8954
QY 2519 -----GlyMet 2520
::: :::
Db 8955 CAGCAGCCGAGCTCGAATACCTTAGAAGAGCGATCTGCAGATCAAGATGAGGGGATAC 9014
QY 2521 LysValAspIleThrAsp----- 2526
::: :::
Db 9015 CGGATCGAGATTTCTGAAGTTTCAAGAGTGTCACTTCAAGTCCCGGTGTCCGGAGAGGT 9074
QY 2527 -----HisPhePheAsnLeuGlyIleHisSerLeuLeu 2537
::: :::
Db 9075 GCAGTCGTTGCCAAGATAGAGAAACAGATACCTATTCGCGAGCCGCTCTCTGTGCT 9134
QY 2538 Ala-----ThrIleLeuIleSerArgIleAsp-----GlnArgLeuLeu 2550
::: :::

Db 9135 GGTACTATACCAAGCAATGAAGATCGAAGCCGATATCTCACTTATCATGAAA 9194
::: :::
QY 2551 ValArgIleThrValIleAspValPheAspHis-----Pro 2562
::: :::
Db 9195 GCAAGGCTTCCAAAGTACATGATGCGCAAGCCACTCTGCTGTGAAAGGCGACTGCT 9254
QY 2563 ValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuGlnIleGlnIleProValSer 2582
::: :::
Db 9255 GTACAGATTAAAGCAAGCTCGACGCTCCGAGA-----TTCCCGAGATTATTAAC 9305
QY 2583 AspGlyGlnGlyGlnAspArgSerAlaHisMetAlaProArgThrGlnIleGluAlaIle 2602
::: :::
Db 9306 GACTCCGCG-----CAGTCTGTGACGCCCAAGCAAGAAATATCGAGGCCAAG 9356
QY 2603 LeuCyAspGluPheAlaValIleGlyPheGln---ValGlyIleThrAspAsnPro 2621
::: :::
Db 9357 ATGTGACAGACTGTGGAAATCCGCTTGGGAATGAGAGATCGGTATCGACGACGCTG 9416
QY 2622 PheAspLeuGlyGlyHisSerLeuMetAlaThrIleLeuAlaValArgIleGlyHisArg 2641
::: :::
Db 9417 TTCAAACTGGGTGGCAGACATCACTTTCGATCTCTGCGCCAGATTCACAAACAG 9476
QY 2642 LeuAspThrThrValSerValIleAspValPheAspHisProValLeuPheGlnLeuAla 2661
::: :::
Db 9477 GTGGGCTGCAAGATCAACCGTTCGGATATATTTGAACAT-----CGTACCGCC 9524
QY 2662 IleAlaLeuAspAsnLeuValGlnSerIleThrAsnGlnIleValGlyIleArgGluMet 2681
::: :::
Db 9525 CGAGCCCTCATATACAGCTTTCATGAAGACTCC-----GACCGG 9566
QY 2682 AlaGluIleSerProPheGlnLeuLeuPheThrGluAspProGluIlePheMetAlaSer 2701
::: :::
Db 9567 AGTAATGTGACTAGTTTCCA-----ACGAACAAAGCGCGGTATCGCGAGGCG 9617
QY 2702 GluIleLeuSerProGlnLeuGlnIleGlnIleAspIleTyrProSerThrGln 2721
::: :::
Db 9618 CCCCTACTCGCG-----ATTCAACACTGGTTTGTCAAAAGCT 9656
QY 2722 MetGlnIleAlaPheLeuPheAspHisThrThrAlaArgProArgProPheValProPhe 2741
::: :::
Db 9657 CTCAGCATCCGATGATGATGATCACT-----TTC 9689
QY 2742 TyrIleAspPheProSerThrSerGluProAspAlaAlaGlyLeuIleIleValIleCysGlu 2761
::: :::
Db 9690 TACGTC-----CGAACCGCAAGCTGAGATGTGATTCCTTAAGCGTCTGTCAGG 9740
QY 2762 SerLeuValAsnHisLeuAspIlePheArg---ThrValPheAlaGluAlaSerGlyGlu 2780
::: :::
Db 9741 GACTTGCACAGATACAGATGATTTTCCGATCGCACTCAAGCGGAGAGTCGATTC 9800
QY 2781 LeuTyrGlnValIleLeuSerCysLeuAspLeuProIleGlnValIleGluThrGluAsp 2800
::: :::
Db 9801 GTGACAGCTCTTGTCTAGACATCTCTCTCGCCACAGCTTGGGTGTGAAAGTAAAGAT 9860
QY 2801 ---AsnIleAsnThrAlaThrAsnGluPheLeuAsp-----GluPheAlaLys 2815
::: :::
Db 9861 GTTGACGGGTCCCGCGCGCTCAAGAGATATGATGAGGTGCGAGTCTGCTTCAACCTT 9920
QY 2816 GluProValArgLeuGlnIleHisProLeuIleArgPheThrIleIleLeuGlnIleThrLysSer 2835
::: :::
Db 9921 GAAACAGCAACCATTTGTTCC-----ATTGGTACTACATAGGATGAAAGCCGATTC 9974
QY 2836 MetArgValIleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGlnIleVal 2855
::: :::
Db 9975 GCGCGAGTCTGTCTCCGTACCATATGCGCATTTGACCCCTCAGCTGCGAGATCTTC 10034
QY 2856 ValArgIleLeuIleMetLeuTyrAsnGlyArgSerLeuLeuProPro----- 2871
::: :::
Db 10035 GTCCGTGACTCGAAGCGCTGACCAAGATGAGAGCTCGAAGCAAGGCGACAGCTTTC 10094
QY 2872 HisGlnPheSerArgTyrMetGln---TyrThrAlaAspIleArgIleSerGlyHisGly 2890
::: :::

DB 10095 CGGAGTGGGCTGAGACCATTCAAATTACAGCGCTCAGACTGTGAGAGAACCAT--- 10151
QY 2891 PheTyrArgAspValIleGlnAsnThrProMetThrIleuSerAspThrValVal 2910
DB 10152 ---TGGAAATAGCTCGTCATGGAACAGCTTCCAGCATATCCGATTCGCTACG--- 10202
QY 2911 AspGlyAsnAspAlaThrCysLysAlaLeuHisLeuSerLysIleValAsnIleProSer 2930
DB 10203 -----TCACCGGCTTCGCGCTGCGCTGAGCAGAACTTTAGAG---CTTGAG 10247
QY 2931 GlnValLeuArgLysSerSerAsnIleIleThrGlnAlaThrValPheAsnAlaLys 2950
DB 10248 AAGACA----- 10253
QY 2951 AlaLeuValLeuSerArgLysAspSerLysAspVal---ValPheGlyArgIleVal 2969
DB 10254 GCGCTACTGATTCAGAGAGAAATCGATCGACAGATGCTCCGTGTACGACTCCCTCGT 10313
QY 2970 SerGlyArgGlnGlyLeuProValGluTyrGlnAspIleValGlyProCysThrAsnAla 2989
DB 10314 ACTTCA---GTTGATTGGGCTCCAAACATATCGCTCCAAACCGGCCA-----AGTATG 10364
QY 2990 ValProValArgAlaHis 2995
DB 10365 GTTACGATCGAGGAGCAT 10382

RESULT 15
US-09-252-991A-9182.
Sequence 9182, Application US/09252991A
Patent No. 6551295
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094,190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9182
LENGTH: 7911
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9182

Alignment Scores:
Pred. No.: 1,42e-126 Length: 7911
Score: 1307.50 Matches: 569
Percent Similarity: 40.15% Conservative: 312
Best Local Similarity: 25.93% Mismatches: 831
Query Match: 8.11% Indels: 484
DB: 4 Gaps: 89

US-09-482-788-2 (1-3129) x US-09-252-991A-9182 (1-7911)
QY 1090 ValIleGlnAspProLeuSerTyrThrLeuIleProLysSerThrHisGluGlyProVal 1109
DB 124 CTGCGAGGGAGGAGATCGATTCTCGCTGTTCCGCTTCGCGCGCGCTGCTTCGCGC 183
QY 1110 GlnGln-----SerTyrSerGlnGlyArgLeuThrPheLeuAspGlnLeuAspVal 1126
DB 184 GAGCGGACCGCGCTGCTCTAGCGCCACAGGACATGCGTTCCCTCGACCTGAGACCA 243
QY 1127 GlySerLeuTyrTyrLeuIleProTyrAlaValArgMetArgGlyProValAsnValAsp 1146
DB 244 CAAAGTGGCCCTTACCACTGCCCGACGCGGTGCGCTGAAACGACGCTGATCGCCAG 303
QY 1147 AlaLeuArgArgAlaLeuAlaAlaLeuGlnGlnArgHisGlnThrLeuArgTyr----- 1164
DB 304 GCGCTGAGGCGGCTTCTGCGACCTGTGCGAGCTCATGAACCTTGCCTACCGTGTTC 363

QY 1165 -----Thr 1165
DB 364 CCGCGCGGCGCGACGACAGACTGGCGAGGCGCCCTGCAACCGCGCTGAGAGTTGCC 423
QY 1166 PheGlnAspGlnAspGlyValGlyValGlnIleValHisGluLysLeuSerGluGluMet 1185
DB 424 TTCGAGGATTGACAGGCGCTGCTGAGCGCGACAGAGAACCCGCTGCGCGAGAGCGG 483
QY 1186 LysValIleAspLeuCysGlySerAspLeuAspProPheGluValLeuAsnGlnGln 1205
DB 484 CAG-----CCGAGATCG 495
QY 1206 ThrThrProPheAsnLeuSerSerGluAlaGlyTyrArgAlaThrLeuLeuArgLeuGly 1225
DB 496 TTCAGCGCGTTCACACCTGTGCGAGGCGCGCTTCGCGGCTCCGCTGATCCCTCGGCG 555
QY 1226 GluAspAspHisIleLeuThrIleValMetHisIleIleSerAspGlyTyrProSerIle 1245
DB 556 GAGGAGCGGATGTGCTGTGTGACCTGATCACAATCGTTCACAGCGGCTGTGATG 615
QY 1246 AspValLeuArgArgAspLeuAsnGlnLeuTyrSerAlaAlaLeuLysAspSerLysAsp 1265
DB 616 AACGTGCTGATCGAAGAATTCAGTCTTCTACAGTCCATTCGACGTGCGCGAGCCC 675
QY 1266 ProLeuSerAlaLeuThrProLeuProIleGlnTyrSerAspPheAlaLysTyrGlnLys 1285
DB 676 GGCCTGCGCGCC-----TTGCGATTCAGTACGCGATTAACGCTGTGCGAGCGC 726
QY 1286 Asp-----GlnPheIleGlnGlnGlyLysGlnLeuAsnTyrTyrLysLysGlnLys 1303
DB 727 AGCTGAGTGGAGCGCGGTGACGAGCGCGCACCTGAGTACGCGCGGCAAGCTCGGC 786
QY 1304 AspSerSerProAla---LysIleProThrAspPheAlaArgProAlaLeuLeuSerGly 1322
DB 787 GAGCGGATCCGCTCGTCCGAGTTCGCGACCGACCGCGGTGCGCGGTCCAGAGTAC 846
QY 1323 AspAlaGlyCysValHisValThrIleAspGlyGluLeuTyrGlnSerLeuArgAlaPhe 1342
DB 847 CGTGGACGCGGTTCAGATTCAGATTCAGATTCAGCGCGCGCTGCGCGAGCGCTGCGCGAC 906
QY 1343 CysAsnGlnHisAsnThrThrSerPheValValLeuLeuAlaPheArgAlaHis 1362
DB 907 GCGCGACGCGGAGGCGCTGACCTGTTATGCTGTCTGCGCGCTTCAATATCTCTG 966
QY 1363 TyrArgLeuThrAlaValGluAspAlaValIleGlyThrProIleAlaAsnArgAspArg 1382
DB 967 CAACGCTATGCGCGGACGACCGACCTGCGGCTGCGCGTCCATCCGCAACCGCAACCGC 1026
QY 1383 ProGluLeuGluAspIleIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIle 1402
DB 1027 GCGGAGGTGGAAGGCTGATCGCGCTGTTCTGTCAACACCGAGTGTGCGCTGATTC 1086
QY 1403 AspHisHisAspThrPheGlyThrLeuIleAsnGlnValLysAlaThrThrThrAla 1422
DB 1087 GAGCGCGGACGTCGTGGCGGACCTGCGCGCGCTGCGCGCTCAAGACACCGTCTTGCGCC 1146
QY 1423 PheGlnAsnGluAspIleProPheGluArgValAlaSerAlaLeuGlnProGlySerArg 1442
DB 1147 CAGCGCATAGATTCGCGCTTCAAGCGCTGTGAGCGCTTCAAGCT---GAGCGC 1203
QY 1443 AspLeuSerSerThrProLeuAlaGln-----LeuIlePheAla 1455
DB 1204 AGCTGAGCAGACCGCGCTGTTCCAGGATGTATCAACACCGACCGCGTGGCGGAC 1263
QY 1456 ValHisSerGlnLysAspLeuGlyArgPheLysPheGlnGlyLeuGluSerValProVal 1475
DB 1264 ATGAGCGCTGACAGCGCGCGCGCTGAGCTTGGCGCGAGCTTCAGCTGG----- 1314
QY 1476 ProSerLysAlaTyrThrArgPheAspMetGluPheHisLeuPheGlnGluThrAspSer 1495
DB 1315 ---AAGAGCGTACACCCAGTTTCAGCTGAGCTGATTAACGAGAAAGGCGGCTCGC 1371

1496 LeuLeuGlySerValAspPheAlaAspGluLeuPheLeuMetGluThrValGluAsnVal 1515
1372 CTGTAGCGCGGTGACCTACCGGACCGACCTGTGACGGCGGACCGGACGATG 1431
1516 ValArgValPhePheGluIleLeuArgAsnGlyLeuGlnSerSerArgThrProValSer 1535
1432 GCCCGCATTTGGACGAACCTGCTGCGCGCATGCTGAAAAACCGCGACGCGGATGAC 1491
1536 IleLeuProLeuThrAspGlyIleValThrLeuGluLeuLeuAspValLeuAsnValLys 1555
1492 TCGCTCCGATGCTGATCGCGAGAGCGCTATCATGTTGCTGGAAGCTGGAACGCACT 1551
1556 HisValAspTyrProArgGlnSerSerLeuAlaAspValPheGlnThrGlnValSerAla 1575
1552 GCGGCGAGATACCGCTGCGCAACGGGCGGTGACCCGTTGTTCCAGAGACAGGTGACGCC 1611
1576 TyrProAspSerLeuAlaValAlaAspSerSerCysArgLeuThrTyrGluLeuAsp 1595
1612 ACACCGACGCGCGCGCTGCGCTTCCGCGAGAGCGCTGGACTACGCGGAGCTGAC 1671
1596 ArgGlnSerAspIleLeuAlaGlyTyrPheLeuArgArgSerMetProAlaGluThrLeu 1615
1672 CGCGGAGCCACCGCTGCGCATGCTTATCGAGCGCGGCTGCGGACCGCTCG 1731
1616 ValAlaValPheAlaProArgSerCysGluThrIleValAlaPhePheGlyValLeuLys 1635
1732 GTGGCGCTGGCCATGAAACCTTCATGAAATGTCGTGGCTGATGGCGATCTCAAG 1791
1636 AlaAsnLeuAlaTyrLeuProLeuAspValArgSerProSerAlaArgValGlnAspIle 1655
1792 GCGGCGCGCTACGTCGCGGTGACCCGAGATCCGAGAGCGCCAGCGCTCATG 1851
1656 LeuSerGlyLeuSerGlyProThrIleValLeuIleGlyHisAspThrAlaProProAsp 1675
1852 CTGAGAGACGCGCGCTGCACTGCTGCAAGCGCATGCGCACTGAAGCTGCGCTGCG 1911
1676 IleGluValThrAsnValGluPheValArgIleArgAspAlaLeuAsnAspSerAsnAla 1695
1912 CAAGCGCTGACGGGATCGACCTG-----GATCGCGGTGCG 1947
1696 AspGlyPheGluValIleGluHisAspSerThrLysPro-----SerAlaThr 1711
1948 CCTGGTTCAG-----GATTACAGTGAAGCGAACCCGGATTCATCTCGATGCGGAG 2001
1712 SerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyArgProGlyValMetIle 1731
2002 AACCTGCGCTATGTCATCTACCTCGCTCCACCGCGCAAGCGCGCGCGGAC 2061
1732 GluHisArgValIleIleArgThrValThrSerGlyCysIle-----ProAsnTyrPro 1749
2062 CGGCATTTGCGCGCTGA--GCACCGCTTGTGCTGATGACAGAGCTTACGGCTGAGCG 2119
1750 SerGluThrArgMetAlaHisMetAlaThrIleAlaPheAspGlyAlaSerTyrGluIle 1769
2120 TCGGCGACAGCGTGTGACAGAG-ACCCGTTGAGCTTCACGTCGTGGAGTTC 2178
1770 TyrSerAlaLeuLeuPheGlyArgThrLeuValCysValAspTyrMetThrThrLeuAsp 1789
2179 TTCTGCGCGTGTAGACCGGCGACGTTTGTGTGTTCCGCGCGGCGACCATCGGAT 2238
1790 AlaArgAlaLeuLysAspValPhePheArgGluHisValAsnAlaAlaSerHisValThr 1809
2239 CCGGCGAAGCTGTGTGAGCTGATCATCGAGGGGGTTCACACGCTGCACTTGTCCG 2288
1810 SerSer-----SerGlnAspValProLeuArgValProArgTyrLeuSerArg 1825
2299 TCGATGCTGAGCGCTTCTGACAGACGAAGACGTGCTTCCTGACACAGCTGAACGC 2358
1826 ThrLeuMetPhePheLeuValValThrAspSerThrAlaProAspAlaLeuAspAla 1845
2359 -----ATCGTTTGACGCGCGAGCGCTGCG-----GCGGAGCGC 2394
1846 Gln-----GlyLeuTyrGlnGlyValGlnCysTyr 1855

2395 CACGAGCAGGTGTTCGCAAGCTGCGCGAGCGCGCTC-----TAT 2436
1856 AsnGlyTyrGlyProThrGluAsnGlyValMetSerThrIleTyrProIleAspSerThr 1875
2437 AACCTATATGGCCCGAACCGAGGGCGGCATGACGTCAACCACTG-----ACCTGATG 2490
1876 GluSerPheIleAsnGlyValProIleGlyArgAlaLeuAsnAsnSerGlyAlaTyrVal 1895
2491 GAGGAGGCGAAGACCGGCTGCGGATGCGCGGCGCATGCGCCATCCGACTGCTGATATC 2550
1896 ValAspProGluGlnGlnLeuValGlyIleGlyValMetGlyGluLeuValThrGly 1915
2551 CTGATGCGCAACTGAGCGCGGTACCGGTGCGGTGCTGCGCGAGCTGACTGCGCGGT 2610
1916 AspGlyLeuAlaArgGlyTyrSerAspLys---AlaLeuAspGluAsnArgPheVal--- 1933
2611 CCGGCGCTGCGCGGTGCTACACACAGCTGCGGCTGACTGCGGAGCTTCTGCGC 2670
1934 ---HisIleThrValAsnAspGlnThrValIleValAlaTyrArgThrGlyAspArgValArg 1952
2671 AGCCCGTTCGTGCTGGGAG-----CGATGACCGCACCGGCGACTGCGCGC 2721
1953 TyrArgIleGlyAspGlyLeuIleGluPhePheGlyArgMetAspThrGlnPheLysIle 1972
2722 TACGCG---GCCAGCGGCTGATGATGATGACCGCGGCGATGACCAACAGTGAACCTG 2778
1973 ArgGlyAsnArgIleGluSerAlaGluIleGluAlaAlaLeuLeuArgAspSerSerVal 1992
2779 CCGGCGCTGCGCATGCTGAGCTGCGCGGATGAGAGCGCGCTGCTGAGCATCCGTGGGT 2838
1993 ArgAspAlaAlaValValLeuGlnGlnAsnGluAspGlnAlaProGluIleLeuGlyPhe 2012
2839 CGGAGCGCGGCTGCTGCGCGGTGACGCGCAGC-----CACTTGTGCTGCTAC 2886
2013 ValValAlaAspHisAspHisSerGluAsnAspLysGlyIleSerAlaAsnGlnValGlu 2032
2887 GTGCTGCTGAGAGCGAGACGAGCGGACCTGCGGGAACCTGACCGCGCATGCGCGCG 2946
2033 GlyTyrGlnAspHisPheGluSerGlyMetTyr-----Ser 2044
2947 AGCCTGCGGAAATACATGTCGCGCGCGACGTGCTGCGTGAAGCGGATCCGCTAGT 3006
2045 AspIleGlyGluIleAspProSerThrIleGlySerAspPheLysGlyTyrThrSerMet 2064
3007 CCGAAGCGCAAGCTGATGCCAAGCGGTGCGCGACCGAAGCTGCGGCGGACAGC 3066
2065 TyrAspGlySerGluIleAspPheAspGluMetHisGluThrPheGluGlyThrThrArg 2084
3067 CATGTCGCGCGGAGATGAATGAATGAGCGACGATGCGCGCGCTGCGGCGGACGTGCTG 3126
2085 ThrLeuHisAspAsnArgSerLeuGlyAsnValLeuGluIleGlyThrGlySerGlyMet 2104
3127 AACCTGAGGAGGTGGCGCGCACCGAACACTTTCCTTGGCTTGGGT---GGCGATTCATC 3183
2105 IleLeuPheAsnLeuAspSerArgLeuGluSerTyrValGlyLeuGluProSerArgSer 2124
3184 GTTTCATTCAGGCTGAGTGCATGCGCTGCG---CGGCGCATCCAG----- 3288
2125 AlaAlaAlaPheValAsnValAlaThrGluSerIleProSerLeuAlaGlyLysAlaLys 2144
3229 -----TTCACTCGGAAGACCTTTCACACACAGACCGATACAGGGGCTGCGCGCA 3279
2145 Val---GlnValGlyThrAlaThrAspIleGlyGlnValAspAspLeuHisProAspLeu 2163
3280 GTGCGCGCGTGAAGGCTGCGGTGCAATGAGACAG----- 3315
2164 ValValLeuAsnSerValIleGlnTyrPheProSerSerGlyTyrLeuAlaGluIleAla 2183
3316 -----GGCGCTGTGAGC 3327
2184 AspThrLeuIleHisLeuProAsnValGlnArgIlePhePheGlyAspValArgSerGln 2203

3328 GGGGACGCGGTGTTGTCGCGG---TTCACGCGGTGTTGTTCTC----- 3366
QY 2204 AlaThrAsnGlnHisPheLeuAlaIaArgAlaIleHisThrLeuGlyLysAsnAlaThr 2223
Db 3366 ----- 3366
QY 2224 LysAspAspValArgGlnLysMetAlaGluLeuGlnAspMetGluGluLeuLeuVal 2243
Db 3367 -----GAAACGCGCATTCGCAATCGCCAGCATCGAACAAGCATATGCTGTTG 3414
QY 2244 GluPro-----AlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGlu 2260
Db 3415 AACCCGCGGACGCGCCCTGAAATGCCAGAGCACTCGAAGCGGCTTGACGCGCCCTGGTGA 3474
QY 2261 HisValGluLeuLeuProLysAspMetGluAlaValAsnGluLeuSerAlaTyrArgTyr 2280
Db 3475 CATCAGACGACATTCGCTGCGCTC-----CATGAACCGACGGAACCTGGCAT 3525
QY 2281 AlaAlaValAlaHisValArgGlySerLeuGlyAspGluLeuValLeuProValGluLys 2300
Db 3526 GCGGAA-----CATGCGGAAGCAACGCTGGCGGCTGCTGCTGCTGCGCGAGCGC 3579
QY 2301 AspAspTrpIleAspPheGlnAlaAsnGlnLeu-----AsnGlnLysSerLeu 2316
Db 3580 -----GTGAGCCGACAAAGCGCTGAGTCGCTTCGACAGAGCTGCAAGCGAGCTG 3630
QY 2317 -----GlyAspLeuLeuLysSer-----SerAspAlaAlaIle 2327
Db 3631 GACCTGGCTGACGCGCCACCTGTTGCGAGCGCTGTTGATGATAGCGGACGCGCGC--- 3667
QY 2328 MetAlaValSerLysIleProPheGluIleThrAlaPheGluArgGlnValAlaIleSer 2347
Db 3688 -----CAGCCTCTGTTGTTGGTATC 3708
QY 2348 LeuAsnSerAsnIleAsp-----GluTrpGlnLeu-----SerThr 2359
Db 3709 CACCATCTGCTGTGAGACGGGGGTCTCTGGCGCATTCCTCGGAGGATTCGCAAGGGCT 3768
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Db 3769 TACCAGACAGACCTCCGCTGGGAAAGCTCCG-----CGGCTGCTC 3807
QY 2380 GlyGluAlaGlyPheArgValGluValSerSerAlaArgGlnTrpSerGlnAsnGlyAla 2399
Db 3808 GGC-----AAGACCAAGCCCTTCAAGCGCTGGGCGC----- 3837
QY 2400 LeuAspAlaValPheHisHisCysCysSerGlnGlyArgThrLeuValAsnPheProThr 2419
Db 3838 -----GGCCGA-----GTG 3846
QY 2420 AspHisIleLeuArgGlySer-----AspLeuLeu 2429
Db 3847 AGGAGACATCCGCTGTGATGATGATGAAGCGCAGTTCGATTTGGCGCGACGCTCTG 3906
QY 2430 ThrAsnArgProLeu-----GlnArgLeuGlnAsnArgIle 2442
Db 3907 GAAGTGGCGCGGCGGACCTTCGCTGCGTCATCCGAAAGCGCTCGAGACGCGTTTC 3966
QY 2443 AlaIleGluValArgGluArgLeu---ArgSerLeuLeuProSerTyrMetIleProSer 2461
Db 3967 GCCATCTCCGTCGAGACTCGCTTCGACCGGACGCTTGACCGAAGC----- 4011
QY 2462 AsnIleValIleLeuAspLysMetProLeuAsnAlaAsnGlyLysValAspArgLysGlu 2481
Db 4012 -----CTGCTGAAGCAAGGCGCGGACGCTACCGTACCAAGTCAACGATCTTCTG 4062
QY 2482 LeuSerArgArgAlaLysValValProLysGlnIleThrAlaAlaProLeuProThrPhe 2501
Db 4063 CTGACCGCCCTGGCGGACAGTGTCTGCTGGAGCGCGCTCT----- 4107
QY 2502 ProIleSerGluValGluValIleLeuCysGluGluAlaThrGluValPheGlyMetLys 2521
Db 4108 -----TCAAGCCTG 4116

QY 2522 ValAspIleThrAspHisPhePheAsnLeuGlyGlyHisSerLeuLeuAlaThrLysLeu 2541
Db 4117 GTACAGCTGGAAGGACAT-----GGCGCGAGGACGCTGTTCCGCTATTCGAC 4164
QY 2542 IleSerArg-----IleAspGlnArgLeuLysValArgIleThrValLysAsp 2557
Db 4165 CTAGTGTGACCGCTCGGTGTTCCACAGTTTGTCCCGGTGCGCTGAC----- 4215
QY 2558 ValPheAspHisProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuValLeu 2577
Db 4216 -----CCGGTC---GGGATCTTGGGAGAGTCCCTGAAGCGATCAAGAAACAG 4260
QY 2578 GlnGlnProValSerAsp---GlyGlnGlyAspArgSerAlaHisMetAlaProArg 2596
Db 4261 TTGCTGCGCATTCGCCAAGAGGCGCTGGATTATGCTGCTGCGCTATCTGCGTGA--- 4317
QY 2597 ThrGluThrGluAlaIleLeuCysAspArgLysPheAlaLysValLeuGlyPhe-----Gln 2614
Db 4318 -----GAGGAAAGTCCCGGCTCTGGCGGGGTTCCGCGAG 4253
QY 2615 ValGlyIleThrAspAsnPhePheAspLeuGlyGlyHisSerLeuMetAlaThrLysLeu 2634
Db 4354 GCGCGATCACTTTCATTAAC-----CTGGCCAGTTGACGCTCAGTTGACAGAGATG 4407
QY 2635 AlaVal-----ArgIleGlyHisArgLeuAspThrThrValSerVal 2648
Db 4408 GCTCTGCTGACCCGCGCTGGCGAAGCGCGGGGCGAGATGACGCC----- 4455
QY 2649 LysAspValPheAspHisProValLeuPheGlnLeuAlaIleAlaLeuAspAsnLeuVal 2668
Db 4456 -----GGCGCTCCGCTGACCACTGGCTG 4479
QY 2669 GlnSerLysThrAsnGlnIleValIleGlyArgGluMetAlaGluTyrSerProPheGln 2688
Db 4480 ---AGTCTCAATGGCGGGGTGTTCAAGCGTGAACGTGACATGACATGACATGACGTG 4536
QY 2689 LeuLeuPheThrGluAspProGluGluPheMetAlaSerGluIleLysProGlnLeu--- 2707
Db 4537 CAGATGTTCCGCGAGGACCAAGTGCCTGCGCTGCGCATGATGATGCTGAGCTGACG 4596
QY 2707 ----- 2707
Db 4597 GCGCTGTGACTTCTGCTGCGATTCTCCAGCGCATGCGCGACGCTTCGATTCCCG 4656
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Db 4657 CTGGCGGGGTGGAACGAGCGCGCTGAGATCCCTCGCGTCCGCTGGAAGAG---GTC 4713
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QY 2754 AlaGlyLeu-----IleLysAlaCysGluSerLeuValAsnHisLeuAsp 2768
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 18:24:23 ; Search time 4856 Seconds
(without alignments)
12431.365 Million cell updates/sec

Title: US-09-482-788-1

Perfect score: 11212
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 172.4 | 1.5 | 6288 | US-10-282-122A-33846 | Sequence 33846, A |
| 2 | 153.4 | 1.4 | 9580 | US-10-282-122A-33351 | Sequence 33351, A |
| 3 | 145 | 1.3 | 10002 | US-10-282-122A-14471 | Sequence 14471, A |
| 4 | 138.4 | 1.2 | 15450 | US-10-282-122A-7449 | Sequence 7449, Ap |
| 5 | 134.8 | 1.2 | 5127 | US-10-156-761-3630 | Sequence 3630, Ap |
| 6 | 134.8 | 1.2 | 902508 | US-10-156-761-1 | Sequence 1, Appli |
| 7 | 133.8 | 1.2 | 3954 | US-10-282-122A-30194 | Sequence 30194, A |
| 8 | 129.6 | 1.2 | 2811 | US-10-282-122A-33871 | Sequence 33871, A |
| 9 | 129 | 1.2 | 10296 | US-10-282-122A-33665 | Sequence 33665, A |
| 10 | 127.8 | 1.1 | 9748 | US-10-282-122A-31388 | Sequence 31388, A |
| 11 | 119.6 | 1.1 | 3789 | US-10-156-761-3185 | Sequence 3185, Ap |
| 12 | 115.2 | 1.0 | 15738 | US-10-329-079-46 | Sequence 46, Appl |

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| 13 | 115.2 | 1.0 | 61944 | US-10-329-079-34 | Sequence 34, Appl |
| 14 | 111.2 | 1.0 | 8138 | US-10-369-493-35302 | Sequence 35302, A |
| 15 | 111.2 | 1.0 | 9683 | US-10-369-493-38492 | Sequence 38492, A |
| 16 | 110.6 | 1.0 | 11007 | US-10-402-842-5 | Sequence 5, Appli |
| 17 | 110.6 | 1.0 | 47988 | US-10-402-842-1 | Sequence 1, Appli |
| 18 | 109.2 | 1.0 | 6522 | US-10-282-122A-31533 | Sequence 31533, A |
| 19 | 104.8 | 0.9 | 8646 | US-10-282-122A-33353 | Sequence 33353, A |
| 20 | 104.6 | 0.9 | 3048 | US-10-156-761-3146 | Sequence 3146, Ap |
| 21 | 104 | 0.9 | 13029 | US-09-815-242-4052 | Sequence 4052, Ap |
| 22 | 104 | 0.9 | 13029 | US-10-282-122A-7240 | Sequence 7240, Ap |
| 23 | 104 | 0.9 | 77536 | US-09-940-3168-1 | Sequence 1, Appli |
| 24 | 101.2 | 0.9 | 7788 | US-10-329-079-8 | Sequence 8, Appli |
| 25 | 101.2 | 0.9 | 37360 | US-10-329-079-6 | Sequence 6, Appli |
| 26 | 99.8 | 0.9 | 135638 | US-10-314-657-1 | Sequence 1, Appli |
| 27 | 99 | 0.9 | 3726 | US-10-282-122A-33927 | Sequence 33927, A |
| 28 | 98.8 | 0.9 | 15738 | US-10-329-079-12 | Sequence 12, Appl |
| 29 | 97.2 | 0.9 | 2460 | US-10-282-122A-30195 | Sequence 30195, A |
| 30 | 95.4 | 0.9 | 7347 | US-09-815-242-7773 | Sequence 7773, Ap |
| 31 | 95.4 | 0.9 | 7347 | US-10-282-122A-7467 | Sequence 7467, Ap |
| 32 | 95.4 | 0.9 | 7347 | US-10-324-967-17 | Sequence 17, Appl |
| 33 | 94 | 0.8 | 11058 | US-10-156-761-3629 | Sequence 3629, Ap |
| 34 | 91.6 | 0.8 | 4020 | US-10-369-493-43172 | Sequence 43172, A |
| 35 | 86.8 | 0.8 | 8244 | US-10-402-842-3 | Sequence 3, Appli |
| 36 | 84.8 | 0.8 | 550 | US-10-425-115-175139 | Sequence 1, Appli |
| 37 | 84.6 | 0.8 | 88421 | US-09-976-059-1 | Sequence 1, Appli |
| 38 | 83.4 | 0.7 | 12951 | US-10-282-122A-31678 | Sequence 31678, A |
| 39 | 83 | 0.7 | 3471 | US-09-974-300-2167 | Sequence 2167, Ap |
| 40 | 82.4 | 0.7 | 4659 | US-10-369-493-42839 | Sequence 42839, A |
| 41 | 80.6 | 0.7 | 9399 | US-10-369-493-42804 | Sequence 42804, A |
| 42 | 80.6 | 0.7 | 18876 | US-10-329-079-42 | Sequence 42, Appl |
| 43 | 80.2 | 0.7 | 135638 | US-10-314-657-1 | Sequence 1, Appli |
| 44 | 79.4 | 0.7 | 7925 | US-10-282-122A-33350 | Sequence 33350, A |
| 45 | 76.4 | 0.7 | 7155 | US-10-329-079-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-282-122A-33846
; Sequence 33846, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining prior application data removed - See File Wrapper or PALM.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 33846
LENGTH: 6288
TYPE: DNA
ORGANISM: Pseudomonas syringae
US-10-282-122A-33846

Query Match 1.5%; Score 172.4; DB 16; Length 6288;
Best Local Similarity 43.9%; Pred. No. 1,1e-42;
Matches 1196; Conservative 0; Mismatches 1481; Indels 45; Gaps 9;

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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 33351
LENGTH: 9590
TYPE: DNA
ORGANISM: Pseudomonas syringae
US-10-282-122A-33351
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Query Match 1.4%; Score 153.4; DB 16; Length 9590;
Best Local Similarity 44.4%; Pred. No. 26-36;
Matches 1199; Conservative 0; Mismatches 1436; Indels 64; Gaps 12;
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DB 3704 ACAGAAACAGTGTGTGTGTCGACCCGACCAACATGCTCCGATGCTGTGTGAGTCC 3763
QY 4007 TGTCTTGCAGCGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4066
DB 3764 GATCATGTTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3814
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; Sequence 14471, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining SEQ ID NOS: 78614
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14471
; LENGTH: 10002
; TYPE: DNA
; ORGANISM: Burkholderia mallei
US-10-282-122A-14471

Query Match      1.3%; Score 145; DB 16; Length 10002;
Best Local Similarity 43.2%; Pred. No. 1.1e-33;
Matches 1186; Conservative 0; Mismatches 1515; Indels 42; Gaps 9;
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Db 5379 CGAGCAACCGGTTCAAGCGCGTGACACCGGATGATGCGCGGGCGCTTGCGCATCGA 5438
Qy 3830 CATTGATCTCTGTGATGTTACAGACCTTGACCCGTTTGAAGTTGTGACCAAG-----ACA 3883
Db 5439 CGATCTGCGGTGGTGCCGACCGCCGCGCGCGCGCGCGCGGATCTTGCGCGGACGCG 5498
Qy 3884 GACTACTCCCTTCAATCTCTCATCTGAGCTGAGTGGAGACGACTTCAAGACTTGG 3943
Db 5499 GAGCGAGCGGTTTGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5558
Qy 3944 TGAAGATGACCAATCTCTCATTTGATGATCATCATATCATCTGAGATGTTGTTAAT 4003
Db 5559 CGACGACGTGACACCGTATGCGTGAAGATCATCATCTGATGCTGCGACCGCTGTGAT 5618
Qy 4004 TGATGCTTGGACGCGGATCTCATATGACCTTCTACTGACGTCGCGCTCAAGACTCAAGA 4063
Db 5619 CGAGGTGTTGCGCGGAGCTGAGCGAGTTGATCGCGCAATTGCGCGCGCGCGCGCGCG 5678
Qy 4064 CCCGCTGTCAGCACTCACTCTTACCTTATCTAGTACAGCGACTTGGCAAAATGACAGAA 4123
Db 5679 CCGGTTCCCGCCGCTGCGCGGTGACATGCGCGCATTTAGCGCGCATGGACGACGCGCAT 5738
Qy 4124 GACCAATTATAGACGAGAGAGCACTCACTACTGAGAGAGCACTCAAGATC 4183
Db 5739 CGCGCGGTGCGCGCTGACCGCGCGCGCAATCTGCGCGGATGCGCTCGCGCGCGCGCC 5798
Qy 4184 TTCCCGACGAAATCCCGACCGACTTTGCGCGCGCGCGCGCGCTTCTGTGAGACGCGAG 4243
Db 5799 GAGCGCTGCGAATGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5858
Qy 4244 TTGCGTACATGTTACATCGACGCGCGAGCTCTACAGTCCCTTCAAGCTTTCGACAGA 4303
Db 5859 GAGCGTGGGCTGCGCGTGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5918
Qy 4304 ACACAACGACCTCTTGTGCTGTTCTTACTGCGGTTCCGTCGCGCTATATCTCT 4363
Db 5919 TCACGCGCGACCTCTTCAATGACCGGTTGCGCGCGTGAGAGGCTGCTGTGCGCCCT 5978
Qy 4364 CACAGCTTTGAAGACGCTGTCTATTGTTACCAATTGCGAATTCGCAACGACCTGAACT 4423
Db 5979 GTGCGCGCAACCGACGTGTGATCGCACGCGAGCGCAACCGCGCGCATGCGCGAT 6038
Qy 4424 GAGGATATCATGCGCGCTTGTTCATACGACGTGATCGAATCAATAGATCATCA 4483
Db 6039 CGAGGCTTATGCGCTTTTTCGTCACACGATCGCGCTCGGTGACCTTCACGCGCG 6098
Qy 4484 CGATACCTTTGGACTTTGATCAACCAAGTCAAGGCTTACGACGACGACGACATTCGAA 4543
Db 6099 GCGGACGTTGCGAGGCTGCTCGCGCGCGGTGAAGGCGCGCGCGCGCGCGCGCGCA 6158
Qy 4544 CGAGATATTCGCTTTGAGCGCGCTTGTATACGACATCAACGCTGATCCAGATCTGTC 4603
Db 6159 TCGAGCATTTCCGTTGAGCATGTGTGACGCGGTGACGCGCGCGCGCGCGCGCTTCGCA 6218
Qy 4604 AAGCACACCTCTGCGACCACTCAATTTTTCAGTGCCTCAAGAGGACCTTGGAGAT 4663
Db 6219 TAGCCGAGTTTTCAGCGCATGTTCCGCTGACGACGCGCTCGCGCGCGAGATGCGCT 6278
Qy 4664 CAAATTCCAGGCTCTCGAGTCCGATCCGTTAGCTTACGAAAGCGTATCACTGATTTGACAT 4723
Db 6279 CGAAGGCTGCGCGCGAGCGCTCGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGAT 6338
Qy 4724 GAGTTTCATCTGTTTCAAGAAACCGACAGCCTTAAAGTAAAGTCACTTTGCCGATGA 4783
Db 6339 GAGCGTGTGCTGCGGAGAGCGCGGATGAGATCGACGCGGCTCTCAATATGCGAGCGC 6398
Qy 4784 GCTGTTCAAAATGAGACTGTTGAAATGTCGTCAGAGTATTTCTTTGAGATTCAGAGAA 4843
Db 6399 GCTGTTGAGCGCGCGACGATCGAGCGCTTTCGCGGCTACTCGCGGCTTTCGCGAGG 6458
Qy 4844 CGGCGTTCAAGTTGCGGACACACAGTCTCAATATCTTCTTTGACGATGAGCATTTGAC 4903
Db 6459 GATGCTGCGCGATGACACGCGCGCTGATGATTCGATTCGCGCGCGCGCGCGCGCGAG 6518
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QY 4904 TCTTGAATAATGATGTTCTCAACGTCACAAATGTCAGTATCCCGAGATTCAGACTT 4963
 DB 6519 GCGGAGATCTGATGAGGCGCGGAACCGGACCGCGCGCGATTCGCGGAACAGCGCGT 6578
 QY 4964 GCGTGAATGTTCTTCCAGACCCAAATCTCTGCTTACCCCGAATAGTGTGGCTGTGAGCTC 5023
 DB 6579 GCAATCGGCTTTCGAGGCGGAGCGGCGCGACCGCCCGAATCCGACCGGATTCGTCAGCG 6638
 QY 5024 CTGTGCGCATGTTGACCTACACCGAGTTGATTCGCGCACTGATATTCCTGCTGGATGGCT 5083
 DB 6639 GCGGACGAGCGCTGACATATGCGCGCTGATGCGCGCGCGAATCCGATTCGACAGCGGCT 6698
 QY 5084 TCGTCGACGCTCAATGCTTCGACAGAGCGCTTTCGAGTATTTGCCCGACGCTGATGTA 5143
 DB 6699 CCGGACGCGCGCGTGGCGCGCGCGATCGGCTGCGCTGATCTCAGCGCTGATCGG 6758
 QY 5144 GACATATGTCGCTTCTTGTGTGTGTAAGGCGAATTTGGCTTATCTTCTCTGATGT 5203
 DB 6759 GCTGCTGCGCGCGAGCTTCGCGGTCTCAAGCTTCGCGCGCGCTTACGTCGCGCTGATGT 6818
 QY 5204 ACGATGCGCTTCGCGGAGGTTGAGATATCTTTCGACTTTCGCGCTTACATGT 5263
 DB 6819 CCGCATTCGCGCGCGCGCGAAGCGCTTCGCGCGAAGACAGCGCGCGC----- 6868
 QY 5264 TTTGATTTGCGCATGATACAGCGCTCCCGATTCGAGGTTACTAACGTCGATTTGTTG 5323
 DB 6869 --GGCTGTGCTGGCGGACCGCGGCGCTGACTGCGCGCGCGCGCGCGCGCGCGCGAGCG 6926
 QY 5324 TATCCGGGATGCGCTGATGACAGCAATGCAATGCTTTGAGTACTTCAGACGACGACG 5383
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 QY 5384 CACAAAGCCCTCAGCGCGAGTCCGATTCGCTGATATTCAGATTCAGATTCAGATTCAG 5443
 DB 6982 CCGCATTCGCGCGCGCGCGAC-AACCGCGATTCAGATTCAGATTCAGATTCAGATTCAG 7040
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 DB 7041 GCGGAGGCGGTGCTGTCAGATTCGCGGATTCGCGCGCGCGCGCGGTGAGAACGCGTTA 7100
 QY 5504 ACCCAATATCTTCGGAAGAGAGATGCTCAGATGCGGACATTCGCTTTGACGCGCGC 5563
 DB 7101 TGGACCTTCGACCGCTTCGAGACCGGTTTCGCTTCGATTCGAAACCGCGCTTCGACGCTC 7160
 QY 5564 ATGTAAGATGATTCAGCGCGCTTTTTCGGAAGACATTCGCTTTCGCTGATCAT 5623
 DB 7161 GACGTTGAGATGTCGCGCGCTTCACAGCGCGCGATTCGCTGAGCGCGA 7220
 QY 5624 GACAACTTCGACGCTGAGACATTCAGATGTCGCTTTTCGAGAGCATGTCACGCGCGC 5683
 DB 7221 CGATCTGCTGATTCGCGCGCGCTTCGCGGAAAC-TGTGCTGATTCGCGCTGACGCTGCC 7279
 QY 5684 AAGTCATGTCACAGCTCTTCTCAAGATGTAACCTTCGAGTCCCGAGAAAGGCTCTGAG 5743
 DB 7280 TGTTCCTCAAGACGCGCTCTTCACCGGTCGCTGTCGATTCGCG--CGATGTCGCT 7337
 QY 5744 AACCTGATGTTCTTCTTTCGCTGTCGAGATTCGACGCGCGCCAGATGCTGCTGATGC 5803
 DB 7338 GCGGCTGCGCTGCTGATTCGCGCGCGAGCGCGCGATTCGCGGCTTACCGGAAGT 7397
 QY 5804 GCAAGGACTTATTCAGGCGCTCAGTGTTCATGATGTTACGCGCGCAACAGAGATGAGT 5863
 DB 7398 GATGGAAGCGCGCGCGCGCGCGCTGTCGTAAGCGGTACGCGCGACGAGACACACAC 7457
 QY 5864 CATGAGTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 5923
 DB 7458 GTTCGCGCGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7517
 QY 5924 ACGAGCTCTGAACAACTCAGAGGCTATGTCGTCGATTCGTCGAGCAACAGCTTGTGCGAT 5983
 DB 7518 GCGGCGCATCGCAATGTCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 7577

QY 5984 TGGTGTGATGAGAGAGCTTGTCTCACTGCGCATGCTCTTGGCGCGGCTTACAGTACAA 6043
 DB 7578 CCGCGTGTACCGGCGGAGATTCACATTCGCGCGCGCGCGGCTGTCGCGCAAGCTTACCTGAACCG 7637
 QY 6044 A---GCCCTTGAAGAGAACCGGTTTGTGACATTCATTCGTCATGACAGACAGTGAAGC 6100
 DB 7638 ACCGCGCTTTCGCGCGGAGGCTTCGTCGCGATTCGTCGTCGTCGTCGTCGTCGTCGTCG 7697
 QY 6101 GTATGCACTGCGCATGAGTTCGCTTACAGATTCGATTCGATTCGATTCGATTCGATTCG 6160
 DB 7698 GTACCGGAGCGGAGACTGCGCGCAT---GGCGCGCGATGCGATGCTGCTGATTCGCG 7754
 QY 6161 ACGTATGACACCCAGTTTCAAGTTGTCGCAATTCGTCGATTCGATTCGATTCGATTCG 6220
 DB 7755 CCGCGCGCACTTCAGATGTAAGATTCGCGCTTTCGATTCGATTCGATTCGATTCG 7814
 QY 6221 GCGCCTTTCGCGGACTCCTTCGTCGAGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 6283
 DB 7815 GTGCTGCTTGAACACGCGCGCTTCGCGCGAGCGCGGCTGTC 7857

RESULT 4 US-10-282-122A-7449

; Sequence 7449, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyckind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7449
 ; LENGTH: 15450
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-7449

Query Match 1.2%; Score 138.4; DB 16; Length 15450;
 Best Local Similarity 44.2%; Pred. No. 2e-31;

Matches 805; Conservative 0; Mismatches 1001; Indels 16; Gaps 5;

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QY 3411 TTCTTGAATCTGGAGAACTCTATCATCTGATCAAGATGCT--GAACTAGCCAGG 3467
Db 7561 TTTTGAATCTGGAGAACTCTCTATCAAGCCAGCCGGGTGCTGCGCCGCGCAG 7620
QY 3468 TCCGTTGATGAGACCTCAAGCTCTTAACATCTACAGACCCGACGTTGGCGGAAT 3527
Db 7621 GACTGAGAGTGAACCTGACCTTGGCGATCTGTTGAGAGCGCGGCTCTGGAGACTTC 7680
QY 3528 TCCGCGGTCTCAAGGGTGAATCTCTG--TCTCACTCTCATCCCAAGTCAATCAT 3584
Db 7681 GCGGCTTCTCCGAGTCCAGCGCGCGAGCGCTGCCCTGTGCTCAAAATTTGCCGCA 7740
QY 3585 GAGGACCTGTTAGACGCTTATTTCAAGCCGACTATGTTCCCTGAGTCAAGTTGAC 3644
Db 7741 GTGCGGAGCTCTTTGTGCAATGCTCAACACGATGTTCTCTGGAACCTGGAG 7800
QY 3645 GTTGGAGTCTGATGATCTGATTTCCATATGCTGTGAGAAATGCGCGGCGCTGCAATGTC 3704
Db 7801 CTTGAAAGCGCGGCTATCATCTCCAGGTACTGACGTTGCGTGGCGTCTGGACAG 7860
QY 3705 GACGCGTTACGTGGGCTCTTGACAGCGCTTGAAACGCGACAGACTCTTGAACGACA 3764
Db 7861 GCGGCGTTGACAGGCTCTGATTTGCTGCTGCTGCGCCAGACGACTTGGCGACCGC 7920
QY 3765 TTGGAAGACAGATGCTGCTGCTGCTCAATTTGTTACAGAAAGCTTCTGAGGAATG 3824
Db 7921 TTGGAAGAGTCAACGCTGACGCGCGCCAGACGATCTGCGCAACATGCGTTGCGCAT 7980
QY 3825 AAGGTCAATGATCTGCTGCTGCTGCTGACCTTGACCTTGACCTTGACCTTGACCT 3881
Db 7981 GTCTGAGAGATTTGCGCGCGCGCGCGAGCGAAAGCAAGTTGCGCGCGCGCGAGGA 8040
QY 3882 CAGACTACTCTCTTAATCTCTCATCTGAAGCTGCTGAGAGCGACGCTTTCAGACT 3941
Db 8041 ATCCGCGAGCTATTCAGCTGCTGCTGCGCGCGCGCTGCTGCGCGCTGCTGCTG 8100
QY 3942 GGTGAAGATACCACTCTCTCATCTATGTCATGATCATCATCTCATGATGTTGCTCA 4001
Db 8101 GCTGGAGAGAGATGTTGCTCATCAACCAAGCAATATCTGTCGAGGTTGCTG 8160
QY 4002 ATTGATGCTCTGCGACGCGATCTCAATCACTCACTCACTCACTCACTCACTCACT 4061
Db 8161 ATGCAAGTATGCTGCAAGCACTCTCAAGGCTTATGCGCGCGCGCGCGCGAGAA 8220
QY 4062 GACCGCTGTCAGCACTCACTCTCTCACTCACTCACTCACTCACTCACTCACTCACT 4121
Db 8221 CCGAGCTGCGCTCATTTGACGCTGCACTGAGTATGCTGCTGCTGCTGCTGCTG 8280
QY 4122 AAGGACCAATTCATAGAGAGAGAGAACTCACTCACTCACTCACTCACTCACTCACT 4181
Db 8281 CTGAGACGCGCGAGAGCGCGCGCGAGCTGATTAAGTGGCTGAGCGCTGAGCG 8340
QY 4182 TCTTCCAGCAAAAGATCCGACCGCACTTTGCCCGCTGCACTTCTGTGAGAGCA 4241
Db 8341 CAAGCGCTCTGGAATCTGCGCGCGCGAGCGGCTGCGCGCGCGCGCGAGCGAG 8400
QY 4242 GGTGGCTATCATGTTACATGACGCGAGCTCAACAGTCCCTTTCAGCGCTTTCGAC 4301
Db 8401 CAGCGTCTGACATGCGGCTGCGCGGTGCTATTCGAGAGAGTCTGCGCGCGCG 8460
QY 4302 GAAACAAACGACCTTTTCTGCTGCTTCTTCTGAGTCTGCTGCTGCTGCTGCTGCT 4361
Db 8461 CCGAGAGGCTGACCCCGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 8520
QY 4362 CTCAGAGCTGTTGAAGAGCGCTGCTATGATGATCACTCACTTGGAAATGCAACCG 4421
Db 8521 TATAGCGGAGAGTCTGAGATCTGCGCTGCGGCTATCTTCCCAACCGCGCGAG 8580
QY 4422 CTGAGAGATATCATCGGCTGCTTCTGCTCAATACGAGTGTATGCAATCAATGATCAT 4481
Db 8581 GTGAGAGGCTGATCGGCTTCTTCTGCTCAATACGAGTGTGCTGCTGCTGCTGCT 8640

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QY 4482 CAGATACCTTTGGAGACTTTGATCAACCAAGCTCAAGGCTACAGACAGACGATTCGAG 4541
Db 8641 GCGCTGCTTTCCGCGATCTACTGCGCGCGCTGCGCGAGCGCGCTGCGCGCGAGCG 8700
QY 4542 AACGAGATATTCGTTTGAAGCGGTTGATATCAAGCTCAAGCTGAGTCAAGATCTG 4601
Db 8701 CACGAGATCTGCGGTTGAGCAATGATGATGCTGCTGAGCGCGCAACCA-----ATC 8755
QY 4602 TCAAGCACACTCTGCGCAACTCATTTTTCAGTGCATCTCAAGAAAGACTTTGAGAA 4661
Db 8756 TCAAGCACAGCGCTGTTTTCAGTGCATGATATCAACCAAGAGCGGAGAGAGATG 8815
QY 4662 TTCAGTTCCAGGCTCTGAGTCCGATCTGCTGCTGCA--AAGCTCACTGATTTG 4719
Db 8816 CCAAGTCAATGATTTGCAATGAGAGATTTTCTGCTGAGTGTGCTGCGCGAGTTG 8875
QY 4720 ACATGAGTTTCATCTGTTTCAAGAAACCGACAGCTTAAAGGTAGCGTCACTTTGCG 4779
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QY 4780 ATGAGCTTTCAAAATGAGACTGTTAAATGTCACAGATTTCTTGAATTTGCA 4839
Db 8936 CCGAGCTGTTGAGCGCGCGAGCGTCAAGCGCATGCGCGCATTTGCGCAACCTGCTG 8995
QY 4840 GAAACGGGCTTCAAAAGTTGCGCGACACAGCTCAATCTTCTTGTGATGAGCAATG 4899
Db 8996 GCGGCTATGCTGAAACCGCGAGCGAGCTCACTGCTGCGCGCTGATGCTGATGCGAG 9055
QY 4900 TGACTCTTGAATAATGATGTTCTCAACGTCAAACATGTCATATCCCGAATCGA 4959
Db 9056 AGCGTGGCGAGTTGCTGAGAAAGCGTGAAGCGCACTGCGCGCGAGTACCGCTGCA 9115
QY 4960 GCTTGGCTGATGCTTTCAGAACCCAGTCTCTGCTTACCCGATAGTCTGCTGCTG 5019
Db 9116 GCGGCAACCGGTTGTTGAGAGAGAGTCAAGCGCAAGCGCGCGCGCGCTGCGCT 9175
QY 5020 ACTCTGTCGCGATGACCTTACACGAGTTGATGCGCGAGTCTGATATCTGCTGAT 5079
Db 9176 TCGCGAGAAACCGCTGAGCTTACCGAGCTGAACCGCGCGCGCGCGCGCTGCGATG 9235
QY 5080 GCGCTTCTGACGCGTCAATGCTGCAAGAGCGCTTGTGCGAGTATTTGCCCGAGCTAT 5139
Db 9236 CCGTGAATGAGCGCGGCGTGTGCGGAGCGCGCTGCGTGTGCGCGAGAGGTTCCA 9295
QY 5140 GTGAGCAATTTGCGCTTCTTTGCTGTTGAAGCGGAACTTGCGCTATCTTCTG 5199
Db 9296 TCGAGATGCTGCGCGCTGATGCGATCTCAAGGCGCGCGCGCTGAGTGGCTG 9355
QY 5200 ATGATGATGCGCGCTGCGGAG 5221
Db 9356 ACCCGAGTACCCCGAGAGCG 9377

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RESULT 5
US-10-156-761-3630
Sequence 3630, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697

Db 4513460 CGCGGGGTGAGGAGCGGGCCGCGCCCTCTCCACAGAGAGCTGCCCTTCAGACGG 4513401
Qy 4566 GTTGTATCAGACATCAAGCTGTGATCCAGAGATCTGTCAAGACACCTCTCGACAACTC 4625
Db 4513400 CTGTCGAGAGAGCTTCAGCCCGAGCGC---GACTGTTCGCGACCCCGCTCTACCAAGTG 4513334
Qy 4626 ATTTTTCAGTGCATCAAGAGAGAGCTTGAAGATTCAGATTCAGAGGCTTCGAGTCC 4685
Db 4513343 GCGTTCAGCTGCACAGCGAGGGGCTGACAGCGCTCTCAACCATGACAGTACGCTGGCC 4513284
Qy 4686 GTACCTGTGCTTACCAAGGCTACCTGATTTGACATGAGATTCATCTGTTTCAAGAA 4745
Db 4513283 GCGTTCGCGAGGCTGCGAGGTCGAGAGCCGATCTGTCTGCTTCATGCGGCAACG 4513224
Qy 4746 ACCGAGC---CCTTAAGGTAGGCTCACTTTCCGATGAGCTGTTCAAATAGAGACT 4802
Db 4513223 CCGGACGGCTCTCTCGAGGGGCTCTGATAGCGCACCTGCTGTTTCGAGCGGGGACCC 4513164
Qy 4803 GTTGAATAATGTCTCAGAGATTTCTTGAATTCGAGAAACGGGCTTCAAAAGTTGCGGG 4862
Db 4513163 GCGGAGCGCATGACCGGCACTTCTCACTCTCGAAGAGGTGGCGAGCAGCCGAG 4513104
Qy 4863 ACACCACTCTCAATCTCTCTTTCAGTGTGACATTTGACTCTTGAATAATTTGATGTT 4922
Db 4513103 ACCCGGCTCGGCGCTCTGAGAGCTCTCTCGCGCAGCAGAACGCCCTCTCTGTCGAG 4513044
Qy 4923 CTCAGCTCAAAACATGTGCACTATCCCGAGAAATCGAGCTTGTGATGTTTCAGAAC 4982
Db 4513043 TGGAAACACA---CGGCGAGAGACACCGAGACCGTACGCTTCGAAAGCTTCGAGAG 4512987
Qy 4983 CAAGTCTCTCTTACCCCGATAGTCTGTGTGTGTGATCTCTGTGTGCGGATTCAGCTAC 5042
Db 4512986 CAGGCGCGCAGCGCGCCCGAGCGACCGCCTGACTTCGCGACCGAGACCGTACGTAC 4512927
Qy 5043 ACCGAGTTGATGCGCAGTCTGATATTTCTGCTGAGATGCGTTCGACCGTCAATGCTT 5102
Db 4512926 GGGGAACTGAGCGCGCGGCGCAACCGGCTGCGCAGACCTGCTGACCCGCTGCGGGC 4512867
Qy 5103 GCAGAGACGCTTGTGCGAGATTTGCGCCACGGCTCATGTGAGACAAATTTGCGCTTCTT 5162
Db 4512866 GCGGAGTCAAGCGCTGCGGCTCTGCTGACCGGGGTCCCGAACTGTGACACCGCGCTCTC 4512807
Qy 5163 GGTGTGTGAAGGGAATCTTGCCCTATCTTCTGATGTGATGATGATGCGCTCGCGAGA 5222
Db 4512806 GCGGTGTGAAGGCGGCGCGGCTATGTGCGGTGACCGGCTCTACCGCGCGAGCGC 4512747
Qy 5223 GTTCAGATATCTTCTGAGACTTTCGGGCTTACATGTTGTTGATTTGGCATGATACA 5282
Db 4512746 ATGCGGCGCA-----TGTGAGACAGCGCGGCGGTACGACGCGGTGAC 4512703
Qy 5283 GCGGCTCCCGATATCGAGGTTACTAACGTGAGTTTGTGCTATCCGGATGCGCTGAAT 5342
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Qy 5343 GACAGCAATGCAATGCTTGAAGTATCGAGACGACAGCAAGAACCCCTCAGCCAGC 5402
Db 4512642 GAGAGCGGAGCAATGCGCGGCGCGCGCGCGCGCGCGCGAGACAGGAGCCGCG 4512583
Qy 5403 A-GTCTGCAATGCTGCTGTATATCTCAGAGTCACTGCGCGACCAAAAGGCGTCAATGAT 5461
Db 4512582 ACGGCTGCGTACCACTTCTTCACTGCGGCTCGACCGGCAACCCAAAGGCGTCAAGT 4512523
Qy 5462 TGAGCACGCTGTCTATTTGAAACAGTCAAGAGTGTATACCAACTATCTCTCGGA 5521
Db 4512522 CACCCACAGAGGTTCCGCAACACGTCGCTGCGCGCGCGCGAGAACTCGCGGAGAG 4512463
Qy 5522 AACGAGATGGCTCAATGCGACCATTCGCTTGAAGCGCGCATCTGACAGATCTACAG 5581
Db 4512462 CTACGCGGCGCGCGCTGTTCTCTGCGCGCGCTGACCTGTCGTCGCGCACTGTG 4512403
Qy 5582 CGGCTTTTGTTCGAAAGACATTTGTTGCTGACTACATGCAACCTCGACGCTAG 5641

Db 4512402 GCGCGCGCTGTGTACCGGCGAGCGGCTGTTCTCTGCTCCGACAGACACCGACATGTCCA 4512343
Qy 5642 AGCACTCAAGATGTGTGTTTTCGAGAGATGTCAAAGCGGCAAGTCAATGTCAAGCTTC 5701
Db 4512342 GTGGGCAAGCGGCTGCGGAGGCGCCAGCGCTTCAAGTTGTCAAGTGAACCCCGGCGCA 4512283
Qy 5702 TTCTCAAGATGTACCTCTCCGAGTCCCGAAGAGCTCTCGAAGAACTTGAATGTTCTTCT 5761
Db 4512282 CTTGACATCTCGCTTCAAGTCAACCGGCGCGAGCGGCGCGCTCGCGCGGCT 4512223
Qy 5762 CTTGTGTGAGAGATTCGAGCGCGCCAGATGCTCTGATG---CGAGGACCTTATCA 5818
Db 4512222 GTGTGTGCGGCGGAGCGCTTCAACCGCGCCACCTCGAGCGCTGCGCGCACTCGCCC 4512163
Qy 5819 AGGAGTCAAGTGTTCATATGAGTTCAGCGCCCAAGAGATGATGATGATGATCAATCTA 5878
Db 4512162 GAGACCGCGCTATACAGAGATACGAGGCGGAGCGAGCGCTCGCGGACAGCGGTGA 4512103
Qy 5879 TCCCATTTGACTGCACTGAGTCTTCAATGAGATTCATGAGATTCAGAGCTTGAACAA 5938
Db 4512102 CGAATTTCCGAGCATG---CGAGCGCGAGTACTGCCCCATCGAGCGCGCTGCGCAA 4512046
Qy 5939 CTCAGAGCGTATGTGTGTGATCTGAGCAACAGCTTGTGGCATGTGTGATGAGAGA 5998
Db 4512045 CATGCGGATGTACTCTTCAACCGCGCTCTCAAGCCCGCTCCGCTCGGAGTCCGCGCA 4511986
Qy 5999 GCTTGTGTCACTGCGAGATGCTTTCGCGGAGCTACAGTCAAAAGC-----CTTGA 6052
Db 4511985 GCTGTACGTGCGGCGGAGCGGCTGTGCGGCGCTACGCGCAACCGCCCGACCTGACGCG 4511926
Qy 6053 CGAAGACGTTTGTGTGCACTTACTGTCAATGACAGACAGTGAAGAGCGTATGCACTGG 6112
Db 4511925 CGACCGCTTCTCCGACCGGACCGGACCGGCGCGCGCGCGCATGATGACGACCGG 4511866
Qy 6113 CGATGAGTGGGATGAGATGAGATGAGTGTGCTCATGAGTCTTCTGAGAGTGTGACAC 6172
Db 4511865 GACCTGTGCTCGCAC---CTCCGAGAGGAAAGTGTGCTTCTCGCGCGGCTGACGA 4511809
Qy 6173 CCAATCAAGATTCGTGCAATGTATGCAATGAGTGAATGAAGAGCGCTTCTGCG 6232
Db 4511808 CCAAGTCAAGATTCGCGGCTATGCGCTGCAATCTGCGGAGATCAAGCGCTGACAGC 4511749
Qy 6233 CGACTCTCTCGTCCGAGATGCTGTGTCTCTTCAAGAGATGAGA 6280
Db 4511748 GCAACCGCGCGTCCGAGCGCGCTGTGACCGGACCGGCGCGAGAA 4511701

RESULT 7
US-10-282-122A-30194
; Sequence 30194, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33871
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Pseudomonas syringae
US-10-282-122A-33871

Query Match 1.2%; Score 129.6; DB 16; Length 2811;
Best Local Similarity 44.5%; Pred. No. 3.8e-29;
Matches 85; Conservative 0; Mismatches 1024; Indels 37; Gaps 7;

QY 4359 CGTCTCAGACCTGTTGAAGCGCTGTCATTTGTAACCAATTTGGAAATCGCAACCGACT 4418
DB 100 CGGTTACGGGGAGATGAGTGTATCGGCACACCGGTGGCAATTCGCCGAGC 159
QY 4419 GAATGAGATATCATTCGGCTGCTTTGTCAATACGAGTGTATGCAATTCATATGAT 4478
DB 160 GAATGAGATATCATTCGGCTGCTTTGTCAATACGAGTGTATGCAATTCATATGAT 219
QY 4479 CATACGATATCTTTGGGACTTTTGTATCAACCAAGCTCAAGGCTACAGACAGCATTC 4538
DB 220 GGGAGCTGAGCGCGCGCGCTTCTGAGAGAGTCAAGCGGTCAATGCTGGCGGCAT 279
QY 4539 GAGAACGAGATATTCGTTTGAAGCGCTGTTATACCACTACAGCTTGATCCAGAT 4598
DB 280 GCCCATGAGACCTGCGCTTGCAGACAGTGTGTGAGCGTGTGAGC---ACCGGAGC 336
QY 4599 CTGTCAAGCAACCTCTCGCAACACTATTTTGCATGTGCACTCAAGAAAGACCTTGA 4658
DB 337 CTGGCCCATATGCGCGATCTTCAGAGTCAATGCTGGCGCTGAACCAACCCCGGCGCGC 396
QY 4659 AGATTCAAGTTCAGAGTCTCGAGTCCGTACTGTGC---CTAGCAAGGCTACACTGA 4715
DB 397 GAATCAAGCTGCGGAGCTGAGCTGAGCGCTGCAAAACCGGCAACAGACAGCCAG 456
QY 4716 TTTGACATGAGTTCATCTGTTTCAAGAAACCGACAGCTTAAAGTACGCTCACTTT 4775
DB 457 TTGACACTGCTGCTTCACTTGTGAGGCGAAGGAGGAGTGTGCTCGGTTCTTGAATAC 516
QY 4776 GCGCATGAGCTTCAAAATGAGACCTGTTGAAATATCTGCAAGATTTCTTGAAT 4835
DB 517 GCGAGCATCTGTTGAGCGGTGCGACATGATGAGTGGGCGCATTTGCAAGTCTT 576
QY 4836 CTGAGAAACGGGCTTCAAGTTCGCGGACACCAAGTCTCAATCTCTTGAATGATGCG 4895
DB 577 CTGAGAAAGATGCTGGGAGTGAACCAAGCGGTCCGAAATCAACGCTGCTGCTGC 636
QY 4896 ATTGTGACTTTGAAAAATGAGATGTTCTCAACGTCAAACATGTGCACTATCCCGAGA 4955
DB 637 GCGCAACGTCGGCGAGTGTGAGACGTTCAACGATACGCGGCGGCTTACCCGCGAGC 696
QY 4956 TCGAGCTTGGCTGATGCTTCCCAAGCCCAAGTCTCTGCTTACCCCGAGTGTGGCTGTG 5015
DB 697 AAGTGTCTTATCAACTGTTTGAAGAGCGGTGGCAACATTCGGAATGCCCTGGCGGTG 756
QY 5016 GTGAGCTCTCTGTCGCGATGACCTTACACCGAGTGTGATCGCAGTGTGATATTCGCT 5075
DB 757 GTGAGTAAAGCCGGAACCTGATCTTATGCGCAACTGATGCTGGGCGGAATCGACTGCA 816
QY 5076 GGAATGCTTGTGTCAGCGTCAATGCTGCAAGACGCTTGTGCAAGTATTTGCCCCACG 5135
DB 817 CATATATCTGATCGGCTGCTGCTGCTCAACCGAGCATGCGGTGCGATCTGCTTCAACGC 876
QY 5136 TCATGTAGACAAATTTGCTGCTTCTTGTGCTGTTGAAGGGAACCTTGGCTATCTTCT 5195
DB 877 AGTCTGAAAAATGCTGCTGCTTCTGCGAAATTTGAAAGCGCGGTGCTATGCTCCG 936
QY 5196 CTCGATGATGAGTCCCTCGCGAGAGTTCAGAGTATATCTTGAAGTCTTCTGGGCT 5255
DB 937 CTGAGCCCTGATATCCGCGAGAGCGGTGCGCTATATGCTGGAAGACAGTGCCTGCTG 996

QY 5256 ACATTTGTTTGAATGGCCATGATPACAGCCCTCCGATATCGAGTGTACTAACGTCGAG 5315
DB 997 GGGTTGCTGTGGAGG-----GGAAACCGGATGTTGTTGGCGAG 1038
QY 5316 TTTGTCGATTCGGGATGCGCTGAATGACAGCAATGACATGAGCTTTGAAGTATCGAG 5375
DB 1039 TTGGCGGTGCGGATCTTGTATCTGCAAGAGGCGATCGGAGGTTGAGCTGATCATAT 1098
QY 5376 CACGACAGCAAAAGCCCTCAGCAGAGTCTGCAATCGTGTGTATACCTCAGATCC 5435
DB 1099 CCGGTGTGCGGACATCAAGCCGAGACCTGGCTATGTGATATACCTCAGGTTCC 1158
QY 5436 ACTGCGGACCAAAAGCGCTGATGAGCAACCGTGTATTTTGAACAGTCACAAT 5495
DB 1159 ACTGTAAACCCAAAGGTGGCCCAACAGCATTAACGCGCTGT---AAACGGTGTGT 1216
QY 5496 GCGGTATACCAATATCTCTGGAACGAGGATGG---CTCATGCGGACCATTTG 5550
DB 1217 GGGCGAGAGTAAATACCACTCGGGCGGAGCATGTGTCTTGCAGAAAGATCTCATTCG 1276
QY 5551 CTTTTGACGCGCATGATGATGATCTACAGCGCCCTTTTGTTCGAAAGACATTTGTT 5610
DB 1277 GCTTCATGATGCTGCTGAGATCTTCTTCTGCTGCTGCGGAGCACAGTGGTCA 1336
QY 5611 GCGTTGACTATGACAAACCTCGAGCTGAGACATCAAGAGTGTGTTTCCGAGAGC 5670
DB 1337 TGCGCGCCCGGAGGACCATCAAGACCTTCACTGATGAGAGTATGAGCGCGAA 1396
QY 5671 ATGTCAACGCGGCAAGTATGATCAGCAGCTCTTCTCAAGATGATACCTCCGAGTCCGA 5730
DB 1397 GCATTGACATGCTGCACTTGTCTTCTTCCATGCTGAGGCTTTGTCAATACAGCCAG 1456
QY 5731 GAAGCTCTGGAACCTTGTATGTTCTTCTTGTGTGACAGATTCAGCGGCCAG 5790
DB 1457 CAGGCGGTGTGACAGCTCAAGCGATATTTGAGTGAAGAAACCTGCCATATCTT 1516
QY 5791 ATGCTCGATGCGGAGGACTTATTCAGGGTCCAGTGTTCATATGTTAGGCCCA 5850
DB 1517 TGCATTTGCAAAACCGGCGCATTTCCGAAAGCGATGCAATATCTTATGAGCCCA 1576
QY 5851 CAGGATGAGATCATGATGATCAATCATCTTCAATGACTGATGATGCTTATCATATG 5910
DB 1577 CCG---AAGCAGCATTTGAGCTCATGATGATGATGATGATGATGATGATGATG 1633
QY 5911 GAGTCCCAATTTGAGAGGACTCTGAACAACTCAGAGCGTATGTCGTGATCTGAGCAAC 5970
DB 1634 TCGTTCGATGCGCGCGTCCGATGAGCAATPACAGGATTTACTGTTGATATGACAGGCC 1693
QY 5971 AGCTTGTGCAATTTGTGTGATGAGAGGCTTGTGTCACTGCGCATGCTTCCCGGG 6030
DB 1694 AGCCAGTGCCTATCGGATCAGCGCGGAAATTAATATCGGCGGAGTGGGGTGCCTGGC 1753
QY 6031 GCTA---CAGTGAACAAAGCCCTTGAAGAGACGTTTGTGCACTTATCTGCAATGACC 6087
DB 1754 GTTATTTGATTCAGACCGGAATTTGACGCGGAGGCTTCTTCTGAGATCTGTTCAATG 1813
QY 6088 AGACATGAAAGGCTATCGCACTGCGGATGAGTGCAGTACAGAGTTGAGATGCGCTCA 6147
DB 1814 GCGCGGCGGCGGAGATGATCAAGAGCGGTGATCTGGGGCGCTGCGGAGCGGCAATA 1873
QY 6148 TCGAGTCTTTCGAGCGATGATGACACCACTTCAAGATTTGCTGCGCAATCTGATGAAATCAG 6207
DB 1874 TCGAGTATCTGGGCGGATMAAGATCAAGTCAAGCTCCGCGGCTTACCGTATGAACTGG 1933
QY 6208 CTGAGATGAAAGGCGCTTCTGCGGAGTCTCCGCTCGAGATGCTGCTGT 6259
DB 1934 GCGAGATGAGTGCAGCTTTCGCGCTTGTCTCGGGGTCAAGGAGGAGTGT 1985

RESULT 9
US-10-282-122A-33665
; Sequence 33665, Application US/10282122A
; Publication No. US20040029129A1

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3365
; LENGTH: 10296
; TYPE: DNA
; ORGANISM: Pseudomonas syringae
; US-10-282-122A-3365

Query Match      1.2%; Score 129; DB 16; Length 10296;
Best Local Similarity 46.3%; Pred. No. 1.6e-28;
Matches 506; Conservative 0; Mismatches 575; Indels 12; Gaps 2;

QY      3603 TCTTATTCACAAAGCCGACATATGTTCTCTGATGATGTTGACGTTGGCAGCTGTGTAT 3662
DB      82  TCCCTTGCTCAACAGCCTCTTGGTTCTTGAGCAATATGAAACCGGCACCTGGCTGTAC 141

QY      3663 CTGATTCATATGCTGTGAGAAATCGCGGCGCTGTCAATGTCAGCGGTTACGTGGGCT 3722
DB      142 AACATCCCGCGCCCTCCCGGATCAACGGTGTGCTGCGGCTGCATATCCTTGAAGCGAC 201

QY      3723 CTTCGACCGCTTGAACAGCAGACGAGACTCTTGAAGCAGATTGAAGCAGAGATGCT 3782
DB      202 CTTAATGCCATCATCGAGCGGCGATGAAGCGCTCATTTTCCGTGATTAAGAT 261

QY      3783 GTGGGTCTAACAATGTTTTCAGAGAAAGCTTTCTAGAGAGA-----TGAAGTCAAT 3833
DB      262 CTACCCGTCGAAGTATCATGCGGAGCGCGCGGTGTCATGACGCGCTGTAAACCTGGCG 321

QY      3834 GATCTGTGTGTTTCAAGCTTGAACCGCTTGAAGGTGTTGAACCAAGAAGACTACTCC 3893
DB      322 GCGCTCTTGAACGGAACCTCACTCTGCAACAGTTTCAATGATGATGAGGCGGCGACGCC 381

QY      3894 TTCATCTTCATCTGAAGCTGCGTGAAGCGACGCTCTTACAGACTGTTGAAGATGAC 3953
DB      382 TTGACCTGAAGCGACCACTGATCCGCGCCACAGCATGAACTCAAGGCGGATGAG 441
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QY      3954 CACATCTCACTATTGTGATGATCATCATCATCATGATGGTGGTCAATGATGTCTTG 4013
DB      442 CATGTCTGTGCTGACGACCTGATCATATGCTTGAAGATGGCTGTGATAGGTGTG 501

QY      4014 CGACGATCTCAATGACTCTTACTGAGTGGCTCAAGAGACTCAAAAGACCCGCTGCA 4073
DB      502 CTGAGCAACTGAGTGGCTCTTCAACGCGAGGTGAACGGCGTGAACGCTTCA 561

QY      4074 GCATCACTCTCTTCACTTATTCAGATGAGGACTTTTGCAAAATGAGCAAGAACCAATTC 4133
DB      562 GCGCTTGAATATCACTATGCGGATGAGGCTGAGGCAAGGAAATGCTGACAGAAAG 621

QY      4134 ATAGACGAGGAGAAAGCAACTCACTCACTGGAAGAAAGCACTCAAAAGACTCTTCCCA 4193
DB      622 GTGTCGAAACCAAGCTGATATATGGAAGATCAAGTCAAGAGATGGCCAAAGTCTT 681

QY      4194 AAGATCCGACCGACTTTGCGCGGCTGCACTTCTGTGGAAGCAGAGTTGGTACAT 4253
DB      682 GAATGCCGACCGACCGGCGGCGGCTGCAAGACTGATATGCGGTTAACCGGTTTAC 741

QY      4254 GTTACCATCGACGCGGAGCTTACCAATCCCTTGAAGCTTTGCAACGAAACAAACAG 4313
DB      742 TTCACTCTCCCGCGCAACTCGAGCGCAACTCCAGAACTCAAGCAACGCACTATGTG 801

QY      4314 ACCCTTTCGTCGTTCTTCTAGCTGCGTCCGTCGCGCTCATTTATGCTTCAAGCTGTT 4373
DB      802 AGCTGTTCACAGAGCTGATATGCTTCAATACGCTGCTGCTGCTTGAAGCAATCAG 861

QY      4374 GAAGACGCTGTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4433
DB      862 CCGATATCTGATATGCGGATATCGGCTGATGCGGCTGATGCGGCTGATGCGGCTG 921

QY      4434 ATGCGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4493
DB      922 ATGCGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 981

QY      4494 GGGACTTGTATCAACCAAGTCAAGGCTTACGAGCGACGACGATTCGAGAAACGAGATAT 4553
DB      982 GCGCTTATCTGCAACGAGACCAATCACTGCTGATGATGATGATGATGATGATGATGATG 1041

QY      4554 CCGTTTGAAGCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4613
DB      1042 CCGTTTGAAGCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1098

QY      4614 CTGCACTCACTATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4673
DB      1099 CTCTTCAAGTCTGTTTCTTCTTCAACAGAGACCTGCGGAGAGACTGACGCTCAGT 1158

QY      4674 GGTCTCGAGTCCG 4686
DB      1159 GGGACAAAGTCCG 1171

RESULT 10
US-10-282-122A-3365
; Sequence 31388, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
```

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31388
LENGTH: 9748
TYPE: DNA
ORGANISM: Pseudomonas putida
US-10-282-122A-31388

Query Match 1.1%; Score 127.8; DB 16; Length 9748;
Best Local Similarity 42.9%; Pred. No. 3.8e-28;

Matches 1166; Conservative 0; Mismatches 1512; Indels 41; Gaps 9;

3566 CATGCCAAGTCACTATAGGAGCCTGTTGACAGCTTTATTCACAGGCGCACTATG 3625
6685 CATCGCTGTGTGTCACGGGAGAGCCCTGCGCTGTGTATGCCAGCAACCTCATG 6744
3626 GTTCCTGATCAGTTGACGCTGTCGTCGTCATCTGATTCATATGCTGAGAAAT 3685
6745 GGTACTGTGCACTGAGCGCGCACAGCGCGCTTACAACTCGCTGCGCTTCACTT 6804
3686 GCGCGGCGCTGTCAATGTCAACGCGTTACGTCGCGCTCTTGCAAGCGTTGAACGCA 3745
6805 GCGCGGCGCGCTGTGATGTGGCGCTGACAGCAAGCGCTTCAAGCGCTTGAAGCGCA 6864
3746 CGAGACTCTTAAGACGACATTTGAAGACAGAGATGTGTGCTGTACAAATTGTTCA 3805
6865 CGAAGCGCTGCGCACCTTTCGTCAGGTGACAGCGGAGCGCGCAGGATTCACGC 6924
3806 GAAGCTTTCGAGAGATGAAGTCATTGATCTGTGTGTTCAACCTGACCGGTTGA 3865
6925 CCGCGAGCGGAGGTGATGCTGCGCAGCGGATGTGATCTGTGATTCAGAGC 6984
3866 GGTGTTGAACCAAGACAGACTACTCCCTTCAATCTCTCATCTGAAGCTGCGTGAAGC 3925
6985 CAGGTGAGACAGTGTGCGCGTGAACCTTTCAGCTGTGACAGCGCACTGATCGCGT 7044
3926 GAGCTCTTAAGACTGTGTGAAGTGAACACATCTCTCACTATTGTCAATGATCATAT 3985
7045 TGACCTTTTCGCTTGAAGCGCGCAGCGCATGTGCTGTGATGAACCTGACACATCAT 7104
3986 CTAGATGTGTGATGATTTGATCTTTCGAGCGGATCTCAATAGGCTTACAGCTGC 4045
7105 CACGATGTGTGATGATGTGAGGTGTGTGTGATCAAGAGTCTGTGCGCTGACAGGCTA 7164
4046 GCTCAAGACTCAAAAGACCGCTGTGACGACTCACTCTCTACTATTCAGTACAGCA 4105
7165 TCGTCAATGGGAGCGCTGTCAAGCTGCGCGCTGTGCGGTGCAATACCGCACTACGCGG 7224
4106 CTTTGCAAAATGGCAAGGACCAATTGATGAGCAGAGAGCACTCACTACGTA 4165

7225 TTGGCAGCGCAATGCTGAGGCGAGCGAGCAAGCGCGCACTGCTTACTGGAGC 7284
4166 GAAGCAACTCAAAAGACTTTCCACAGCAAAAGATCCGACCGCACTTTGCCCGCTCACT 4225
7285 AAGTGTGGGCGGTGAACAGCGCGGTGTGGAATTCGACCGCACTTACCGCGCGCGCA 7344
4226 TCTGTGAGAGCGCAGGTTCGTATCATGTTACATGACGAGGAGCTTACAGTCCCT 4285
7345 GCCAAGCGCGCTGCGCGCAGTGTGAGCCGTGCGTGAAGCGCGCGCTGTGAGGCACT 7404
4286 TCGAGCTTGTGAAGAAACAAACAGACCTTTCTGTCTCTTCTGCTGCTGCTGCG 4345
7405 CAGCGCGAGCGCGAGCGCGCGCTGACCTGTTTCAATGTTCTGTGCGCACTTCCA 7464
4346 TGCGCTCATTTATGCTCTCAAGCTGTGAGAGCGCTGTATGTTACCAATTCGAA 4405
7465 GACCTGCTTCACTGTTTACTGACTAGCGCGCAATCCGCTGCGCGCTGCGTGAAC 7524
4406 TCGCAACCGACTGAACCTGAGGATATCATGCGCTGCTTGTCAATPACGATGTATCG 4465
7525 TCGCAGCGCGCGGAAACCGAAGGCTGTGCGCTTCTGTCAATPACGAGGTGCAAA 7584
4466 AATCAATGATCATACGATACCTTTGAGACTTTGATACCAAGTCAAGCTACAG 4525
7585 GCGCGAGTTTCACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7644
4526 GACAGCAGACTTTCAGAACAGAGATATCCGTTTGAAGCGCGCTTATCAGCACTACAG 4585
7645 GCTGATATGCCAGCGCGCATACAGACCTGCGCTTGAACAGTGTGTGCGCGCTTGAAC 7704
4586 TGAATCCAGATCTGTCAAGCAACACCTCTGCAACAACTGATTTTGGAGTCACTACA 4645
7705 GGCAGCGATCTCAACCAAAACCGCTGTC---CAGGTATGTTCAACCAACAGCGCG 7761
4646 GAAGACCTTGAAGATTAAGTTTCAAGGCTGAGTCTGAGTCTGCTGCTGCTGCAAGC 4705
7762 GGCAGAGCGCGCGCGCGAGAGTGCAGGCGCTGCAAGATGAGCGCTGCACTGCGAGT 7821
4706 GTA---CACTGATTTGACATGAGATTCATCTGTTTCAAGAAACGACAGCTTAAAG 4762
7822 GCACAGACCGCAATTTGACCTGCGCTGATACCGCGAGCAGCTGAGCGCATGACGCG 7881
4763 TAGGCTCACTTTGCGGATGCTGTTCAAAATGAGACTGTTGAAATGCTGTCAGAT 4822
7882 AGCTTTTACCTTGCCACCCGACCTGATGACAGCCCGACAGCATGAGCAATGCGCGCA 7941
4823 ATTCTTGAATCTGAGAAACGCGCTTCAAAATTTGCGGACACAGTCTCAATACTTC 4882
7942 CTGCGCAATCTGCTCCAGGCGCATGCTGCGAGCGCAACAGGTGTGCGCACTGCC 8001
4883 TTGACTGATGAGATGTGACTCTTGAATAATGATGTTCTCAAGCTCAAAATGTCGA 4942
8002 GATGTGATGATCTGAGAGCAGTGCATGCTGATGATGATGAGACCGCAAGTGGC 8061
4943 CTATCCCGGAATTCAGCTTGTGATGCTTTCAGAACCAAGTCTTGTATCCCGCA 5002
8062 CTACCGGAGCGCGCTGCTGATCAATTTGTCAGAGATCAAGCCAGCGTATCCGCA 8121
5003 TAGTGTGCTGTGTGATCTCTCTGCGCATTTGACCTTACAGAGTGTGATGCGCAGTC 5062
8122 GCGCGCGCTGATATTTTCCCGATGCACTTTAGTATACCAAGTGTGATGCGTGC 8181
5063 TGATATTTCTGCTGATGAGCTTGTGTCAGCGGTCAATGCTGAGAGCGCTTGTGCACT 5122
8182 CAACCGCTGTGCAAACTGCTGATGAGAGGTGTGCGCGGAGTGTGATTTGGCT 8241
5123 ATTTGCGGAGCTCATGTGAGCAATGCTGCGCTTCTTGTGTGAGAGCGCACTT 5182
8242 GCGGATGAAAGAGCTGGAATGTGATGAGCTGATGCGCTGCTCAAGCGCGCGG 8301
5183 GCGCTATCTCTCTGCA--TGTACATGCGCTGCGGAGATTTCAAGATTAATCTTCT 5240
8302 CGCTTATGATCGCTGAGCCCGGATTAACCGAGCAGCGCTGCTTACATGATGAGGA 8361

QY 5241 GGAATTCTGGGCTTACATGTTTGTGATGGCCATGATACAGCGCTCCCGATATCGAG 5300
DB 8362 CAGCGGATCGGCTGCTGCTCAGCCAGCAAGCATTTGCGGAGCGCTCCGCGGCGG-- 8419
QY 5301 GTTACTAAGCTGAGTTTGTCTGATTCGGGATGCGCTGATATGACAAATGACAGATGCG 5360
DB 8420 -----GACGCGGTACCTATCTCTGCTGACCAAGACCGCGAGTGGCTGGCC 8467
QY 5361 TTGAAGTCAATGAGCAGCAGACGAAAGCCCTCAGCCAGAGTCTCGATACGTGCTG 5420
DB 8468 GGGTATGCGACACCGCCCTGAGGTGAGCTTCGCTCCCACTGGCTTATGATC 8527
QY 5421 TATACCTCAGATCACTGCGCAGCAAAAGGCGTCATGATGACACCGTCTCATATT 5480
DB 8528 TACACCTCGGTTCCACAGGCGCGCCCAAGGCGCGGCAACCCACGAGGCGCTCT- 8586
QY 5481 CGAAGCTCAGAGTGGCTGTATACCACTATCTTGGAAAC-----GAGATGGCTC 5535
DB 8587 -CAACGCGCTGAGTGTGATGCAAGGCGCTATGCGCTGATGCGACGACGAGTGGCTGC 8645
QY 5536 ACATGGCAGCATGCGTTTGAAGGCGATCGTACGAGATCTACAGCGCCCTTTTGTTCG 5595
DB 8646 AGAAACCCCTTACGTTGATGTGCTGATGCTGCTGAGGATCTTCTGCGCTGATGACCG 8705
QY 5596 GAAAGCACTTGTGCTGCTGATGATCAATGACAAACCTCGACGCTAGACACTCAAGATG 5655
DB 8706 GCGCGGCGCTGCGCGGCTGCGCTGCGCGGATACCGCGACCGCGCGCTGTGCCAGA 8765
QY 5656 TGTGTTTCCGAGCATGTCACGCGGCAAGTCACTGACAGCTCTTTCAGATGATAC 5715
DB 8766 CCATCATCGACCAACAGTGAAGCAGCCTGACCTTCCGCTGATGCTCAGGCTTCA 8825
QY 5716 CTCTCGAGTCCGAGAAAGCTCTCGAAGCTTGAATGTTCTTCTTGTGTGTGACAG 5775
DB 8826 TGCCACGCGCGAGTTCAGACAGTCCGACGCTTCCGCGCGGTGTGCAATGCGGAG 8885
QY 5776 ATTCGACGCGCCAGATGCTCTGATGCGAGGACTTTCAGAGGGGTCAAGTATACA 5835
DB 8886 CGCTGCGCGCGCTGATGCTGCGCAACAGTCCGCGAGCGCTGCTCAAGCGGGTGTACA 8945
QY 5836 ATGTTACGCGCCCAAGAGATGAGTCAATGATACATTCATTCATTCATTCATTCAT 5895
DB 8946 ACCTGACGCGCCGACGAGCGCGCATCGACGATCCCACTGAGCTGCGGCGACAGC 9005
QY 5896 AGTCTTTCATCATGAGTCCCAATGAGAGCTGGAACCACTCAGAGCGGATGCG 5955
DB 9006 AGGAGCTTCA-----GCGTCCGATCGGCAACCGATCGAACCTGCGACCCCAATCC 9059
QY 5956 TGGATCCTGAGCAACAGCTTGTGAGCATTTGATGAGGAGCTTGTGTCACTGGCG 6015
DB 9060 TCGAACCCGACCTGCTGCGCGCTGCGCGCGCGCTCAATGGAGAGCTTACTGCGCGCA 9119
QY 6016 ATGATCTTGGCGCGGCT--ACAGTGAACAAAGCCCTTGAAGAACCGTTTGTGACA 6072
DB 9120 TTGGCGCTGCGCGGCTTACAGGCTGCGCGGAGCTGAGCGGCTTGTGTGCGCG 9179
QY 6073 TTAATCTCATGACCAAGAGTGAAGCGCTATGCGACCTGCGATGAGTGGCGGTACA 6132
DB 9180 ATTCGTTGAGAGCAGGCGGCTGCTGTATACCGCATGCGACCTGCGCGCTGATG-- 9237
QY 6133 TTGAGAGTGGCTCATGAGTCTTGGAGGTATGACACCGCATTCAGATTCGTTGCGCA 6192
DB 9238 -CCCGAGCGGTGATGATGATTAAGCGCGGCGGTATGACACAGGTAAATTTGCGCGCC 9286
QY 6193 ATGATTCAGATGAGTGAAGTGAAGCGGCTTCTGCGCGATCTCTCGCTCGAGATG 6252
DB 9297 TGGGTATCGAGTGGGTGAAGTGAAGCAGACGAGTGGCGGACGCCCAAGTGGCGAGG 9356
QY 6253 CTGCTGTGCTTTCAGCA 6271
DB 9357 CAGTGTGCTGCGCCAGGA 9375

RESULT 11
US-10-156-761-3185
; Sequence 3185, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3185
; LENGTH: 3789
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3789)
US-10-156-761-3185

Query Match 1.1%; Score 119.6; DB 15; Length 3789;
Best Local Similarity 45.7%; Pred. No. 8,2e-26;
Matches 619; Conservative 0; Mismatches 714; Indels 21; Gaps 5;

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DB 800 GGTGCGCGCGGCGGAGAACCGGTGCGCTGCTGCGGCGCGGAGCCACCTGCTGCTGCG 859
QY 5155 CGTCTTGTGATGTTGAGAGCGCAACTGAGCTTATCTTCTCTGATGATGATGCGCTT 5214
DB 860 CCGCGCTCGGCTGCTTCAAGCGCGGCGGCTTATCTGACCTGCGGCTGACCCGACTACCCG 919
QY 5215 CGCGAGAGTTCAAGATATATCTTCTGACTTCTGAGGCTTACCATTTGTTGATTTGCC 5274
DB 920 CCGACCGGATGGGTATCTCTGCGGACAGCGGTGCGCGGCTGCTGACCTGACGCG 979
QY 5275 ATGATACAGCGCTCCGATATG-----AGGTACTAAAGTGAAGTTGTTGTA 5325
DB 980 ACCTGCGCGGCGCACTCAAGCGGTCCAGACCGGTGCGGAGATGACCTCAGCGTCTCG 1039
QY 5326 TCGCGAGTGGCTGATGATGACGACGATGAGTGGCTTGAAGTCAATGAGCAAGACGCA 5385
DB 1040 CCTTCGACACTTGGAGTGGCGACGAGCCCGCGGACGCCCGGTGCGCGCGGAGCGCC 1099
QY 5386 CAAGCGCTCAGCGACGAGTCTGCAATAGTGTGATATCTGAGATTCAGTGGCGGAC 5445
DB 1100 GCGCGGAGCGCGGCTGAGCGGCTTACTGATGACCTTCCGATGACCGGCGGAGC 1159
QY 5446 CAAGGCGCTCATGATGAGCAACGATCTATTAATTCGACAGTCAAGTGGCTGATATAC 5505

Db 1160 CCAAGGCGCTGCTGCTCCCGCATCGGGCATCAGCGCTGCTGACGGGAGTGGCTATG 1219
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Db 1220 TAGCGCTGAGACCGACAGCAGATGCGAGGTGGGACAGACCGGTTTGAGCGCTCCG 1279
Qy 5566 CGTACGAGATCTACAGGCGCTTTTGTTCGGAAGAACATTTGTTGGCTTGAATCAATGA 5625
Db 1280 TGTGGAGATGTGGGGCGCTGCTCGGCGCGCGCACCTGTGCATCTTGAACGCGAGA 1339
Qy 5626 CAACCCCTGACGCTAGAGACACTCAAGATGTGTTTTCCGAGACATGTCAACCGGCAA 5685
Db 1340 CCTGCTGACACGAGAACTCGGCGGCGCTGCGGAAACGACATCAACCGC-C 1398
Qy 5686 GTATGTCACCACTCTTCTCAAGATGTAACCTTCGAGTCCGAGAAGCTTCGAGAA 5745
Db 1399 CTGTTCACCTCGGCGCTGTTGACCGGCTGCGCGAGGAGC--GTACCTGTGTCGTC 1456
Qy 5746 CTTGATGTTCTTCTTCTTGTGTGTAACATTTGACGGCCCGCAGATGCTTCGATCGC 5805
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Qy 6226 TTCTGCGGACTCCTCCGTCGAGATGCTGCTG 6259
Db 1928 TGTCCGCGCTGCCGCGGCTGGGCGCGCGCGCT 1961

RESULT 12

US-10-329-079-46

; Sequence 46; Application US/10329079

; Publication No. US20030198981A1

; GENERAL INFORMATION:

; APPLICANT: FARNET, Chris

; APPLICANT: ZAZOPOULOS, Emmanuel

; APPLICANT: STAFEA, Alfredo

; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES

; FILE REFERENCE: 3002-11US

; CURRENT APPLICATION NUMBER: US/10/329, 079

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 46

; LENGTH: 15738

; TYPE: DNA

; ORGANISM: Streptomyces refuineus

US-10-329-079-46

Query Match

1.0%; Score 115.2; DB 15; Length 15738;

Best Local Similarity 45.8%; Pred. No. 6.5e-24;

Matches 451; Conservative 0; Mismatches 518; Indels 15; Gaps 1;

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Db 92 TGGGATGATCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 151
Qy 3739 AGCGACACGAGACTTTTGAACACATTTGAAGACAGATGATGATGATGATGATGATG 3798
Db 152 GGGCGCACGAGACGCTCCGACGATGCTTCCGACGCGCGGACGCGGCGCGGACGAG 211
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Db 212 TCTGCG 271
Qy 3859 CGTTTGAAGTTTGAACCAAGAACAGACTCTCCCTTCAATCTCTCATGAGAGTGGCT 3918
Db 272 TCCCGCGCTCTTGGCCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 331
Qy 3919 GAGAGCGAGCTTTTACAGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 3978
Db 332 TGAAGGCGGCGCTCTGCGCTGCGGAGACGAGACGAGCTGCTGCTGATGATGATG 391
Qy 3979 ACATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4038
Db 392 ACATGCGACGAGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 451
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Db 452 CCGCGCGAGCGAGGCG 511
Qy 4099 ACAAGCACTTTGCAAAATGCGAGAGACCAATTTACAGAGAGAGAGAGAGAGAG 4158
Db 512 ACAACCTGTGAGCGGAGAGCTGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAGAG 571
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Db 572 GCCAGACGCGGTCTGGAAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
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Db 632 TCAACG 691
Qy 4264 ACGGCGAGCTCTTCAAGTCCCTTTCAGGCTTTCAGACCAAGACCAACAGACCTTTTCG 4323
Db 692 CGCGCGGAGACCAAGAGCGGATGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 751
Qy 4324 TCGTTCTTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4383
Db 752 TGTGTGTGAGCGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
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Qy 4444 TTGTCAATAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4503
Db 872 TGTGTAACACCTG 931
Qy 4504 TCAACCAAGTCAAGGCTTACAGACAGACAGACATTTGAGAAAGAGATTTCCGTTGAGC 4563
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Qy 4564 GCGTTGATGAGACTTACAGCTG 4587
Db 992 GCGTGTGAGAGACTTCCCGCG 1015

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 10:54:02 ; Search time 780 Seconds
(Without alignments)
10217.135 Million cell updates/sec

Title: US-09-482-788-1

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1306.8 | 11.7 | 46899 | 1 US-08-471-119A-1 | Sequence 1, Appl1 |
| 2 | 408.2 | 3.6 | 1713 | 1 US-08-471-119A-4 | Sequence 4, Appl1 |
| 3 | 136.6 | 1.2 | 7527 | 4 US-09-252-991A-71 | Sequence 71, Appl1 |
| 4 | 136.4 | 1.2 | 6573 | 4 US-09-252-991A-9183 | Sequence 9183, Ap |
| 5 | 104 | 0.9 | 77536 | 4 US-09-410-551B-1 | Sequence 1, Appl1 |
| 6 | 104 | 0.9 | 77536 | 4 US-09-940-316B-1 | Sequence 1, Appl1 |
| 7 | 103.8 | 0.9 | 10023 | 4 US-09-252-991A-8892 | Sequence 8892, Ap |
| 8 | 97.8 | 0.9 | 3315 | 4 US-09-252-991A-8892 | Sequence 8892, Ap |
| 9 | 97.8 | 0.9 | 7911 | 4 US-09-252-991A-9182 | Sequence 9182, Ap |
| 10 | 95.4 | 0.9 | 7374 | 4 US-09-252-991A-9100 | Sequence 9100, Ap |
| 11 | 94 | 0.8 | 4242 | 4 US-09-252-991A-7056 | Sequence 7056, Ap |
| 12 | 82.8 | 0.7 | 4236 | 4 US-09-252-991A-7057 | Sequence 7057, Ap |
| 13 | 80.2 | 0.7 | 792 | 4 US-09-252-991A-9098 | Sequence 9098, Ap |
| 14 | 79.4 | 0.7 | 2219 | 3 US-08-510-646B-17 | Sequence 17, Appl1 |
| 15 | 79.4 | 0.7 | 1172 | 3 US-08-861-774E-17 | Sequence 17, Appl1 |
| 16 | 67 | 0.6 | 532 | 4 US-09-252-991A-8884 | Sequence 8884, Ap |
| 17 | 67 | 0.6 | 532 | 4 US-09-252-991A-8886 | Sequence 8886, Ap |
| 18 | 67 | 0.6 | 1239 | 4 US-09-252-991A-8991 | Sequence 8991, Ap |
| 19 | 65.2 | 0.6 | 1494 | 4 US-09-252-991A-8992 | Sequence 8992, Ap |
| 20 | 65.2 | 0.6 | 1260 | 3 US-08-861-774E-85 | Sequence 85, Appl1 |
| 21 | 62.8 | 0.6 | 178 | 1 US-08-471-119A-3 | Sequence 3, Appl1 |
| 22 | 62.8 | 0.6 | 993 | 4 US-09-252-991A-9093 | Sequence 9093, Ap |
| 23 | 61.6 | 0.5 | 648 | 4 US-09-252-991A-9095 | Sequence 9095, Ap |
| 24 | 61.6 | 0.5 | 759 | 4 US-09-252-991A-8775 | Sequence 8775, Ap |
| 25 | 61.4 | 0.5 | 1222 | 3 US-08-861-774E-83 | Sequence 83, Appl1 |
| 26 | 61 | 0.5 | 1368 | 4 US-09-252-991A-64 | Sequence 64, Appl1 |
| 27 | 61 | 0.5 | 4403765 | 3 US-09-103-840A-2 | Sequence 2, Appl1 |

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| C | 28 | 61 | 0.5 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appl1 |
| | 29 | 60.4 | 0.5 | 474 | 2 | US-08-403-852D-14 | Sequence 14, Appl1 |
| | 30 | 60.4 | 0.5 | 474 | 3 | US-08-510-646B-14 | Sequence 14, Appl1 |
| | 31 | 60.4 | 0.5 | 474 | 3 | US-09-231-818B-14 | Sequence 14, Appl1 |
| | 32 | 60.4 | 0.5 | 474 | 4 | US-09-635-359B-14 | Sequence 14, Appl1 |
| | 33 | 60.2 | 0.5 | 810 | 4 | US-09-252-991A-8770 | Sequence 8770, Ap |
| | 34 | 60.2 | 0.5 | 951 | 4 | US-09-252-991A-8774 | Sequence 8774, Ap |
| | 35 | 60.2 | 0.5 | 1857 | 4 | US-09-252-991A-8888 | Sequence 8888, Ap |
| | 36 | 60.2 | 0.5 | 2025 | 4 | US-09-252-991A-8891 | Sequence 8891, Ap |
| | 37 | 59.6 | 0.5 | 1171 | 3 | US-08-861-774E-81 | Sequence 81, Appl1 |
| | 38 | 58.6 | 0.5 | 378 | 4 | US-09-252-991A-8993 | Sequence 8993, Ap |
| | 39 | 57.6 | 0.5 | 741 | 4 | US-09-252-991A-7023 | Sequence 7023, Ap |
| | 40 | 57.2 | 0.5 | 741 | 4 | US-09-252-991A-27 | Sequence 27, Appl1 |
| | 41 | 57.2 | 0.5 | 1204 | 3 | US-08-861-774E-87 | Sequence 87, Appl1 |
| | 42 | 56.8 | 0.5 | 1122 | 4 | US-09-252-991A-1175 | Sequence 1175, Ap |
| | 43 | 56.8 | 0.5 | 2484 | 4 | US-09-252-991A-1388 | Sequence 1388, Ap |
| | 44 | 56.8 | 0.5 | 6858 | 4 | US-09-252-991A-1219 | Sequence 1219, Ap |
| | 45 | 56.6 | 0.5 | 681 | 4 | US-09-252-991A-8887 | Sequence 8887, Ap |

ALIGNMENTS

RESULT 1
US-08-471-119A-1
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Letener, Ernest
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoergerdorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoft, Welynn
; REGISTRATION NUMBER: 26,369
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Toxoplasma murium
; STRAIN: ATCC 34921
; US-08-471-119A-1
Query Match 11.7%; Score 1306.8; DB 1; Length 46899;
Best Local Similarity 58.4%; Pred. No. 0;

Matches 2680; Conservative 0; Mismatches 1822; Indels 90; Gaps 19;

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Db 25464 GCGTTGTGACCGGCAAGGCGTTCGCGACGCTTTCGAGACACGATGGGTTGT 25523
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QY 3903 TCACTGAAGCTGCTGGAAGCAGCGCTTTACGACTTGGTGAATGACACATCTTC 3962
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Db 25704 TCTATGCTTATGCAACCAATTTCTGATGCTGACGCTGTTGATGCTACAGCAAGAA 25763
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QY 4677 CTCGAGTCCGTACCTGTGCTTACAAAGCTTACACTGATTTGACATGAGAGTTCATCTG 4736
Db 26421 ATGACGACCAAGCTCTGGAAGCGCGCTGTGACAGAGCTGACCTTGAAGTTCACCTC 26480
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5994 GAGAGCTGTGTGACTGTGAGTGTCTTGCGGGGCTACAGTGAACAAAGCCCTTGAC 6053
27729 GAGAAATTTGCTTACCGGTGATGTGCTTGCCTGTGCTATACAGCTCAGCCCTGAC 27788
6054 GAGAACCGTTTGTGCACTTACTGTGCA--TGACGAGACAGTGAAGGCGTATCGACT 6110
27789 GAGAGCGGTTTGTGCTGATCAGATCGATGTGAGGAAATATCAAGGCTATCCGAAC 27848
6111 GCGGATGAGTGGGTGACAGATTTGAGATGAGCTTATCGAGTCTTGTGACATGAGAC 6170
27849 GGTGATGAGTCCGCTACCGGCCCAAGACTTTGAGATTTGAAATCTTCCGCGATGAT 27908
6171 ACCAGTTCAAGATTTGTGGCAATGTATGCAATCAGTGTGATGTAAGCGGCTCTG 6230
27909 CAACAGGTGAGATTTGAGTCAACGCTGTGCTGTGCTGCTGAAAGCAAGAAATCAAGAAC 27968
6231 CGGACTCTCCGTCGAGATGTGCTGTGCTGCTTCAAGCAATGAGATCAAGCGCT 6290
27969 GGCACAGCTTGTGTGATGATGAGTGTGCTGTGCTGCTGCTGAAAGCAAGAAATCAAGAAC 28028
6291 GAGATCTTGGGCTTGTGTGTGCTGATCATGATATTTGAGATGACAGGCAATCT 6350
28029 GAGATGATCTTCTTATCACCAGCCAGGAAAGACGAGCT--ATCGAGCAGCATGATGCA 28085
6351 GCCAATCAAGTCGAAGATGCGAAGACCAATTTGAGAGTGGCATGTATTCGACATGGC 6410
28086 AACAGCAGGTCCAGGCTGGGAGAGCATTTGACGTAACAGAGTATGCTGATATCAG 28145
6411 GAAATTCACCGCTGACGATTTGTGAGCACTTCAAGGCTTGGACATCATATGATGGA 6470
28146 GATCTGACACTTCTTACCTTTGTGACAGACTTTTGGGATGGAATGATATGAGGGA 28205
6471 AGTCAATTCGATCTGATGATGACAGAGTGTGCTTGTGATGATACCCGCACTCAT 6530
28206 GTTGACATTTCTGTCAACGAGATGAAAGAGTGGCTTGTGAAATCTACGCGCTCTCTTA 28265
6531 GACAATGCTCTGAGCAATGCTTGAATTTGAAACAGGTAGCGGATGATCTCTTC 6590
28266 GACAAACGCGCACTGTGATATCTGAGATGAGAGCGGAACTGGCATATTTCTATCT 28325
6591 AACCTTGACA-----CAGGCTTGAAGTTCAGTGTGCTTGAACATTCAGATGACA 6644
28326 AACCTGGGCAAAAGTCAACGAGCTTACAGAGATATGCTGTGACCCGCGCTCCTGAGCC 28385
6645 GCTGCAATTTGTCAACAAAGCTACGAGTCTATACATCGCTTGTGAGAAACCGAGTT 6704
28386 GCAATCTTGTCAACGAAAGCGGTCTGCTGCAAGTCTAGCGCGGTAAGCCCGGTA 28445
6705 CAGGTTGAACAGCTACGATATTTGTGCAAGTCC-----ATGACTTACACCTTGACTC 6758

28446 CTGTGGAACGCGCTGATATCGGTTCTGTGACAAAGATGATGATCAACCTGAGCTT 28505
6759 GTGTTCTCAACTCAGTATTCAGTATTTCCGCTTCCGAGATACCTTGACAGAAATGCA 6818
28506 GTGTTATCAACTCCGAGCCAGTACTTCCCAATCAAGATGATGATCAAGTGTGTC 28565
6819 GACACCTTGAATTCAGCTCAACGTCAGCGAGATTTCTTGGGAGTGTCCGATCCGAG 6878
28566 AAGCTTGTGAAAGTCCAGGCTCAGAGCTCAGAGTGTCTTGTGGGATATCAGATCCAG 28625
6879 GCCACCAAGCACTTCTTGTGCGAGGCTATCCACACACTGGGAAAGATGACAAG 6938
28626 GCCCTTAAAGGAGCTTCTTGTGAGCTGTGCGGTTGTGCGTGTGAGCAATGTAGC 28685
6939 AAGGACATGTTGACACAGAAATGCGAATTTGAGAGACATGAGAGAGAGTCTGTT 6998
28686 AAGAGCAGATCCGGGAAAGATCGCAGAGCTCGAAGAGCGAAGAACTTCTGCTG 28745
6999 GAACCTGCTTCTTCACTCGTTGAAGAGAGGTTTCAGGCTGTGGAACATGTTAG 7058
28746 GACCAAGCTTCTTCTGAGCTTGAAGCAGCTGCTCCAAATCAAG---CAGTTGAG 28802
7059 ATCTGCAAAAGACATGAGAGCTGTGATGAGCTCAGTGTGATGATGCTGTT 7118
28803 GTCTGCAAGAGTATGAGAGGCGCACCAAGAGTGTGCTGTGATGATGCTGCGTT 28862
7119 GTGCACTTGGGCTTACTTGTGAGATGAGCTGTGCTCGG---TTGAAAGATGAC 7175
28863 CTACACATCAGCCCAACGAAGAGAGCAGCTGTCTATACAGATATGATCCACAGCA 28922
7176 TGATGACTTTTCAAGGAATCAATGAAACGAAGTCACTGGGTGACTTCT---CAAG 7232
28923 TGGTTGACTTGTGAGAGAGCAAGAAAGATCTCAGCTGTGAGAACTTTCTAACAA 28982
7233 TCTTCAAGTCTGTATCATGAGCAGTCAAGAAATTCCTTTCGAATCAGCGCTTGA 7292
28983 GAGAGATATGATGATGATGAGTGGGTGCGGAAATCCCGTATCAGCAAGACATGTGAG 29042
7293 AGACA-----GTCGTGCTTCTCTCAATAGCAATCATGATGAGTGCAG 7337
29043 GACACATTTATGAACTCTTGTGACCAAGATCATCTCACTCATGACGGGACATCTGTG 29102
7338 CTATCAACATTTGGTCCAGGCGGAGGAGCTCATCACTATCGTTCGCAATCTT 7397
29103 ATCTCAAGTGTGATGAGCGGCTGCAATGTGACTTGTGACGACACCGGCTTACG 29162
7398 CGCATGCTGGGGAAGCCGGGTTCCGTGTGAGGTCACTTGTGACGACAGTGTCTGAG 7457
29163 CAGTTGGCCAAAGAGAGGAGATTCGGGTTAGATGAGTGGGCGGACAGAGATCTCAA 29222
7458 AATGTCATTTGAGCGCTGTTTTCATCAT-----TGTGCTCCCAAGG 7502
29223 AACGGCCCTCGATGTCGCTTTCACCGCTTTCGCAACGATGCAAAATGCGAGCGAGT 29282
7503 CGTACTGTGCACTTTCCTACGAGCAATCACTTGAAGGCTGATCTCTGACCAAT 7562
29283 CGTGTCTGTGACCTTCCCTTACCGACATCAAGGTGACAACTTGCACCTTACGAAAC 29342
7563 GCAACCTTTCAGCACTGCAAAACCGTCTGATTCGCAATGCAAGTCCGAGAGGCTTGG 7622
29343 CGGCACTTCAGAGAGTCAAGAGCGGCGGTATGAGTCAAGATCTTGTGAGGCACTGAG 29402
7623 TCTTACTTCCATGATCATGATCCATCGAATCGTGTGCTTGTGACAGATGCTCTC 7682
29403 ACAGCACTGCGGCTTCAATGATCCATTCGGCTTATGCTGCTCCGCAATGCGAGC 29462
7683 AAGCCCAATGTTAAGTTGACCGGAGAACTCTCTGCGAGGCAAGGTTGTACCGAG 7742
29463 AACCCCAAGCAAGTGAAGGAAACGCTCTGCGCGCGAGGTTGTGCGAG 29522
7743 CAGGACAGAGCGCGTTTACGACATTTCCCATGAGTGAAGTCAATCTTGTGC 7802

Db 29523 AGAAG--GCACTGTCAGCGCGCTTCCGCTCTGTAATGACACCGAGATAGTTCTTTC 29579
Qy 7803 GAAGAACCACTAGAGTGTGGCATGAGTTAGACATTAACCATCACTTCTTCAATCTC 7862
Db 29580 GAGGAATACCAATATCTTGAAGAACTGAAGTTGGCATCAAGCAACTTCTTGAATG 29639
Qy 7863 GGTGGACACTCTCTCTTGGCCAGAGCTCAATTTCTGTATGCAACGATCAAGATC 7922
Db 29640 GGGGGGCAATTCATCATGAGCTACGAAAGCTCGACCCGACCTAAGCCGGGCACTGATACC 29699
Qy 7923 CGATACCTGTCAGAGATGCTTGAACATCCTGATTTGGGATCTAGCATCTGTATC 7982
Db 29700 CGGGTTCAGGTCAAGAGGAGTGTGATTAACCCGCTCTGCTGACTGCTGCTTGCATC 29759
Qy 7983 CGTCAAGGCTGGGTTTGAACAACCCGTTTC 8014
Db 29760 GAACAGGCTCGACACCTCATCTGCTTATTC 29791

RESULT 2
US-08-471-119A-4
; Sequence 4, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Lettner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoerendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaesenoef, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Necosmospora vasinfecta
; US-08-471-119A-4

Query Match 3.6%; Score 408.2; DB 1; Length 1713;
Best Local Similarity 57.3%; Pred. No. 4e-115;
Matches 950; Conservative 0; Mismatches 638; Indels 69; Gaps 9;

Qy 6403 ACATGGCGAAATGACCCGTCGACGATGGTGTAGCGACTTCAAGGTTGACATCAATGT 6462
Db 1 ACATGGCGGATTTGATTCGCGATGCCCTCGGACGAGACTTCTTATCTTGACATCATGT 60

Qy 6463 ATATGAGAACTCAATTCGACTTCGATGATGACGAGTGGCTTGTGAGACTACCCGA 6522
Db 61 ACAGCGGCTCATGATATCCCCGGGAGAGATGACGAAATGGCTCAGGCACTATGACT 120
Qy 6523 CACTTCATGACATCGCTCTCTAGGCAATGTCTTGAATTTGGAACAGATAGGCGATGA 6582
Db 121 CACTTCCTGCAACACAGCCACCCGGAAAGATGTCTGAGATCGGAACCTGTACCGGTATGG 180
Qy 6583 TCCCTTCAACTTGAACA-----GCAGGTTGAGAGTTAGTGTGTGCTTGAACATCCA 6636
Db 181 TGCCTTCAATCTCTGGGAGGTTGAGGAGCTACAGACTATGCCGCTTGAACCTCGC 240
Qy 6637 GATCAGCAGCTGATTTGTCAACAAAGCTACCGAGTATATACATGCTTGTGGAAG 6696
Db 241 GCTCCGCTGCTGCTGGGTTTACAAAGCAATCAAACTTTCCCAAGCTGGCAGAAAGC 300
Qy 6697 CCAAGCTTCAGTTTGAACAGCTACAGATTTGCTCAAGTCATGATTTACCCCTGACC 6756
Db 301 CCGAGTCCAGTTGGAACCGCGAGAGTGTCACTCATTAATGACTGCTGCGATC 360
Qy 6757 TCGTGTCTCAACTAGTCAATTCAGTATTTCCGCTTCGAGTACCTTGCAAAATCG 6816
Db 361 TCGTTGTGATCAACTCGGTGCCCAATATCTTCCAACTGAGATATCTGCTGAGCTGA 420
Qy 6817 CAGACACTTGAATTCATCTGCTTAACGCTGACGCGAATTTCTTGGCGATGCCATGCG 6876
Db 421 CGGCAACTTGAATTCGACTGCCGCGGTCAAGCGTATTTCTTGGCGCATGAGAACT 480
Qy 6877 AGGCCAACACGAGCACTTCTGCTGCCAGGCTATCCACACTGCGGGAATAATGCA 6936
Db 481 ATGCAACCAATTAAGACTTTCTGTGACAGACAGTCCATTAAGGTTCAATGAT 540
Qy 6937 CGAAGACGATGTTGACAGAAATGAGCAGAAATTTGAGACATGAGAGAGATGCTTGC 6996
Db 541 CTAAAGCCATGTTCTGACACACAGTGGCCAACTTGAAGATGACAGGAAGATGCTTG 600
Qy 6997 TTGAACCTGCTTCTTCACTCTGTTGAAGACAGTTTCCAGGCTGTGTTGAAATGTTG 7056
Db 601 TTGACCTGCTTCTTCACTGCTGAGCTGAGCAGACTGCTTCCAGAAATCAACACGCTG 660
Qy 7057 AGATCTGCGCAAGAAACATGGAAGCTGTGAATGAGCTCACTGCTATGATGCTGCTG 7116
Db 661 AGATCTGCGCAAGAAAGAGATGCGCGACCAACAACTCACTTACCGAATGCTGCTG 720
Qy 7117 TTGACAGTTCGGGG-----TTCACTTGAAGATGAGCTTGTCTTCCGTTG 7164
Db 721 TTATTCATGTGGAGGCGACAGATGCCGAATGGGAGATGAGATTAACATAGGCTG 780
Qy 7165 AGAAGAT-----GACTGATGCACTTTCAAGCAATCAATTGAACCAAGAT 7212
Db 781 TCAAGATATGATTCGAAAGGCTGGGTGACTTCCGCGGACAGAGATGAGACGCTGAG 840
Qy 7213 CACTGGGTACCTTTCATGCTTCA-----GATGTGCTATCATGCGCAGCAAAA 7266
Db 841 CTCTCTTGGAGCTCTTCAGAGCCGCCAACGTGCAATGAGCTGTGCTCGCTGATACA 900
Qy 7267 TTCCTTGAATTCAGCGCTTGAAGACAGGTGCTGCTTCCCTCAATAGCAACATCG 7326
Db 901 TCCCATACAGCAAGACATATGAGAGGCCATCTGTCTGACTCATTTGAAGATGACGAG 960
Qy 7327 ATG-----AGTGAGCTATTCACATTCGTTCCAGCGCGAGG 7365
Db 961 ACAGCACTTCAGATGACAGCAAGCAAGCCCTGATATGCGCACTCAATACAGGCGAAG 1020
Qy 7366 GCGACTCATCATCTGCTTCCGACATCTTTGCACTGCTGGGGAAGCCGGTTCGCTG 7425
Db 1021 AATGCCCTGCTCTCTAGTGGCGACCTGATTAAGATTTGATTAAGGAGATGAGCTTCCAG 1080
Qy 7426 TCGAGGTCACTTTCAGACGACAGTGTCTCAGAAATGATGATGACGCTGTTTCCATC 7485
Db 1081 TTGAGACCACTGGGCTCGACAAACATCCAGCGCGGAGCTCGATGCTGTTTCCACC 1140

| | | | |
|----|------|---|------|
| Qy | 4857 | TCGGGGAACACAGTCTCAATACCTTCCTTGACTGATGGCAATTGGACTCTTGA | 4916 |
| Db | 6373 | CCGACGACCGAGCTGACCTCGCTGCCATGCTCGATGCCAGAGACCTGGCACTTGCTG | 6432 |
| Qy | 4917 | GATGTTCTCAACGTCCAAACATGTCAGCTATCCCGAGATCCGAGATCGACTTGATGTCCTC | 4976 |
| Db | 6433 | GAAAGCTTGAAACGCCACATGCTGACAGTACCCTGCGCAACCGCGCGTGCACACGGTTGTC | 6492 |
| Qy | 4977 | CAGACCCCAAGTCTCTGCTTACCCCGATATGTTGGCTGTGGTGAACCTCTCGTCCGATTG | 5036 |
| Db | 6493 | GAGAGGCGGTGTGAGCGCAGCCCGACCGCGCGCGCTGCGCTTCGCGAGAGACGCGCTG | 6552 |
| Qy | 5037 | ACCTAACCCGAGTTGATGCGCAGCTGATATATTCCTCGCTGGATGGCTTCCTGCACGGCTCA | 5096 |
| Db | 6553 | GACCTAACCGAGCTTGAAACCGCCCGGCGCAACCGCTGCGCGCATGCCCTGATTCAGACCGGG | 6612 |
| Qy | 5097 | ATGCCCTGCAGAGACGCTTGTGCGAGTATTTGCCCAACGGTCATGTGAGACAATTTGTCGGC | 5156 |
| Db | 6613 | GTCGGTGGGGAACCGCTGTGTGGGCGTGGCCATGAGACGCTCATTCAGAGATGTGTGTGGCC | 6672 |
| Qy | 5157 | TTCTTTGGTGTGTGAAGCGCAACTGGCCTATCTTCTCTCGATGTACATTCGACCTTCG | 5216 |
| Db | 6673 | CTGATGGGATTCCTCAAGCGCGGCGCGCCTACGNGCGGTGGACCCGAGATATCCGAG | 6732 |
| Qy | 5217 | GCGAG 5221 | |
| Db | 6733 | GAGCG 6737 | |

RESULT 4
US-09-252-991A-9183
; Sequence 9183, Application US/09252991A

```

? APPLICANT: Marc J. Rubenfield et al.
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
? TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 107196.136
? CURRENT APPLICATION NUMBER: US/09/252,991A
? CURRENT FILING DATE: 1999-02-18
? PRIOR APPLICATION NUMBER: US 60/074,788
? PRIOR FILING DATE: 1998-02-18
? PRIOR APPLICATION NUMBER: US 60/094,190
? PRIOR FILING DATE: 1998-07-27
? NUMBER OF SEQ ID NOS: 33142
? SEQ ID NO 9183
? LENGTH: 6573
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (5574)
? OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-9183

```

| | | | | |
|----------------------------|--------|--------------------|------------|--------------|
| Query Match | 1.2%; | Score 136.4; | DB 4; | Length 6573; |
| Best Local Similarity | 43.6%; | Pred. No. 2.2e-30; | | |
| Matches 1271; Conservative | 0; | Mismatches 1552; | Indels 50; | Gaps 13; |

| | | | |
|----|------|--|------|
| OY | 3392 | GATCAATGTTGGGGAACTTTTGTGAACCTGGAGAAAATTATACATGCTATCAAGT | 3455 |
| Db | 3129 | GATCGGCCTTACCGAACAATTCTTGAAATTTGGGCGACACTGCTGTGGCCACCGCCT | 3186 |
| OY | 3452 | GGT---GAACATGCGAGAGTCGGTGTATGAGCACTCAAGGCTCTTAACATCTACAGA | 3508 |
| Db | 3189 | GGTCTCGGGGATTCGCCAAGATCTCGGTAATGCAAGTCAAGCTTGAAGACCTTTTGAGCA | 3248 |
| OY | 3509 | CCCGACGCTTGGGGGAATTTCCGCGGATCGTCAAGGATGATCTCTGTCTTACACTTGAT | 3566 |
| Db | 3249 | GCCGGTCTCTGACAGGATTCGTGGAAGCCTGGGCGAGAACCCGGGGAGGTTCCGCCGAT | 3308 |
| OY | 3569 | CCCCAAGTCACTCATGAGGACCTGTTGAGCAGCTTATTCAAGGCCGACTATGGTT | 3626 |

| | | | | |
|----|------|--------------|--|------|
| Db | 3309 | CATCCCGCTTAA | CCCGGAGAGAGCCGCGTGGCTTCTCTTAATGCAACGAGAGCGGCAGTGGTT | 3368 |
| Qy | 3629 | CTTGAAATCA | GTGGAGCTTGTGGCACTCTGTGGTATCTGAATTCATATGCTGTGAAATGCG | 3688 |
| Db | 3369 | CCTCTGGCAAT | TGGAAACGGGAGAGCGGGCCCTTATCAATTTCCGCCGCCCTGCGCTTGGCG | 3428 |
| Qy | 3689 | CGGGCCGTG | CAATGTGCAACCGCTTAAAGTCCGGGCTCTTGACAGCGGTTAAACAGGCAACGA | 3748 |
| Db | 3429 | CGGGGCGCT | CGATGTCTGTCCGGCTACAGCCGAGTTTGAGCGGCTTCACACAGCCTCACGA | 3488 |
| Qy | 3749 | GACTCTTAGA | ACGACATTTTGAAGACACAGATGAGTGTGCTGTATCAAAATTTGTCACAGAA | 3808 |
| Db | 3489 | GTCTGTGCG | TATACCGGCTTCCGGCAGAGAGGCTGTGCAATCCGTTACAGGTGTGATATCCGA | 3548 |
| Qy | 3809 | GCTTTCAG | GAGATGGAAGTGCATTTGATCTCTGTGTTCAAGACTTGAACCCGTTTGAAGT | 3868 |
| Db | 3549 | TGGCAGTGT | GAGGTTTCCGGGCACTACCTGGCAATGTGCATGACCGCGTGTCAAGGCG | 3608 |
| Qy | 3869 | GTTGAACCA | GAAGACAG---CTACTCCCTTCAATCTCTCATCTGAAGTGTGAGAGAC | 3925 |
| Db | 3609 | GGCAGTGA | AGACGGAATGGCCAGGCCCTTTCGACTACGGGCGGATCCGTTGCTGGAT | 3668 |
| Qy | 3926 | GAGCCTCT | TAACGATTTGATGATGACCAATCCTCACTATTGTCAATGCACTCATCAT | 3985 |
| Db | 3669 | CAGTCTGT | TGGAAGTGGCTCCGAATGACATGTCTGTCTATGTTCCAGCACCAATATGCT | 3728 |
| Qy | 3986 | CTCAGATG | TGTTGTCATATTGATCTTTCGACAGCGGATCTCAATAGCTCTATCTGAGTGC | 4045 |
| Db | 3729 | CTCCGAGG | TGTTGGTCATGACGTTGATGTGTCGAAGACTGTGATCAGCTCTACGCGCCTA | 3788 |
| Qy | 4046 | GCTTAAGA | ACTCAAAAACCCGCTGTACGACATCTCTCTACTCTATCCAGTACAGCA | 4105 |
| Db | 3789 | CAGCACA | GGGGCGCCAGACCGGCCCTGCGGGCT---GCCATTAAGTATCCGACTATGC | 3845 |
| Qy | 4106 | CTTTGCA | AAAAATGGCAGAAAGCCAAATTCATAGACAGAGAAAGCACTCAACTCTAGAA | 4165 |
| Db | 3846 | CGTCTGG | ACGCGCAATGATGATGAGGCCCGAGAGAGGAGCGCAATTTGGCGTACTGAT | 3905 |
| Qy | 4166 | GAAACCA | CTCAAGACTCTTCCCGACGA---AGATCCGACCGACTTTGGCCGCGCTGC | 4222 |
| Db | 3906 | CGGCTGT | GGGTGGCGAACAGCCGGGTGCTGAGACTGCCGTTGATGTCGCCGCTCTGC | 3965 |
| Qy | 4223 | ACTTCTGT | CTGAGAGCCGAGGTGTGCTATGTTACATGACGCGGAGCTCTACCACTC | 4282 |
| Db | 3966 | GGAACA | AGGCTTTCGCGCGCGCTGAGTTGCAACTGGCCGCCACGAGCGGCGCAAGCG | 4025 |
| Qy | 4283 | CCTTCAG | ACCTTTCGCAACGAAACAACAAGCACTCTTGTGTGCTTCTTACGTGGGTT | 4342 |
| Db | 4026 | GCTAAG | CGCTTGGCCCAACGGGAGTACCTTATGTTGCTGTGCGGTGCTT | 4085 |
| Qy | 4343 | CCGTGCG | CTCATTTATGCTCTCACAGCTGTTGAAGCGCTGTCAATTTGATACCAATTTGC | 4402 |
| Db | 4086 | CCAGGCG | CTGTATGTCTACACAGCGGTCAAGCCGATATCCGTGTCCGCGTCCGGTCTGC | 4145 |
| Qy | 4403 | GAATCG | AACCTGAACCTGAACCTGAGGATATCATGCGTCTGTTGTCAATAACGAGTGTAT | 4462 |
| Db | 4146 | CAATCG | CAACCGGGTCCAAACCGAGCACTGATGGGTTCTTCTGTCAACCCAGGTGCT | 4205 |
| Qy | 4463 | GCGAAT | CAACTAATATCATCACGATACCTTTGGGACTTTTGATCAACCAATGCAAGCTAC | 4522 |
| Db | 4206 | CAAGCG | CACTATCATGAGGAGATGGGTTTCGACCGATTCCTGCAACAGGTTCCGACGCG | 4265 |
| Qy | 4523 | GACGAC | GACAGCACTTTCAGAACAGGATTTCCGTTTGAAGCGCTTGTATTCAGACTACA | 4582 |
| Db | 4266 | CTCCGT | GAGCGGAGCGACACAGGACTTGGCGTTTGAGCACTGTGTGAGAGCTTTGCA | 4325 |
| Qy | 4583 | GCTTGAT | TCAGAGATCTGTCAAGCACACTCTTCGCAAACTCAATTTTTCGAGTGCATC | 4642 |
| Db | 4326 | ACCGGA | GCGAGGTCTACGACACAGCCGCGTGTTCAGATGTCTAATCACTACAGGCGGA | 4385 |
| Qy | 4643 | ACGAGA | GAAGACTTCAAGTTCCAGGGTCTCGAATCCGTACTGTGCTTAGCA | 4702 |

Db 4386 GCGGGGCGAGCAGCGCTTCCGGAAGTCGGGAGCTGAGCAGTCAAGAGCAGCGCTGGGA 4445
 Qy 4703 AGCGTCA---CTGATTTGACATGAGATTCCATCTGTTTCAAGAAACGACACCTTAA 4759
 Db 4446 AAGCCATACGCGCGACATTGACCTGGGCTGGATGACTGTGATCCGAGTCGACATCTG 4505
 Qy 4760 AGGTACGCTCAACTTGGCCGATGAGCTGTTCAAAATGAGACCTTTGAAATGTGCTCAG 4819
 Db 4506 GGGGGGGGTGTATATGCGACGATCTATTCATGCTTGCACGCGAGAGGCGCTGGTAGC 4565
 Qy 4820 AGTATTTCTTGAATTTGAGAAACGGGCTTCAAAGTTCCGCGACACCACTTCATACT 4879
 Db 4566 GCATTTGGCAGAACCTCTGATGATCCCTGGCGATGCTCGAGCTCGCTGGGAGAGCT 4625
 Qy 4880 TCCCTTGACATGAGCATGTGTGATCTCTTGAATAATGGAGTGTCTCAAGCTTCAACATGT 4939
 Db 4626 GGCATGCTGCTCGGAGAGAGCGGAGATCATCGGCACTCTGGAACCGCAGCGATTC 4685
 Qy 4940 CGACTATCCCGAGAAATCGAGCTTGGCTGATCTTCCAGACCCAAAGTCTCTGCTTACC 4999
 Db 4686 GGGCTATCCGCGCAACCGCTGATGACACGAGTGGCCGAGCGGGGTATGGGCGC 4745
 Qy 5000 CGATGATCTGCTGTGTGATCTCTCTGCGCATTTGACCTTACCGAGTTGATGCGCA 5059
 Db 4746 GATGCGGTGGCGGTGATCTTCAAGAGAAACTCACTACGCGAGCTGATGAGCCG 4805
 Qy 5060 GTTGATATTTCTGCTGTGATGCTCTGCGATGCTGCAATGCTGCGAGAGCTGTGCGC 5119
 Db 4806 GGCCAACCGCTGCGCCAGTGTGATGCGCCAGAGCGTGGCCCGCAATGGCGGTGCG 4865
 Qy 5120 AGATTTTGGCCCAAGGTCATGAGACAAATTTGCTTGTGTTGTTGAAAGCGAA 5179
 Db 4866 GATGCGCATGACGAGCGCGAGATCATGTGCGCTTCTGCGGTGTGAAAGCGCG 4925
 Qy 5180 CTTGCCCTTATCTTCTCTGATGATGATGCGCTTGGCGAGAGTTGAGATTAATCTTC 5239
 Db 4926 CGCGGCTTACGTGCGCTGTGATTCGAATACCGCGAGCGCTGCTGATCAATGCA 4985
 Qy 5240 TGAATCTTGTGGGCTTACCATTTGTTGATTTGGCCATGATACAGCGCTCCCATATCGA 5299
 Db 4986 GGCAGCTGCGGCGCACCTGCTGTGACCCATGACCACTCTGAGGCTGTGCCGATCC 5045
 Qy 5300 GGTATTAACGTCGATGTTTGTGATCCGGATGCGGATGACGATGACAGATGCGATG 5359
 Db 5046 CGAGGGGTGTCTGCTGTGCGGTGATTCGCGAGAGGATGGGCGGCTTCCCGCTCA 5105
 Qy 5360 CTTTGAATCATGAGCAGCAGCAGCAAAACCTCTAGCCAGAGTCTGCTATGCTGT 5419
 Db 5106 TGATCCAGAGGTGGCGCTGACAGCGCCAA-----CCTGGCTATGTGAT 5150
 Qy 5420 GTTATCTTCAAGATTCATCTGCGGACCAAAAGGCTGATGATGAGCACTGTGATAT 5479
 Db 5151 CTACACTCTCGGCTTCAACCGGATGCGCAAGGGGTGGCGGTGTCCACGCTCGTTGAT 5210
 Qy 5480 T---CGAAGCTCAAGAGCTGTATATACCACTATCTTTCGAAACAGAGATGCTCA 5536
 Db 5211 CGCCCATATGTGTGACCGCGGACGCTTACAGATATACCCCGAGAGACTGCGAGCTGCA 5270
 Qy 5537 CATGCGGACCATTTGCGTTTGAACCGCGCATGTATGAGATCTAACGCGCCCTTTTGTG 5596
 Db 5271 CTTCATGTGCTTGGCTTTCAGCGTTCCAGAAAGGTGTGATGACCCGTTGATCAACGG 5330
 Qy 5597 AAGACACTTGTGCTTGTGATGATGACCACTTGAAGCTTGAAGACTCAAGATGT 5656
 Db 5331 CGCGCGGTGTCTATCGGACGACGCTGTGCTCCGGAACGACCTAACCGCGAT 5390
 Qy 5657 GTTTTCCGAGCATGTCAACGCGGCAATGATGATCAGCAGCTTCTCAAGATGATAC 5716
 Db 5391 GCATGCGC-ACGGGTATACGTGGGGGTGTTCCGCGCGGTATCTGACCACTGGCG 5449
 Qy 5717 TCTCCAGTCCGAGAGGCTCTCGAAGAC---TTGATGTTCTTCTTGTGTGTGA 5772
 Db 5450 AGCATGCGGAGCGGAGGCAATCCGCGCGGTATGCTTGGCGGCGAGC 5509

Qy 5773 CAGATTCAGCGGCCCCAGATGCTCTGATCCGAGGAGACTTTATCAAGGGGTCCAGTGT 5832
 Db 5510 CGGTGGCGGAGGCGACACTTATGACTGCGGTGGGGCGGTGAAGCCGAGTACTGT---T 5566
 Qy 5833 ACAATGTTACGGCCCAACAGAGATGAGTCAATGATCAATCTATCCCATTTGACTCGA 5892
 Db 5567 TCAACGATTAACGCGCCGACCGAGACGCTGTGTGCGCGCTGTGTGAAAGCAGGGCGG 5626
 Qy 5893 CTGAGTCTTCAATGATG---GTCCAAATGGAAGAGTCTGAACTCAAGAGCGT 5949
 Db 5627 GCGATGCTGCGGCGCGGCTACATGCTCCGATCGGTACGCTGTGGCAACCTGAGCGCT 5886
 Qy 5950 ATGTGATGATCTCTGAGCAACAGCTTTGATGCTGTGTGATGAGAGAGCTTGTGCA 6009
 Db 5687 ACATCTCGACGCGGAGTTGAACTCTGCGGTAGCGGTGGGGCGGAACTGTACTG 5746
 Qy 6010 CTGGCAGATGCTTGGCGCGGAGCTTACATGTA---CAAAGCTTGAACGAAACCGTTT 6066
 Db 5747 GCGGGGAAGGGGTGGCGCGGCTTACCTGGAGCGTCCGGGCTGACCGCGAGCTTTCG 5806
 Qy 6067 TGCATTAATCTGATGATGACACAGATGAGCGCTATGCACTGGCGATCGAGTGGGT 6126
 Db 5807 TGCAGAACCTTGTGCGCGCGCGGAGCGGCTGTACCGGACGAGCGGACCC---TGACC 5863
 Qy 6127 ACAGATGAGATGAGCTCTCATGAGTCTTTCGACGATGAGACACCCAGTTCAAGATT 6186
 Db 5864 GTGGGCGTGGATGGGTGTGTGATGACTCTCGGACGGGTGTGACACAGGTGAAGATCC 5923
 Qy 6187 GTGCAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6246
 Db 5924 GAGCTTCCGATCGAATGAGAGATGAGAGCGCGCTTCCGCGATCCGCGGTG 5983
 Qy 6247 GAGATGCTGCTGTCTCTTCAAGCAATGAG 6279
 Db 5984 GCGAGCGGTGTGTGTGCGCCAGCGGTGCGG 6016

RESULT 5

US-09-410-551B-1

; Sequence 1, Application US/09410551B

; Patent No. 6503737

; GENERAL INFORMATION:

; APPLICANT: KOSAN BIOSCIENCES, Inc.

; APPLICANT: REEVES, CHRISTOPHER

; APPLICANT: CHU, DANIEL

; APPLICANT: KHOSLA, CHAITAN

; APPLICANT: SANTI, DANIEL

; APPLICANT: WU, KAI

; TITLE OF INVENTION: POLYMERASE SYNTHASE ENZYMES AND RECOMBINANT DNA

; FILE REFERENCE: 30062-20026.00

; CURRENT APPLICATION NUMBER: US/09/410, 551B

; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/139,650

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: US 60/123,810

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/102,748

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 77536

; TYPE: DNA

; ORGANISM: Streptomyces hygroscopicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52275)...(71465)

US-09-410-551B-1

Query Match 0.9%; Score 104; DB 4; Length 77536;
 Best Local Similarity 47.1%; Pred. No. 1.8e-19;

Matches 465; Conservative 0; Mismatches 505; Indels 18; Gaps 4;

QY 3589 GACCTGTTGAGCATCTTATTACAAAGCCGACATAGTCTTGATCAGTTGACCTTG 3648

Db 47870 GCCCGGCTCTTGTCTTGTGACACAGGGGAGATCTGCTTCTCCAGCAATTGGACCCGG 47929

QY 3649 GCAGCTGTGTGATCTGATTTCCATATGCTGTGAAATGCGCGGCTGTCAATGTGACG 3708

Db 47930 AGAGCAACGCTTAATCTCCCGCTGTGCAACGCCGCGGCTATTGTGAGCGCCGG 47989

QY 3709 CGTTAGTGCGGCTCTTGGACGCGCTTGAACAGCAACGAGACTCTTGAACAGCAATTG 3768

Db 47990 CCTTGAGCGGTGTGCGCTGCTGTCTGCGGCGCCAGAGCGTTGCGAGCGGTTCG 48049

QY 3769 AAGACCAAGATGATGTGCTGTGTAACAAATGTTCAAGAACTTTCTGAGAGATGAAAG 3828

Db 48050 ACACCGCGGAGCGGAGCCCTTCCAGGGGCTTCCCGCC---CGGAACCTCTCTGC 48106

QY 3829 TCATTGATCTGTGTGTTGACACTTGACCCGTTTGAAGTTGAACCAAGAACAGACTA 3888

Db 48107 GCCACGCGCGGCGGAGGAGGAGGAGCGCCGCGCTGTCTCCGAGAGATCGCCG 48166

QY 3889 CTCCTTCAATCTCTCATCTGAAAGCTGTGAGAGGAGCGCTTACAGCTTGTGTAAG 3948

Db 48167 CGCGGTTGCACTGTGCGACCGGCGGCTTGAATCAGGCGCTGTGATCCGCTCGGTGACG 48226

QY 3949 ATGACCAATCTCTCATCTGATTTGTGATGATCATCATCATCTGATGTTGTTCAATTGATG 4008

Db 48227 ACAGACCACTTCTGTGCGGTGACCTGTGACCATGTGTGCGCGGAGCGGTGCTTGTGCGGC 48286

QY 4009 TCTTGGCAGCGGATCTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4068

Db 48287 TCTTCCCAATGAACTCGACGCCCACTAAGCGGCGCTGCGCGA-----CACTGCGCGCC 48340

QY 4069 TGTGACACTCATCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4128

Db 48341 CTGCGCAACTGCGCGCTGTGCGGTGAGTACGCGGCTGTGCGCGCTGTGAGAGCGCGCG 48400

QY 4129 AATTCA-----TAGACAGAGAGAGAGCACTCACTCACTCACTCACTCACTCACTCACTCACT 4179

Db 48401 AACTTCAACCGGCGCGGAGTGTGACAGAGGCTGTGCGCTCACTGTGCGGAGCACTCCGGGGCG 48460

QY 4180 ACTTCTCCGAGCAAGATCTCCGACGCACTTGTGCGCGCTGTGCTGTCTGTGAGAGCG 4239

Db 48461 CCGCGGCGGCTGTGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 48520

QY 4240 CAGGTGCGTACATGTTACATGACGAGCGGAGCTCTACAGTCCCTTCCAGCTTCTGCA 4299

Db 48521 CGGCGCATGTGCGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 48580

QY 4300 ACGAACACACACGACCTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 4359

Db 48581 GCGACTCTCGGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 48640

QY 4360 GTCTCAGCTGTGTTGAAGAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 4419

Db 48641 GCGAGGCGGAGCGCGGAGCGGTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 48700

QY 4420 AACTGAGGATATCATGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 4479

Db 48701 CGTACGAGGCTGTGATGGAATGTTGTCAACAGCTGTGCGCGCGCGCGCGCGCGCGCGCG 48760

QY 4480 ATCAGCATCTTGTGAGACTTGTGATCAACCAAGTCAAGGCTCAAGACAGACAGCATTTG 4539

Db 48761 GCGATCTGTGTCTGTGCGGAACTCTTCAACGCTGTGCGGCGCGCGCGCGCGCGCGCGCG 48820

QY 4540 AGAAGAGATATTCGTTGAGCGCGT 4567

Db 48821 CCGACGCGGAGCTGTGCGTTGAGAACT 48848

Sequence 1, Application US/09940316B

Patent No. 6759536

GENERAL INFORMATION:

APPLICANT: KOSAN BIOSCIENCES, Inc.

APPLICANT: REEVES, CHRISTOPHER

APPLICANT: CHU, DANIEL

APPLICANT: KHOSLA, CHAITAN

APPLICANT: SANTI, DANIEL

APPLICANT: WU, KAI

TITLE OF INVENTION: POLYKETIDES ENCODING THE FBA GENE OF THE PK-520 POLYKETIDE SYNTH

TITLE OF INVENTION: GENE CLUSTER

FILE REFERENCE: 30062-20026.11

CURRENT APPLICATION NUMBER: US/09/940,316B

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/410,551

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: US 60/139,650

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 60/123,810

PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/102,748

PRIOR FILING DATE: 1998-10-02

NUMBER OF SEQ. ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 77536

TYPE: DNA

ORGANISM: Streptomyces hygroscopicus

FEATURE:

NAME/KEY: CDS

LOCATION: (52275)...(71465)

US-09-940-316B-1

Query Match 0.9%; Score 104; DB 4; Length 77536;

Best Local Similarity 47.1%; Pred. No. 1,8e-19;

Matches 465; Conservative 0; Mismatches 505; Indels 18; Gaps 4;

QY 3589 GACCTGTTGAGCATCTTATTACAAAGCCGACATAGTCTTGATCAGTTGACCTTG 3648

Db 47870 GCCCGGCTCTTGTCTTGTGACACAGGGGAGATCTGCTTCTCCAGCAATTGGACCCGG 47929

QY 3649 GCAGCTGTGTGATCTGATTTCCATATGCTGTGAAATGCGCGGCTGTCAATGTGACG 3708

Db 47930 AGAGCAACGCTTAATCTCCCGCTGTGCAACGCTGTGCGGCTGTATGTGAGCGCCGG 47989

QY 3709 CGTTAGTGCGGCTCTTGGACGCGCTTGAACAGCAACGACTCTTGAACGCAATTG 3768

Db 47990 CCTTGAGCGGTGTGCGCTGCTGTCTGCGGCGCCAGAGCGTTGCGAGCGGTTCG 48049

QY 3769 AAGACCAAGATGATGTGCTGTGTAACAAATGTTCAAGAACTTTCTGAGAGATGAAAG 3828

Db 48050 ACACCGCGGAGCGGAGCCCTTCCAGGGGCTTCCCGCC---CGGAACCTCTCTGC 48106

QY 3829 TCATTGATCTGTGTGTTGACACTTGACCCGTTTGAAGTTGAACCAAGAACAGACTA 3888

Db 48107 GCCACGCGCGGCGGAGGAGGAGGAGCGCCCGCGCTGTCTCCGAGAGATGCGCG 48166

QY 3889 CTCCTTCAATCTCTCATCTGAAAGCTGTGAGAGCGCTTACAGACTTGTGTAAG 3948

Db 48167 CGCGGTTGCACTGTGCGACCGGGCGTGTATCAGGCGCTGTGATCCGCTCGGTGACG 48226

QY 3949 ATGACCAATCTCTCATCTGATTTGTGATGATCATCATCTGATGTTGTTCAATTGATG 4008

Db 48227 ACAGACCACTTCTGTGCGGTGACCGTCAACATGTCCCGCGAGCGGCTGTGCGGCG 48286

QY 4009 TCTTGGCAGCGGATCTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4068

Db 48287 TCTTCCCAATGAACTCGACGCCCACTAAGCGGCGCTGTGCGG-----CACTGCGCGCC 48340

QY 4069 TGTGACACTCATCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4128

Db 48341 CTGCGCAACTGCGCGCTGTGCGGTGAGTACGCGGCTGTGCGCGCTGTGAGAGCGCGCG 48400

QY 4129 AATTCA-----TAGACAGAGAGAACACTCACTACTGAGAGAACAACTC---AAG 4179
DB 48401 AACTCACCGGCGCGGAGTCTGGAAGAGCGGTCTGGCTCTGCGGAGAACAACTCCGGGGCG 48460
QY 4180 ACTCTTCCCAAGAAAGATCCGACCGACTTTGCGCGCTTCTGTCTGAGACG 4239
DB 48461 CCCCCGGCGGCTCGCCCTCCGACCGCTCCCGCGCGGCTGCGGACCGGACG 48520
QY 4240 CAGGTTCGTACATGTTACATGACGAGCGAGCTCAAGTCCCTTCAGGCTTTCGA 4299
DB 48521 CGGCGATGCGCGAGTGGCGCGCGCGCGCGCTGCGGACCGCGCTTCACTCCGCG 48580
QY 4300 ACGAACACAAACAGACCTCTTCTGCTCTTCTTACGTGCGTCCGCGCTCATATTC 4359
DB 48581 GCGACCTCGGTGGGTCTGCTGTATGACCTGCTGGGGGCTTCAAGCGGTCTCTGCC 48640
QY 4360 GTCTCACAGCTTTGAAGAGCGCTGTCACTGGTACACCAATTGGGAATGCAACGACCTG 4419
DB 48641 GCGAGCGGCGACGCGGAGCGTGTGCTGCGGACCGCGGCGAACCGTACCGGCGG 48700
QY 4420 AACTGAGATATCATGCGCTTGTGCAATACGAGTATGCGAATCAACATAGATC 4479
DB 48701 CGTACGAGGCGCTGATGCGATGTTGTTCAACAGCTGCGGCTGCGGCGGACCTTCG 48760
QY 4480 ATCAGCATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACGACTTCG 4539
DB 48761 GCGATCGGTGCTTCCGGAACTCCTGACCGGCTGCGGCGGACGACGAGCGGCTTCG 48820
QY 4540 AGAACGAGATATTCGTTGAGCGCT 4567
DB 48821 CCCACGCGACCTGCGTTGAGAACGT 48848

RESULT 7

US-09-252-991A-6997
; Sequence 6997, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6997
; LENGTH: 10023
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6997

Query Match 0.98; Score 103.8; DB 4; Length 10023;
Best Local Similarity 44.8%; Pred. No. 3.9e-20;
Matches 460; Conservative 0; Mismatches 552; Indels 15; Gaps 1;

QY 3585 GAGGAGCTTGTGAGAGCTTATTCACAGCGGAGTATGTTCTGTAGTCAAGTGGAC 3644
DB 4777 GAGCAGCGGCTGCGGCTCTCTACTGCAAGAGGATGTTCTCTGGCAACTGGAG 4836
QY 3645 GTTGGCAGTGTGTGATCTGATTCATATGCTGTGAATCGCGGGCTGTCAATGTC 3704
DB 4837 CCGGACAGCGCGGCTACCAAGTCTGCGGCGCTGCAAGCGGCGGCTGAGCTG 4896
QY 3705 GAGCGTACAGTGTGGGCTTTGAGAGGCTTGAACAGGACAGGACGACTTTTGAAGACA 3764
DB 4897 GCGCGCTTGAAGCGCGGCTTACAGAGGCTTGTGAGGCGGACGAGACCTTGGACACG 4956
QY 3765 TTGAAGACGAGATGTTGTGCTGATCAAAATGTTTCACGAGAGCTTTCTGAGGAGATG 3824

DB 4957 TTCCCGACGCTGACGCGCTGCGGTACAGCGGCTGACGAGCGAGTGGCGGCTGACATG 5016
QY 3825 AAGGTATATGATCTGTGTGTTGAGACTTGAACCCGTTTGAAGTTGAACA----- 3877
DB 5017 GACTGGCAGGACTTCTCCGCTGACCGGACGAGCCGACGACCTGACAGACCTTC 5076
QY 3878 -----AGAACAGACTACTCCCTTCATCTGTCAATCTGAAGCTGGCTGAGAGCGAG 3929
DB 5077 GCGGACAGAGGAGGACCGGCGCTTGAACCTTGAAGAGCGGCGGTTGCTGGGCTGCG 5136
QY 3930 CTCTTACAGTCTGTGTAAGATACACATCTCTACTATTTGTATGATCAATCATATTC 3989
DB 5137 ATGGTGAAGTGGCGGAGCGGAGCTACTAGTGTGACCTGTGACACATGCTAC 5196
QY 3990 GATGTTGTGCAATGATGTTGTCGACGAGATCTCAATAGCTTACTAGCTGCGCTC 4049
DB 5197 GAAGCTGGGCGATGACATCTTCCCGGAACTGGGCGGCTTACGAGGCTTCTTC 5256
QY 4050 AAGGACTCAAAAGACCGCTGTGACACTCTCTTACTTATCCAGTACAGGACTTT 4109
DB 5257 GAGGACCGGAGATCGCGCTGAGAGCGGTTCCGGTCCAGTACCTGACCTACAGGTGTG 5316
QY 4110 GCAAAATGCAAGAGCAATTCATATGACGAGAGAGCACTCACTACTGAGAGAG 4169
DB 5317 CACGCGAGTGTGCTGAGAGCGGCGGAGCGGACCGGCTGACCTAGTAAAGGCCAG 5376
QY 4170 CAATCAAAATCTTCTCCGAGAAAGTCCGACGACTTTGCGCGGCTGACTTCTG 4229
DB 5377 CTGGGCAACGAGATCGCTGCTGCAATGCTCGGCGGACCGGCGGCGGCTGAG 5436
QY 4230 TCTGAGACGACAGTGTGCTGATGTTACATGACGCGGAGCTTACAGTCCCTTGA 4289
DB 5437 AGCCACAGGCGGACCTTACCGCTTGCATGACCTGACCGGAGCTGCGGCGGCTGCT 5496
QY 4290 GCGCTTGCAGAGAACACACAGACTCTTCTGCTGTTCTTACGCTGCTTCCGCTCC 4349
DB 5497 CGCTTCAACCGCCCGCGGCTGACCATGTTATGACATGACCGGCACTTGGCGGCG 5556
QY 4350 GCTCATATGCTCTCACAGTGTGTAAGAGCGTGTATTTGATACCAATTGGGAATCG 4409
DB 5557 TTGCTTACCGCTACAGCGGCGGACGAGACTGCTGATCGGCGGCGGAGGAGCGG 5616
QY 4410 AACGACCTGAAGTGAAGTATCATGCGCTGCTTGTCAATACGAGTATGCAATC 4469
DB 5617 ATCCGCGGAGAGGAGGAGGCTGATGCGGCTTCTCTCAATACGAGTGTGCGCTGC 5676
QY 4470 AACATGATCATGATGATCTTGGGACTTTGATCAACCAAGTCAAGCTTACGAGACA 4529
DB 5677 CGGCTGACGAGATGATGACGCTGCGGAGCTGTTGAGCAGGCTGCGGACGCTGATC 5736
QY 4530 GCAAGATTCAGAGAACAGATATTCGTTGAGCGGCTTATACAGACTACAGCCTGGA 4589
DB 5737 GATGGCAGTGCAGACGAGACTGCGTTGACCACTGTGGAAGCCTTGAACCTCCG 5796
QY 4590 TCCAGAG 4596
DB 5797 CGCAGCG 5803

RESULT 8

US-09-252-991A-8892/c
; Sequence 8892, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8892
 ; LENGTH: 3315
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8892

Query Match 0.9%; Score 97.8; DB 4; Length 3315;
 Best Local Similarity 42.7%; Pred. No. 1,2e-18;
 Matches 703; Conservative 0; Mismatches 917; Indels 25; Gaps 3;

QY 3600 CAGTCTTATTCACAAAGCCGCACTATGCTTCTGATGAGTTCAGTTGACGTTGGCAGTCTGTGG 3659
 DB CTGCTTACAGCCCGCAGCCGATGTGTTCTCTGACCTGAGCCACAGATGGGCGC 3148
 QY 3660 TATCTGATTCATATGCTGTGAGAAATGCGGGGCTGCTCAATGTTCAGCGTTACGTGG 3719
 DB 3147 TACAACTGCGCCAGCGGGGTGGCTGAAACGACCGCTGATTCGCGAGGGCTGGAGCGC 3088
 QY 3720 GCTCTTGACAGGCTTGAACAGCAGACGACGACTCTTGAACGACATTTGAAGACAGGAT 3779
 DB 3087 GCCTTGCCAGCCTGTGTGACGCTGATGAAACCTGCTGACGTTGTTCCGCGGGCGCC 3028
 QY 3780 GGTGTGCTGTACAAATTTTTCAGAGAAAGCTTTCTGAGAGATGAAGTCAATGATCTC 3839
 DB 3027 GACGACAGCCTGGCGCAGGCGCCCTGCAAGCCCGCTGAGAGTGTGCTTTCAGAGATTGC 2968
 QY 3840 TGTGCTT-----CAGACTTGAACCCGTTTGAAGTGTGAACCAAGAACAG 3884
 DB 2967 AGCGGCTGCTGAGCGCCGAGCAGAAAGCCGCTGCGCGAGGCGCAGCGGAGTGC 2908
 QY 3885 ACTACTCCCTTCAATCTCTCATCTGAAGCTGGCTGAGAGCGACTTTTACGACTTGTG 3944
 DB 2907 TTGGAGCGCTTTCAGCTGTGTGAGAGGGCCGTTGCTGGGGTCCCGCTGATCCGCTGGC 2848
 QY 3945 GAAGATGACCAATCTCACTATTTGTATGATGATCAATCATCTGATGTTGTCAATT 4004
 DB 2847 GAGGAGGGGATGTGTGTGTGACCTGTGATCAATCTGTGTCGAGCGGTGTGATG 2788
 QY 4005 GATGTCTTGGAGCGGCTTCAATCAGCTCTTCACTGCTGGCTCAAGAACTCAAAAGC 4064
 DB 2787 AAGGTGTGATCGAAGAAATTCAGTCTTTCAGTGTCTTATGCGACTGGGCGGAGCC 2728
 QY 4065 CCGCTGTGACGACTCACTCTCTACTATCCAGTACAGCAGCTTTCAGAAATGGCAGAA 4124
 DB 2727 GGCTGTGCGGCTTGGCGGATCAAGTACGCGATTAACGCTGTGGCAGCGAGCTGTG 2668
 QY 4125 GACCAATTCATAGACAGAGAGCAACTCACTACTGAAAGAACAACTCAAAAGCTT 4184
 DB 2667 GAGGCGGATGACAGAGCGCCAGCTGGAATCTGGCGCGGCAAGTCTGGGCGAGCGCAT 2608
 QY 4185 TCCCCAGCAAAAGTCCCGACCGACTTTGCCCGCCCTCACTTCTGTGTGAGAGAGCAGT 4244
 DB 2607 CCGGTCTGAGTGTGCGACCGACCCCGGTGCGGGGTTCACAGTACCGTGGAGC 2548
 QY 4245 TCGGTATCATGTTCATCATGACGAGGAGCTCTAACAGTCCCTTCAGGCTTTCGACAGAA 4304
 DB 2547 CGTTACAGATTCAGATCGAGCGGCGCTGCGCAGGCGCTCGCGGACCGCCGAGCGC 2488
 QY 4305 CACAAACGACCTCTTGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4364
 DB 2487 CAGGCGGTGACCTGTTCTATCTGTGTCTGCGGCTTCAATATCTCTTCTCAACGCTAT 2428
 QY 4365 ACAGCTTTGAAGCGCTGTCTATGTATACCAATTGGAAATGGCAACCGACCTGAATCTG 4424
 DB 2427 AGCGGCGAGACCGCTGCGGGTGGGCTCCCAATCGCAACCGCAACCGGCGGAGGTG 2368
 QY 4425 GAGGATATCATCGGCTGCTTGTCTCAATACGAGTATGCAATCAACATGATCATCAC 4484
 DB 2367 GAAGGCTGATCGGCTGTCTGTCAACACCGAGTGTGCTGCTGTGATTCGACGCGCC 2308
 QY 4485 GATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACGACGATTCGAGAAC 4544

DB 2307 ACGTGCTGCGACCCCTGTGCGCGGCTTCAGAGAACCCGTGTGCGCGCCAGCGCCAT 2248
 QY 4545 GAGGATATTCGTTTGGAGCGCTTGTATGACGACTACAGCCTGATTCAGATCTGTCA 4604
 DB 2247 CAGGATCTGCGTTTCAGACCCCTGTGTGAGCGCTTCAAGTTCAGAGCGACCTGAGCCAC 2188
 QY 4605 AGCAACCTCTC-----GCACAACTCATTTTTCAGAGTCACTCAAGAGAGACTTGG 4656
 DB 2187 AGCCCGCTGTTCAGAGTATGATCAACACACAGCCGCTGTGCTCCAGATCGAGCGCTG 2128
 QY 4657 GAAGATTCAGTTCCAGGCTGTGAGTCCGTACTGTGCTTACGAAAGCTTACATCTGAT 4716
 DB 2127 GACAGCGTGGCGCGCTGACCTTTCGCGACCTGCACTG--GAAGACCGTACACCAAGT 2070
 QY 4717 TTGACATGAGATTCATCTGTCTTCAAGAAACGACAGCCTTAAAGTAGAGTCACTTGG 4776
 DB 2069 TCGACTGAGCTGTGATCTTACGAAAGGCGGTGCTGTATGCGCGCTGACTACG 2010
 QY 4777 CCGATGAGCTGTTCAAATGAGACTGTGAAATGTCTGACAGATATCTTTGAGATTTC 4836
 DB 2009 CAGCCGACTGTTTGAGGCGCGGACCGTCAAGGCAATGGCGGCAATGGCAGAACTTC 1950
 QY 4837 TGAGAAACGGGCTTCAAGTTCCGCGACACCACTTCAATCTTCTTGTACTGATGCA 4896
 DB 1949 TGGCGGCTATGTGAAACCCGACGCGCAGCTGCACTGCTGCGGATGCTGATGCG 1890
 QY 4897 TTGTGACTCTTGAATAATGATGTCTCAACGCTCAAAACATGTCGACTATCCCGAGAT 4956
 DB 1889 AGAGCGCTATCAGTGTCTGAAAGCTGGAACCCCACTGCGGCGAGTACCCCTGCAAC 1830
 QY 4957 CGAGCTTGCTGATGTCTTTCAGACCCCAAGCTCTGCTTACCCCGATGTTCTGCTGG 5016
 DB 1829 GCGGCGTACCGGCTTGTTCAGAGAGAGGTGAGCGCACACCGAGCGCGCGCTGG 1770
 QY 5017 TGAATCTCTGTGCGCATTTACCTACACCGATTTGATGCCCATGCTGATATCTGCTG 5076
 DB 1769 ATGCGCTGATCGAGCGCGGGGTGCGTGGGACCGCTGTGTGGCGCATGGAAGCTT 1650
 QY 5077 GATGCTTCTGCGAGGCTCAATGCTGTGACAGAGAGCTGTGCGAGTATTTGCCCGCAGT 5136
 DB 1709 ATGCGCTGATCGAGCGCGGGGTGCGTGGGACCGCTGTGTGGCGCATGGAAGCTT 1650
 QY 5137 CATGTGACAAATTTGCGCTTCTTGTGTGTTGAAGGGGAACTTGGCTTATCTTCTC 5196
 DB 1649 CCAATGAGATGTGTGTGCGCTGATGCGCATCTCAAGGCGCGGCGCTTACGTGCGG 1590
 QY 5197 TCGATGTACATGCGCTCTGCGGAG 5221
 DB 1589 TGAACCGAGATATCCCGAGAGACG 1565

RESULT 9

US-09-252-991A-9182
 ; Sequence 9182, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/74,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 9182
 ; LENGTH: 7911
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9182

Query Match 0.9%; Score 97.8; DB 4; Length 7911;
Best Local Similarity 42.7%; Pred. No. 2.4e-18;
Matches 703; Conservative 0; Mismatches 917; Indels 25; Gaps 3;

QY 3600 CAGCTTATTCACAAAGCCGACTATGTTCTGTGATCAGTTGAGCGTTGACGTTGTG 3659
DB 196 CTGTCTACAGCCAGAGCCAGTGTGTTCTGTGACCTGGAGCCAGAGAGTGGGCC 255
QY 3660 TATCTGATTCATATGCTGTGAGAAATGCGGGCTGTCAATGTCCAGCGTTACGTGG 3719
DB 256 TACAACTGCTCCAGCGGGTGGCTTAAAGGACCGCTGATCGCCAGGGGCTGGAGCGC 315
QY 3720 GCTCTTGACAGCGCTTGAACGACGACGAGCTTTAGAAAGCAATTTGAAGACAGAT 3779
DB 316 GCTCTTGACAGCGCTTGTGACGCTTATGAACCTGTGTAAGGTTTCCCGCGCGGCC 375
QY 3780 GGTGTGCTGTACAAATTTTCAAGAGCTTTGTGAGAGATGAAGTCAATTGATCTC 3839
DB 376 GACGACAGCTGGGCGAGGGCCCTGCAAGCCCGGTGAGAGTTGCTTGAGGATTCG 435
QY 3840 TGTGTT-----CAGACTTGAACCCGTTTGAAGTTGAACCAAGACAG 3884
DB 436 AGCGGCTGCTGAGCGCGAGAGAGCCGCTGCGAGAGGAGCGAGCGGAGTGC 495
QY 3885 ACTACTCCCTTCAATCTCTCATGTGAAGCTGGCTGAGAGAGAGCGCTTACAGCTTGT 3944
DB 496 TTGCAGCTGTTCACCTGTGCGAGGGGCCGTTGCTGGGGTCCGCTGATTCGCTGGGC 555
QY 3945 GAAGATGACCAACCTCTCACTATTTGTCATCATCATCTCAATGTTGTTGTCATTT 4004
DB 556 GAGGAGGGGATGTGCTGTGTTGACCTGTGATCATCTGTGTCGAGCGGTGGTCAATG 615
QY 4005 GATGTCTTGGAGCGCATCTCAATCAGCTTCACTCAGCTGGCTCAAGACTCAAAAAG 4064
DB 616 AAGGTGTGATTCAGAAATTCAGTCTTTTACAGTCCCTATGCGATGCGCGAGACCC 675
QY 4065 CCGGTGTGACAGCTCACTCCCTTCACTCACTCACTGAGAGAGCGCTTTGAAATGGCAG 4124
DB 676 GCGCTGCGGCTTGGCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 735
QY 4125 GACCAATTCATAGAGAGAGAGAGCACTCAACTACTGAGAGAGCAACTCAAGACTCT 4184
DB 736 GAGGCGGATGAG 795
QY 4185 TCCCGAGCAAAAGATCCCGAGCTTTGCCGCCCTGCACTTGTCTGAGAGCAGGT 4244
DB 796 CCGGTCTGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 855
QY 4245 TGGGTATCATTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4304
DB 856 CGTTACAGATTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 915
QY 4305 CACAACAGCACTTCTTGTGCTTCTTCTAGCTGCTTCCGTCGCTCAATTCGTCTC 4364
DB 916 CAGGGGCTGAGCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
QY 4365 ACAAGCTGTGAAGAGCTGTCTATTTGTAACCAATTCGAAATGCAACCGAAGCTG 4424
DB 976 AGCGGAG 1035
QY 4425 GAGGATATCATTCGCTGCTTGTTCATATGAGAGATATGAGAAATGAGATCATAC 4484
DB 1036 GAAAGGCTGATCGCTGCTGTCTCAACCAAGGTGCTGCTGCTGCTGCTGCTGCTG 1095
QY 4485 GATACCTTTGGAGCTTGTATCAACCAAGTCAAGGCTGAGAGAGAGAGATTCGAGAC 4544
DB 1096 AGCTGCTGAG 1155
QY 4545 GAGGATATTCGTTTGAAGCGGTTGATCAGCACTACAGCTGAGATCAAGATCTGTCA 4604
DB 1156 CAGATATGCTGCTGAG 1215

QY 4605 AGCAGACCTCTC-----GCACAACTCATTTTTCAGATGCACTCAGAGAGACCTTG 4656
DB 1216 AGCCCGCTGTTCAGAGGATATGTAACCAACAGCCCGCTGTGGCTGAGAGAGCTG 1275
QY 4657 GAAGATTCAGATTCAGAGGCTGTGAGTCCGTACCTGTGCTTACAAAGCTACATCTGAT 4716
DB 1276 GACAGGCTGAGCGCTGAGCTTGTGAGCTTGTGAGCTGAGCTGAGCTGAGCTGAG 1333
QY 4717 TTGACATGAGATTCATCTGTTCAGAAACGACAGCCTTAAAGGTAGGCTCACTTTC 4776
DB 1334 TCGACTGAGCTTGAATCTTACAGAGAGGCGGTGCTGTACGCGCTGACTTACG 1393
QY 4777 CCGATGAGCTGTTCAGAAATGAGAGCTGTTGAATATGCTCAGAGATTCCTTTGAGATTC 4836
DB 1394 GAGACAGCTGTTTGAAGCGCGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1453
QY 4837 TGAAGAGCGGCTTCAAGATTCGCGAGACACAGTCTCAATATCTTCTTTGAGATTC 4896
DB 1454 TGGCGGCTATGTGAGAAACCCGAGGCGAGCTGCACTGCTGCTGCTGCTGCTGCTG 1513
QY 4897 TTGTGACTTGAAGAAATGAGATTTCTCAAGTCAACATGTCATATCCCGAGAT 4956
DB 1514 AGAGGCTATTCAGTTGCTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1573
QY 4957 CGAGCTTGTGATGCTTCTTCCAGAGCCAGTCTCTGCTTACCCGATGCTGAGTGTG 5016
DB 1574 GCGGCTGAG 1633
QY 5017 TGAATCTCTGCTGAGATTCAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5076
DB 1634 CTTTGGCGAG 1693
QY 5077 GATGCTTGTGAG 5136
DB 1694 ATCCCTGATGAG 1753
QY 5137 CATGTGAGCAATTTGTCAGCTTCTTTGTTGTTGAGAGAGAGAGAGAGAGAGAGAG 5196
DB 1754 CATGAGATGATGCTGTGCGCTGATGCGCATCTCAAGAGAGAGAGAGAGAGAGAG 1813
QY 5197 TCGATGAGATGAGCTTCTGCGAGAG 5221
DB 1814 TGAAGCGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1838

RESULT 10
US-09-252-991A-9100
; Sequence 9100, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9100
; LENGTH: 7374
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9100

Query Match 0.9%; Score 95.4; DB 4; Length 7374;
Best Local Similarity 44.2%; Pred. No. 1.2e-17;
Matches 445; Conservative 0; Mismatches 556; Indels 6; Gaps 1;

QY 3581 TCATGAGGAGCTGTGAGAGCTTATTCAGAGAGCGGACTATGTTCTGTGATCAGTT 3640

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7057
LENGTH: 4236
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7057

Query Match 0.7%; Score 82.8; DB 4; Length 4236;
Best Local Similarity 45.0%; Pred. No. 6.4e-14;
Matches 309; Conservative 0; Mismatches 377; Indels 0; Gaps 0;
QY 3891 CCCTTCATCTCATCTGAAAGCTGGCTGAGAGCGACGCTTACGACTTGTGTAAGAT 3950
DB 2433 CCGTTGACCTGGAAAAGGGCGCGCTGCGGGTCACTGGTGGCGCTGAGAACAG 2374
QY 3951 GACCACTCTCTCACTATGTCATGATCATCATCTCAATGATGTTGTCATTTGATGTC 4010
DB 2373 GACCACTCTCTGAGTCACTGATCATCATCTGATGATGTTGTCATTTGATGTC 2314
QY 4011 TTGCGACGCGATCTCAATCACTGCTCTACTGAGCTGCGCTCAAGACTCAAAAAGCCGCTG 4070
DB 2313 CTCTGACGACATTTCTGCGCGCTCTACGCGAAGCTCTGCGCGCGCGAGCCGCGACTG 2254
QY 4071 TCAGCACTCACTCTCTACTTACCTATTCAGTACGCGACTTTGCAAAATGGCAGAAAGCA 4130
DB 2253 GCGCGCTGGAATGTCAGTACGCGAGTTGCTGCTGCGAGACGCGAGTGGTGGAGCGG 2194
QY 4131 TTCATAGACAGAGAGAACTCACTCACTGAGAAAGCACTCAAAAGACTCTTCCCA 4190
DB 2193 GCGAGAGGCGCGCGCAACTGAGCTGAGCGGAAAGCTGAGCGAGCAAGCGCGCGGTG 2134
QY 4191 GCAAAATCCCGACCGACTTGGCCGCGCTGCACTTCTGTGTGAGAGCGAGTTGGTGA 4250
DB 2133 CTGGAATGCGCACCGACCACTCGCGAGCGCGCGCGCGCGCGCGCGCTGAC 2074
QY 4251 CATGTTACATCGACGCGAGCTCTACCACTCCCTTTCAGACCTTTCGACAAACAAC 4310
DB 2073 AGCTCGGGGTGACCAAGAGCTGCGCGCGGCTATCCGCGAGCGCGCGCTGAGACGAG 2014
QY 4311 AGCACTCTTTCGCTCTTCTTCTGAGCTGCGCTGCGCGCTCATTAATGCTTACAGCT 4370
DB 2013 GCGAGTGTCTTCACTGAGCTGCTGCGCGCTTCCAGGCGCTGCTGACGCGACAGCGG 1954
QY 4371 GTTGAAGACGCTCTATGTTGTACCACTTGGCAATGGCAACCGACTGAACTGGAGAT 4430
DB 1953 CAGGCGAGATCCGCACTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1894
QY 4431 ATCATCGGCTCTTTCATTAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 4490
DB 1893 CTGCTGCGCTCTTCACTCAACCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1834
QY 4491 TTTGGGACTTTGATCAACCAAGTCAAGGCTTCAAGCAAGCAAGCAAGCAAGCAAG 4550
DB 1833 TTGCGCGCATTTCTGCGCGAGGCTGCGAGGCGAGCCTCGCGCGCGCGCGCGCGAG 1774
QY 4551 ATTCCGTTGAGCGCGCTTGTATCAGC 4576
DB 1773 CTGCGCTTCAAGCAAGGCTGCTGCGCGC 1748

RESULT 13
US-09-252-991A-9098
Sequence 9098, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9098
LENGTH: 792
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9098

Query Match 0.7%; Score 80.2; DB 4; Length 792;
Best Local Similarity 47.4%; Pred. No. 1.1e-13;
Matches 306; Conservative 0; Mismatches 333; Indels 6; Gaps 2;
QY 3953 CCACATCTCACTATGTCATGATGATCATCATCATCATCATCATCATCATCATCATCAT 4012
DB 1 CCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 4013 GCGACGCACTCTCAATCACTGCTCTACTGAGCTGCGCTCAAGACTCAAAAAGCCGCTGTC 4072
DB 61 GCTGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 4073 AGCACTACTCTCTCACTATGATGATGATGATGATGATGATGATGATGATGATGATG 4132
DB 121 GCGCGCTG---CCGATACAGATCCGAGCTATGCGCTGCGAGCGCAAGATGATGAGGC 177
QY 4133 CATAGACAGAGAAAGCACTCACTATGAGAAAGAAAGCACTCAAAAGCTCTTCCAG- 4191
DB 178 CGAGAGAGAGAGCGCGCACTGAGTGGCTGATGAGTGGCTGAGTGGCTGAGTGGCTGAG 237
QY 4192 --CAAGATCCGACGCACTTTCGCGCGCTGCACTTCTGTGTGAGAGCGAGTTGGCT 4249
DB 238 GCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297
QY 4250 ACATGTTACATGACGCGAGCTCTACCACTGCTTTCAGACCTTTCGACAAACAACA 4309
DB 298 GAGATTCGAACCTGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357
QY 4310 CAGGACTCTTTCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4369
DB 358 TGGAGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 4370 TGTGAAGACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4429
DB 418 TCAGCGGATATCCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 477
QY 4430 TATCATCGCTCTTTCATTAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 4489
DB 478 ACTGATCGGCTTCTTCTGTAACACCGAGTGTCAAGCGCGCATGATGAGTATGAGT 537
QY 4490 CTTTGGGACTTTGATCAACCAAGTCAAGGCTTCAAGCAAGCAAGCAAGCAAGCAAG 4549
DB 538 GTTCGACCGATTTCTCAACCAAGTTCAGCAAGCTGCTGCTGAGGCGCGAGCGAGCA 597
QY 4550 TATTCGTTTGAAGCGGCTTATCAGACATCAAGCTGATTCAG 4594
DB 598 CTGCGCTTCAAGCACTGATGAGAGCTTTCAGAACCGAGCGAG 642

RESULT 14
US-08-510-646B-17
Sequence 17, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Veronique
APPLICANT: Crouzet, Joel

APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved in The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS: 45
ADDRESSEE: Fimegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION DATA:
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S. virginiae
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2219
OTHER INFORMATION: /product = "virginiamycin s synthase gene"
US-08-510-646B-17
Query Match 0.7%; Score 79.4; DB 3; Length 2219;
Best Local Similarity 43.3%; Pred. No. 4.3e-13;
Matches 764; Conservative 0; Mismatches 961; Indels 38; Gaps 7;
QY 3470 CGTTGGATGAGACTCAAGGCTCTTAACATCTACAGACCGGAGGCTGGGGAATTC 3529
Db 14 CTTGGGAGCGGAGATCGGGGCTCGTACCTGTTGAGGACCCACCGTCGAGCCCTTGC 73
QY 3530 CGCGGTGCTGAAGGATGATCTCTGTCTCACTCTCATCCCAAGTCAACTCATGAGG 3589
Db 74 CGAAACCTCGAAGAGGCGCGGAGGTCGCGCCCGCTGCGCGCCGCGACCGCCCGA 133
QY 3590 ACCTGTGAGCAGTCTTATTCAAGGCCGACGTATGTTCTTGATCAGTTGACGTTGG 3649

Db 134 ACAGTCCGCTGTCCTTGCCCGGCGGCGCTGTGTTCTTCGACCGCTGGAAGACC 193
QY 3650 CAGTCTGTGATCTGATTCATATGCTTGGAATGCGGCGGCTGTCAATGTCAAGC 3709
Db 194 CAACTCAGCTTAACAATCCCGCTCCGCTCCGCTCGCGGGGAGCTGACCGACCGGC 253
QY 3710 GTTACGTGGGCTCTTTCGACGCGCTTGAAACGACACAGACTCTTGAAGCATTTGA 3769
Db 254 GTTGCAACAGGCGCTCAACGACCTGACGACCGCCGCAAGAGCTCGGCGCTCAACC 313
QY 3770 AGACAGATGATGTGGGTATCAATTTGTACAGAAAGCTTTGAGGATGAAGT 3829
Db 314 GAGCGCGGACGCGCGGCTTACGACAGCTCTTCGACCGCAGAGCCGAGCCGCT 373
QY 3830 CATTGATCTCTGTGTTAGACCTTGACCCGTTGAGTGTGAACCAAGACGACTAC 3889
Db 374 GTGTGTGTCGCGCGGACGAGAGCGGAGCTCGCGGAGATGTCTGGCGAGCGCGCGCA 433
QY 3890 TCCCTTCATCTCTCATCTGAGCTGAGAGGAGCGCTCTTACAGCTTGATGA 3949
Db 434 CGAGTTCAGTCACTCCGACCGCGCGCTGCGGCTCTCTGTTCACTTCGACCGGA 493
QY 3950 TGAACATGCTCACTATTGTCAATGATCAATCATCTCAGATGTTGTGATTAATG 4009
Db 494 CGAGCAGCTCTCTCTCTGCTGCTGACACATGCGCGGAGCGCTGTGCTCGACC 553
QY 4010 CTTCGACGCGATCTCAATGAGCTTCACTGAGCTGCGCTCAAGACTCAAGACCGCT 4069
Db 554 ACTCAGCGGAGCTCAACCGCGGCTTACACCGCGCGGAGAGGCGCGCGCGCGCTG 613
QY 4070 GTACAGCTCACTCTCTTACCTTATCCAGTACAGC-----GACTTTCGAAATG 4117
Db 614 GGAAGCCCTCCGCTCAGTACGCGGACGCTACACCTCTGCGACAGAGATGCTCGCTC 673
QY 4118 GCAGAGGACCAATTTATAGAGAGAGAGAGCACTCACTACTGGAAGCACTCA 4177
Db 674 GCGGAGAGCTCCGAGAGCTCGCGCGCGCGGACGCTGACACCTGCGCGCTGCTG 733
QY 4178 AGACTCTTCC---CGAACAAGATCCGACCGACTTTCGCGCGCTGCACTTGTCTGG 4234
Db 734 CGCGGCGCGGAGCACTGGAATGCGCCACCGACCAACCGCGCGCGCGCGCGCA 793
QY 4235 AGACGAGTGGTGGTACATTTACATCGACGCGGAGCTTACAGTCTCTTGAGCTT 4294
Db 794 CCAAGCGCGGACCGCTCCCTTCCACTGAGCGCGGAGCTGACAGAGCGGCTCAGCGCT 853
QY 4295 CTGCAAGAACACAAACAGACGCTTTTCGCTTCTTCTAGCGCGCTCCGCGCTCA 4354
Db 854 GGCAGGCTCTGAGAGCGCGGCTGTTCATGTCTGACGCGCGCTGCTGCTGCT 913
QY 4355 TTATGCTCTCAGCTGTGGAAGAGCGCTGCTCATTTGTATCAACCAATTGCGAATGCA 4414
Db 914 CACCAAGCAGGATGCGCGGACGCAACATCCGATCGGAGCGCGCGCGCGCA 973
QY 4415 ACCTGAACCTGAGAGATATATGCGCTGCTTGTCAATACGAGTATGGAATCAACAT 4474
Db 974 CGAGGCGCTGAGAGATGCTGCGGTTCTTCGTCACACCTGCTGCTGCGACGAC 1033
QY 4475 AGATCATCAGATACCTTTGGGACTTTGATCAACCAAGTCAAGGCTTACGACGAGC 4534
Db 1034 CTCGCGGATCGACCTTCCGCAACTGTTGACGACCGCGCGCACTGCGCGC 1093
QY 4535 ATTGGAAGAGAGATATTCGTTTGAAGCGCTGTATACGACTACAGCTGATTCAG 4594
Db 1094 ATACGACACCAAGACCTGCTTCGAGAGAGCTGT-----GAGAGCTTCAACCGC 1146
QY 4595 AGATCTGTCAAGCACTCTCGCAACTCATTTTTCAGTCACTACAGAAAGACT 4654
Db 1147 AGCGTGTGCTGCGCGGACCGCTGTTCAGAGTACGTGCGCTTTCAGAGAGATGCCA 1206
QY 4655 TGAAGA-TTCAAGTTCAAGGCTGAGATCGCTTACTGTGC---TAGCAAGCGTACA 4710
Db 1207 CGGACAGCGCGCTGCTGCGCGCTGAGCTGTCAAGAGCGGCTCGCTGAGATTCG 1266

QY 4711 CTCGATTGACATGAGTTCCATCTGTTTCAAGAAACGACGCTTAAAGTAGCGTCA 4770
DB 1267 CCAAGTTGACCGCGCCCTGGCCGCGAGAAAGGACCGCGACGCGCGCGGTCCG 1326
QY 4771 ACTTTCGCGATGAGCTGTTTCAAAATGAGACCTGTTGAAAATGTCGACGATTTCTTG 4830
DB 1327 TGGCGCGCACTGGGAGTTTCAAGACCGACCTGTTTCAAGGAGGACCGTGGAGGCTTCG 1386
QY 4831 AGATTCGAGAAACGGGCTTCAAAAGTTGCGGACACCAAGTCTCAATATTCTTTGA--- 4887
DB 1387 GGGCCAGGCTCAACCGCTCTGCTGCGCTGCTCGCCGCGACCGCCGACCGCATCGGAC 1446
QY 4888 CTGATGCGATTTGATCTTTGAAAATTTGATGTTTCAACGTCACCAATGTCGACTATC 4947
DB 1447 GGGTGGGCACTCTGACACCGCGCGAAGCCACCGCATCTCTCAACCTGGAAGACACT 1506
QY 4948 CCGC-----AGATGAGCTTGGCTGATGTTCTTCCAGACCCAAAGTCTGCTTACC 4998
DB 1507 CCGCGCCCGCGCGGACGCGACCTGCGCGGAGCTGTTCCAGGCGCGCGCGCGAGCAC 1566
QY 4999 CCGATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5058
DB 1567 CCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1626
QY 5059 AGTCTGATATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5118
DB 1627 GGGCCCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686
QY 5119 CAGTATTTGCCCCGAGTCATGTGAGCAATTTGCGGTTCTTTGTTGTGAGGCGA 5178
DB 1687 CCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746
QY 5179 ACTTGGCTTATCTTCTCTCGAT 5201
DB 1747 GCGCGCTTACCTGCGCTGAT 1769

RESULT 15

US-08-861-774E-17/C
; Sequence 17, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Clone ps32
US-08-861-774E-17

Query Match 0.7%; Score 74.8; DB 3; Length 1172;
Best Local Similarity 54.1%; Pred. No. 6.8e-12;
Matches 198; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

QY 5917 CAATTGACAGCTGACCACTGAGAGCGTATGCTGATCTGACCAAGCTTG 5976
DB 688 CGATCGCGCTCGCTGACCAAGCTTCAAGTCTGATGAGGCACTGAGCCG 629
QY 5977 TTGGCAATGGTGTGATGAGAGAGCTTGTGTCACTGGCGATGGTCTTGGCGGCGCTA-- 6034
DB 628 TTCCGCGCGGCTGATCGGAGACTGTACATCGTGGCGAGAACTTGGCGGCTATG 569

QY 6035 -CAGTGACAAAGCCCTTGAAGAGACCGTTTGTGACATTTACTGTCAATGACGACAG 6093
DB 568 TCATGATGCGCGCTTCAACCGAGCGCGGTTGTATCCGATTCATTCGGTGACCTGGCT 509
QY 6094 TGAAGCGTATCGCACTGGCGATGAGTGGGTACAGATTGAGATTGAGTGGCTTATGACT 6153
DB 508 CGCGCTGTACCGGACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
QY 6154 TCTTGGAGGTATGACACCCAGTTCAAGATTGCTGCAATGCTATGCAATGAGTGA 6213
DB 451 TCATCGGCGCGGATCATCAGTCAAGATCCGCGCTTCCGATCGAGCTGGTGAGA 392
QY 6214 TTGAAGCGGCTTCTGCGGACTCTCCGTCGAGATGCTGTGCTTCAAGAGA 6273
DB 391 TGAAGCGGCGCTGGCGATACCCCGGTGTGAGACGCGCTGCTGCTGCTGCTGCTGCTG 332
QY 6274 ATGAGG 6279
DB 331 AGCGGG 326

Search completed: November 5, 2004, 19:12:46
Job time: 803 secs

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